



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/12, C07K 14/47, A61K 38/17, C12N 5/10, C12Q 1/68	A2	(11) International Publication Number: WO 98/45435 (43) International Publication Date: 15 October 1998 (15.10.98)
(21) International Application Number: PCT/US98/06954 (22) International Filing Date: 10 April 1998 (10.04.98) (30) Priority Data: 08/835,913 10 April 1997 (10.04.97) US (71) Applicant: GENETICS INSTITUTE, INC. [US/US]; 87 CambridgePark Drive, Cambridge, MA 02140 (US). (72) Inventors: JACOBS, Kenneth; 151 Beaumont Avenue, Newton, MA 02160 (US). MCCOY, John, M.; 56 Howard Street, Reading, MA 01867 (US). LAVALLIE, Edward, R.; 113 Ann Lee Road, Harvard, MA 01451 (US). RACIE, Lisa, A.; 124 School Street, Acton, MA 01720 (US). MERBERG, David; 2 Orchard Drive, Acton, MA 01720 (US). TREACY, Maurice; 93 Walcott Road, Chestnut Hill, MA 02167 (US). SPAULDING, Vikki; 11 Meadowbank Road, Billerica, MA 01821 (US). AGOSTINO, Michael, J.; 26 Wolcott Avenue, Andover, MA 01810 (US). (74) Agent: SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US).		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). Published. <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: SECRETED EXPRESSED SEQUENCE TAGS (sESTs)		
(57) Abstract Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.		

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece			TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	NZ	New Zealand		
CM	Cameroon			PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakhstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

SECRETED EXPRESSED SEQUENCE TAGS (sESTs)

FIELD OF THE INVENTION

5 The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

BACKGROUND OF THE INVENTION

10 Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed *in vivo*, and (2) that efforts to sequence genes and other portions of the genome of target organisms which are not actually expressed wastes substantial effort on areas not likely
15 to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they were transcribed.

20 Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect. Since the EST approach theoretically identifies all expressed proteins, it produces an EST
25 library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators searching for secreted proteins because they must separate the secreted "wheat" from the non-
30 secreted "chaff", wasting effort and resources in the process.

35

40

Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent discloses a "signal sequence trap" which selectively identifies ESTs for secreted proteins,
5 namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

SUMMARY OF THE INVENTION

The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide
5 comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ
ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID
NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ
ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ
10 ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ
ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ
ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ
ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ
ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ
15 ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ
ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ
ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ
ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ
ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ
20 ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ
ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ
ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ
ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ
ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ
25 ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100,
SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID
NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109,
SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID
NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118,
30 SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,
SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,
SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID

NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145,
SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID
NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID
5 NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
10 SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID
NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190,
SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID
NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID
15 NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
20 SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,
SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID
NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244,
SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID
25 NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253,
SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID
NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262,
SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID
NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271,
30 SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID
NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280,
SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID
NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289,
SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID

NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298,
SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID
NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307,
SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID
5 NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316,
SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID
NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325,
SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID
NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334,
10 SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID
NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343,
SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID
NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352,
SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID
15 NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361,
SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID
NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370,
SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID
NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379,
20 SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID
NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388,
SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID
NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397,
SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID
25 NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406,
SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID
NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415,
SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID
NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424,
30 SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID
NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433,
SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID
NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442,
SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID

NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451,
SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID
NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460,
SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID
5 NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469,
SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID
NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478,
SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID
NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487,
10 SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID
NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496,
SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID
NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505,
SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID
15 NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514,
SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID
NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523,
SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID
NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532,
20 SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID
NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541,
SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID
NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550,
SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID
25 NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559,
SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID
NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568,
SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID
NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577,
30 SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID
NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586,
SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID
NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595,
SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID

NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604,
SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID
NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613,
SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID
5 NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622,
SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID
NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631,
SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID
NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640,
10 SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID
NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649,
SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID
NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658,
SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID
15 NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667,
SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID
NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676,
SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID
NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685,
20 SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID
NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694,
SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID
NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703,
SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID
25 NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712,
SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID
NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721,
SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID
NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730,
30 SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID
NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739,
SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID
NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748,
SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID

NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757,
SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID
NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766,
SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID
5 NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775,
SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID
NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784,
SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID
NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793,
10 SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID
NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802,
SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID
NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811,
SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID
15 NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820,
SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID
NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829,
SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID
NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838,
20 SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID
NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847,
SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID
NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856,
SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID
25 NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865,
SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID
NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874,
SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID
NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883,
30 SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID
NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892,
SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID
NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901,
SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID

NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910,
SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID
NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919,
SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID
5 NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928,
SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID
NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937,
SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID
NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946,
10 SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID
NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955,
SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID
NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964,
SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID
15 NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973,
SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID
NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982,
SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID
NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991,
20 SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID
NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000,
SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ
ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID
NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID
25 NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID
NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID
NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID
NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID
NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID
30 NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID
NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID
NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID
NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID
NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID

NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID
NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID
NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID
NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID
5 NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID
NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID
NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID
NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID
NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID
10 NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID
NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID
NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID
NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID
NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID
15 NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID
NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID
NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID
NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID
NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID
20 NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID
NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID
NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID
NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID
NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID
25 NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID
NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID
NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID
NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID
NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID
30 NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID
NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID
NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID
NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID
NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID

5 NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID
NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID
NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID
NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID
NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID
NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID
NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID
NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID
10 NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID
NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID
NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID
NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID
NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID
NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID
15 NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID
NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID
NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID
NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID
NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID
20 NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID
NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID
NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID
NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID
NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID
25 NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID
NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID
NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID
NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID
NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID
30 NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID
NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID
NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID
NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID
NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID

NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID
NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID
NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID
NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID
5 NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID
NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID
NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID
NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID
NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID
10 NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID
NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEQ ID
NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID
NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID
NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID
15 NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID
NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID
NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID
NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID
NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID
20 NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID
NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID
NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID
NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID
NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID
25 NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID
NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID
NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEQ ID
NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEQ ID
NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID
30 NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID
NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID
NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID
NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID
NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID

NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID
 NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID
 NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID
 NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID
 NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID
 NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID
 NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID
 NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID
 NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID
 NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;

or a complement of said sequence.

In other embodiments, the present invention provides an isolated polynucleotide
 consisting of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ
 ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID
 NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ
 ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ
 ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ
 ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ
 ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ
 ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ
 ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ
 ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ
 ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ
 ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ
 ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ
 ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ
 ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ
 ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ
 ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ
 ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ
 ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ
 ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100,
 SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID

NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109,
SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID
NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118,
SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID
5 NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,
SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,
SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID
NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145,
10 SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID
NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID
NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
15 NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID
NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190,
20 SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID
NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
25 NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,
30 SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID
NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244,
SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID
NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253,
SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID

NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262,
SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID
NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271,
SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID
5 NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280,
SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID
NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289,
SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID
NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298,
10 SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID
NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307,
SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID
NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316,
SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID
15 NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325,
SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID
NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334,
SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID
NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343,
20 SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID
NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352,
SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID
NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361,
SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID
25 NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370,
SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID
NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379,
SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID
NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388,
30 SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID
NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397,
SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID
NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406,
SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID

NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415,
SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID
NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424,
SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID
5 NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433,
SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID
NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442,
SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID
NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451,
10 SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID
NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460,
SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID
NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469,
SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID
15 NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478,
SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID
NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487,
SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID
NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496,
20 SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID
NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505,
SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID
NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514,
SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID
25 NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523,
SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID
NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532,
SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID
NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541,
30 SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID
NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550,
SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID
NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559,
SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID

NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568,
SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID
NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577,
SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID
5 NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586,
SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID
NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595,
SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID
NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604,
10 SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID
NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613,
SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID
NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622,
SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID
15 NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631,
SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID
NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640,
SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID
NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649,
20 SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID
NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658,
SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID
NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667,
SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID
25 NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676,
SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID
NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685,
SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID
NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694,
30 SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID
NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703,
SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID
NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712,
SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID

NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721,
SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID
NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730,
SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID
5 NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739,
SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID
NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748,
SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID
NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757,
10 SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID
NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766,
SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID
NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775,
SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID
15 NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784,
SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID
NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793,
SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID
NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802,
20 SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID
NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811,
SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID
NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820,
SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID
25 NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829,
SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID
NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838,
SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID
NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847,
30 SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID
NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856,
SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID
NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865,
SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID

NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874,
SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID
NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883,
SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID
5 NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892,
SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID
NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901,
SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID
NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910,
10 SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID
NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919,
SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID
NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928,
SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID
15 NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937,
SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID
NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946,
SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID
NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955,
20 SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID
NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964,
SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID
NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973,
SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID
25 NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982,
SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID
NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991,
SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID
NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000,
30 SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ
ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID
NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID
NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID
NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID

NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID
NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID
NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID
NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID
5 NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID
NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID
NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID
NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID
NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID
10 NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID
NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID
NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID
NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID
NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID
15 NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID
NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID
NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID
NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID
NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID
20 NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID
NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID
NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID
NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID
NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID
25 NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID
NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID
NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID
NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID
NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID
30 NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID
NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID
NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID
NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID
NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID

NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID
NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID
NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID
NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID
5 NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID
NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID
NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID
NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID
NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID
10 NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID
NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID
NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID
NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID
NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID
15 NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID
NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID
NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID
NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID
NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID
20 NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID
NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID
NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID
NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID
NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID
25 NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID
NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID
NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID
NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID
NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID
30 NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID
NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID
NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID
NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID
NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID

NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID
NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID
NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID
NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID
5 NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID
NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID
NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID
NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID
NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID
10 NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID
NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID
NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID
NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID
NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID
15 NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID
NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID
NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID
NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID
NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEQ ID
20 NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID
NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID
NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID
NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID
NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID
25 NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID
NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID
NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID
NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID
NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID
30 NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID
NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID
NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID
NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID
NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID

5 NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEQ
NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEQ I
NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ I
NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ II
NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID
NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID
NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID
NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID
10 NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID
NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID
NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID
NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID
NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID
15 NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID
NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID
NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID
NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID
NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;
or a complement of said sequence.

20 In further embodiments, the present invention provides an isolated polynucleotide
consisting essentially of a nucleotide sequence selected from the group consisting of:

25 SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ
ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID
NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ
ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ
ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ
ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ
ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ
ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ
ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ
ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ
ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ
ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ
30 ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ

5 ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ
ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ
ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ
ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ
ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ
ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ
ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100,
SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID
NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109,
10 SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID
NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118,
SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,
SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
15 NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,
SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID
NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145,
SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID
NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
20 SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID
NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
25 NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID
NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190,
SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID
NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
30 SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID

NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,
SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID
5 NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244,
SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID
NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253,
SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID
10 NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262,
SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID
NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271,
SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID
NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280,
15 SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID
NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289,
SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID
NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298,
SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID
20 NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307,
SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID
NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316,
SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID
NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325,
25 SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID
NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334,
SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID
NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343,
SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID
30 NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352,
SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID
NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361,
SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID
NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370,
SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID

5 NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379,
SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID
NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388,
SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID
NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397,
SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID
NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406,
SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID
10 NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415,
SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID
NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424,
SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID
NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433,
SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID
15 NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442,
SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID
NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451,
SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID
NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460,
20 SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID
NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469,
SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID
NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478,
SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID
25 NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487,
SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID
NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496,
SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID
NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505,
30 SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID
NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514,
SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID
NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523,
SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID

5 NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532,
SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID
NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541,
SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID
NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550,
SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID
NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559,
SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID
10 NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568,
SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID
NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577,
SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID
NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586,
15 SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID
NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595,
SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID
NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604,
SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID
20 NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613,
SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID
NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622,
SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID
NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631,
25 SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID
NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640,
SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID
NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649,
SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID
30 NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658,
SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID
NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667,
SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID
NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676,
SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID

5 NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685,
SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID
NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694,
SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID
NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703,
10 SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID
NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712,
SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID
NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721,
SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID
NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730,
15 SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID
NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739,
SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID
NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748,
SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID
NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757,
SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID
20 NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766,
SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ
NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775,
SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID
NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784,
25 SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID
NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793,
SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID
NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802,
SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID
30 NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811,
SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID
NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820,
SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID
NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829,
SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID

5 NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838,
SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID
NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847,
SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID
NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856,
SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID
NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865,
SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID
10 NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874,
SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID
NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883,
SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID
NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892,
SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID
15 NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901,
SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID
NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910,
SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID
NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919,
20 SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID
NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928,
SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID
NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937,
SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID
25 NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946,
SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID
NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955,
SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID
NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964,
30 SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID
NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973,
SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID
NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982,
SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID

NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991,
SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID
NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000,
SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ
ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID
NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID
NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID
NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID
NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID
NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID
NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID
NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID
NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID
NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID
NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID
NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID
NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID
NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID
NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID
NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID
NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID
NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID
NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID
NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID
NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID
NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID
NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID
NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID
NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID
NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID
NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID
NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID
NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID
NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID

NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID
NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID
NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID
NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID
5 NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID
NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID
NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID
NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID
NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID
10 NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID
NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID
NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID
NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID
NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID
15 NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID
NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID
NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID
NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID
NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID
20 NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID
NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID
NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID
NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID
NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID
25 NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID
NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID
NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID
NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID
NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID
30 NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID
NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID
NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID
NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID
NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID

NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID
NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID
NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID
NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID
5 NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID
NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID
NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID
NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID
NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID
10 NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID
NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID
NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID
NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID
NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID
15 NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID
NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID
NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID
NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID
NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID
20 NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID
NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID
NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID
NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID
NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID
25 NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID
NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID
NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEQ ID
NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID
NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID
30 NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID
NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID
NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID
NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID
NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID

NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID
 NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID
 NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID
 NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID
 5 NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID
 NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID
 NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID
 NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID
 NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEQ ID
 10 NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEQ ID
 NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID
 NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID
 NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID
 NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID
 15 NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID
 NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID
 NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID
 NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID
 NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID
 20 NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID
 NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID
 NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID
 NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID
 NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID
 25 NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID
 NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;

or a complement of said sequence.

In yet other embodiments, the present invention provides an isolated polynucleotide
 comprising a nucleotide sequence which hybridizes to a sequence selected from the group
 30 consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ
 ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID
 NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ
 ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ

5 ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ
ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ
ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ
ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ
ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ
ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ
ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ
ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ
10 ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ
ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ
ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ
ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ
ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ
ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ
15 ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ
ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100,
SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID
NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109,
SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID
20 NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118,
SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,
SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,
25 SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID
NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145,
SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID
NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID
30 NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,

SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID
NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190,
SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID
NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
5 SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID
NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
10 NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,
SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID
NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244,
15 SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID
NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253,
SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID
NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262,
SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID
20 NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271,
SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID
NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280,
SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID
NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289,
25 SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID
NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298,
SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID
NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307,
SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID
30 NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316,
SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID
NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325,
SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID
NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334,

SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID
NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343,
SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID
NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352,
5 SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID
NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361,
SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID
NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370,
SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID
10 NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379,
SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID
NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388,
SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID
NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397,
15 SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID
NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406,
SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID
NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415,
SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID
20 NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424,
SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID
NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433,
SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID
NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442,
25 SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID
NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451,
SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID
NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460,
SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID
30 NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469,
SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID
NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478,
SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID
NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487,

SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID
NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496,
SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID
5 SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505,
SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID
NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514,
SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID
NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523,
10 SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID
NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532,
SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID
NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541,
SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID
NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550,
15 SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID
NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559,
SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID
NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568,
SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID
20 NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577,
SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID
NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586,
SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID
NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595,
25 SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID
NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604,
SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID
NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613,
SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID
30 NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622,
SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID
NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631,
SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID
NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640,

SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID
NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649,
SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID
NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658,
5 SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID
NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667,
SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID
NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676,
SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID
10 NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685,
SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID
NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694,
SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID
NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703,
15 SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID
NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712,
SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID
NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721,
SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID
20 NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730,
SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID
NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739,
SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID
NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748,
25 SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID
NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757,
SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID
NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766,
SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID
30 NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775,
SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID
NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784,
SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID
NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793,

SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID
NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802,
SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID
NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811,
5 SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID
NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820,
SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID
NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829,
SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID
10 NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838,
SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID
NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847,
SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID
NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856,
15 SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID
NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865,
SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID
NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874,
SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID
20 NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883,
SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID
NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892,
SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID
NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901,
25 SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID
NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910,
SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID
NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919,
SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID
30 NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928,
SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID
NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937,
SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID
NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946,

SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID
NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955,
SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID
NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964,
5 SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID
NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973,
SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID
NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982,
SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID
10 NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991,
SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID
NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000,
SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ
ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID
15 NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID
NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID
NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID
NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID
NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID
20 NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID
NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID
NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID
NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID
NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID
25 NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID
NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID
NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID
NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID
NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID
30 NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID
NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID
NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID
NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID
NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID

NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID
NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID
NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID
NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID
5 NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID
NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID
NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID
NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID
NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID
10 NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID
NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID
NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID
NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID
NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID
15 NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID
NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID
NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID
NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID
NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID
20 NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID
NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID
NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID
NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID
NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID
25 NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID
NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID
NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID
NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID
NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID
30 NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID
NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID
NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID
NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID
NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID

NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID
NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID
NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID
NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID
5 NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID
NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID
NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID
NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID
NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID
10 NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID
NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID
NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID
NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID
NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID
15 NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID
NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID
NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID
NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID
NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID
20 NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID
NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID
NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID
NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID
NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID
25 NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID
NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID
NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID
NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID
NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID
30 NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID
NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID
NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID
NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID
NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID

NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID
NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEQ ID
NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID
NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID
5 NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID
NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID
NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID
NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID
NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID
10 NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID
NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID
NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID
NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID
NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID
15 NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID
NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID
NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID
NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEQ ID
NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEQ ID
20 NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID
NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID
NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID
NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID
NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID
25 NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID
NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID
NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID
NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID
NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID
30 NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID
NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID
NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID
NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID

NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;

or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described
5 polynucleotides.

DETAILED DESCRIPTION

The nucleotide sequences of the sESTs of the present invention are reported in the Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each
10 SEQ ID NO: in the Sequence Listing.

Table 2

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.) followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

15	1	B11	21	C3	41	C639	61	D148
	2	B18	22	C32	42	C641	62	D154
	3	B21	23	C141	43	C642	63	D167
	4	B26	24	C143	44	C645	64	D179
	5	B40	25	C180	45	D4	65	D188
20	6	B115	26	C195	46	D7	66	D196
	7	B121	27	C293	47	D14	67	D200
	8	B124	28	C312	48	D15	68	D203
	9	B125	29	C539	49	D27	69	D233
	10	B142	30	C544	50	D68	70	D252
25	11	B196	31	C547	51	D69	71	D286
	12	B208	32	C571	52	D81	72	D303
	13	B224	33	C604	53	D100	73	D304
	14	B227	34	C607	54	D101	74	D305
	15	B232	35	C608	55	D104	75	D310
30	16	B236	36	C610	56	D105	76	D311
	17	B238	37	C617	57	D115	77	D318
	18	B255	38	C626	58	D121	78	D327
	19	C1	39	C627	59	D133	79	D329
	20	C2	40	C636	60	D143	80	E1

	81	E4	115	H291	149	J139	183	M141
	82	E5	116	H306	150	J143	184	M152
	83	E11	117	H383	151	J156	185	M194
	84	E12	118	H426	152	J168	186	M230
5	85	E14	119	H438	153	J297	187	M273
	86	E18	120	H541	154	J317	188	M292
	87	G1	121	H545	155	J322	189	M301
	88	G12	122	H657	156	J422	190	M313
	89	G16	123	H698	157	J435	191	M328
10	90	G20	124	H758	158	J509	192	M338
	91	G21	125	H770	159	J512	193	O7
	92	G26	126	H849	160	J532	194	O47
	93	G31	127	H920	161	J546	195	O67
	94	G40	128	H978	162	J598	196	O75
15	95	G46	129	H999	163	J635	197	O99
	96	G53	130	H1004	164	J638	198	O135
	97	G55	131	H1010	165	J708	199	O139
	98	G58	132	H1045	166	J731	200	O268
	99	G68	133	H1052	167	M4	201	O276
20	100	G85	134	H1075	168	M6	202	O289
	101	G86	135	H1096	169	M43	203	O338
	102	G99	136	H1116	170	M60	204	O349
	103	G103	137	H1165	171	M68	205	O351
	104	G107	138	H1301	172	M71	206	O372
25	105	G108	139	H1408	173	M88	207	O386
	106	G112	140	H1413	174	M97	208	O417
	107	G114	141	H1456	175	M100	209	O418
	108	H45	142	I5	176	M114	210	O463
	109	H162	143	I28	177	M120	211	S10
30	110	H165	144	I32	178	M121	212	S34
	111	H171	145	J5	179	M125	213	S70
	112	H174	146	J54	180	M126	214	S169
	113	H225	147	J66	181	M128	215	S185
	114	H236	148	J135	182	M137	216	S195

	217	AA20	251	AJ6	285	AM72	319	AP137
	218	AA35	252	AJ8	286	AM93	320	AP76
	219	AB10	253	AJ52	287	AK679	321	AP87
	220	AA240	254	AJ53	288	AK684	322	AP90
5	221	AA244	255	AJ54	289	AK699	323	AP150
	222	AA246	256	AJ78	290	AM155	324	AP159
	223	AA287	257	AJ80	291	AM167	325	AP160
	224	AA299	258	AK368	292	AM207	326	AP162
	225	AA318	259	AJ127	293	AM217	327	AP168
10	226	AB45	260	AJ142	294	AM224	328	AP179
	227	AA36	261	AJ143	295	AM226	329	AP197
	228	AA363	262	AC339	296	AM235	330	AP215
	229	AA365	263	AC370	297	AM259	331	AP224
	230	AA351	264	AL14	298	AM266	332	AP226
15	231	AB290	265	AK401	299	AM267	333	AP242
	232	AC41	266	AK438	300	AM277	334	AP250
	233	AC18	267	AK583	301	AM279	335	AQ11
	234	AC175	268	AK585	302	AC387	336	AQ2
	235	AC114	269	AK598	303	AC395	337	AQ21
20	236	AC111	270	AK604	304	AC410	338	AQ23
	237	AC100	271	AK609	305	AC412	339	AQ3
	238	AC222	272	AK620	306	AC423	340	AQ34
	239	AC325	273	AM10	307	AJ146	341	AQ5
	240	AI44	274	AM104	308	AJ147	342	AR15
25	241	AI6	275	AM123	309	AJ156	343	AR22
	242	AI86	276	AM137	310	AJ168	344	AR28
	243	AJ1	277	AM15	311	AJ169	345	AR3
	244	AJ10	278	AM16	312	AJ172	346	AR34
	245	AJ13	279	AM30	313	AJ173	347	AR42
30	246	AJ15	280	AM38	314	AJ174	348	AR54
	247	AJ20	281	AM39	315	AK528	349	AR61
	248	AJ21	282	AM42	316	AP116	350	AM282
	249	AJ26	283	AM46	317	AP120	351	AM307
	250	AJ27	284	AM66	318	AP135	352	AM349

	353	AM372	387	AR310	421	AM616	455	AM921
	354	AM392	388	AR323	422	AM622	456	AM931
	355	AM400	389	AR324	423	AM625	457	AM973
	356	AM430	390	AR325	424	AM666	458	AM996
5	357	AP11	391	AR349	425	AM686	459	AS56
	358	AP2	392	AR360	426	AM704	460	AS61
	359	AP56	393	AR364	427	AM726	461	AS63
	360	AP57	394	AR400	428	AM728	462	AS65
	361	AP58	395	AR415	429	AM735	463	AS83
10	362	AP60	396	AR417	430	AM741	464	AS85
	363	AP67	397	AM558	431	AM742	465	AS86
	364	AP7	398	AM566	432	AM754	466	AS88
	365	AQ53	399	AM600	433	AM781	467	AT107
	366	AQ54	400	AR420	434	AM795	468	AT111
15	367	AQ61	401	AR437	435	AM814	469	AT138
	368	AQ64	402	AR440	436	AM833	470	AT140
	369	AQ71	403	AR446	437	AM838	471	AT142
	370	AQ73	404	AR450	438	AT16	472	AT146
	371	AQ83	405	AR452	439	AT19	473	AT151
20	372	AM1075	406	AR455	440	AT20	474	AT157
	373	AM1076	407	AR463	441	AT4	475	AT181
	374	AM1083	408	AR464	442	AT53	476	AT97
	375	AR100	409	AR467	443	AT63	477	AS239
	376	AR69	410	AR474	444	AT64	478	AT226
25	377	AM1017	411	AR475	445	AT74	479	AT259
	378	AM1032	412	AS15	446	AT94	480	AT260
	379	AM1036	413	AS20	447	AT95	481	AT265
	380	AM1045	414	AS23	448	AM1000	482	AT280
	381	AM1060	415	AS31	449	AM856	483	AT340
30	382	AM1067	416	AS47	450	AM885	484	AT351
	383	AR253	417	AS48	451	AM889	485	AT352
	384	AK642	418	AS7	452	AM892	486	AT356
	385	AK647	419	AM610	453	AM910	487	AT359
	386	AK650	420	AM614	454	AM91°	4°8	AT361

	489	AS252	523	AU161	557	AW106	591	BE28
	490	AS263	524	AU164	558	AW107	592	BE3
	491	AS264	525	AZ285	559	AW109	593	BE34
	492	AS268	526	AZ286	560	AW133	594	BE9
5	493	AS271	527	AZ287	561	AW140	595	AZ12
	494	AS294	528	AZ290	562	AW92	596	AZ22
	495	AS301	529	AZ188	563	AW95	597	AZ32
	496	AS330	530	AZ191	564	AW98	598	AZ45
	497	AS144	531	AZ204	565	BA185	599	AZ46
10	498	AS152	532	AZ219	566	BA204	600	BF143
	499	AS157	533	AW170	567	BA210	601	BF146
	500	AS162	534	AW176	568	BA226	602	BF157
	501	AS164	535	AW178	569	BG1	603	BF160
	502	AS167	536	AW179	570	BG13	604	BF169
15	503	AS180	537	AW182	571	BG3	605	BF171
	504	AS186	538	AW185	572	BG33	606	BF176
	505	AS187	539	AW189	573	BG36	607	BF178
	506	AU36	540	AW192	574	BG37	608	AS196
	507	AU39	541	AW194	575	BG40	609	AS202
20	508	AU43	542	AW199	576	BG43	610	AS209
	509	AU47	543	AW222	577	BG48	611	AS216
	510	AU50	544	AW231	578	BG58	612	AS230
	511	AU59	545	AZ261	579	BG72	613	AS232
	512	AU71	546	AZ264	580	BG73	614	AX101
25	513	AU101	547	AZ302	581	BF101	615	AX104
	514	AU102	548	AZ303	582	BF132	616	AX107
	515	AU105	549	AK649	583	AZ69	617	AX109
	516	AU106	550	AK663	584	BD51	618	AX122
	517	AU107	551	AR336	585	BD53	619	AX124
30	518	AU115	552	AR356	586	BD65	620	AX127
	519	AU118	553	AR398	587	BD66	621	AX128
	520	AU122	554	AR399	588	BD73	622	AX130
	521	AU138	555	AM1016	589	BD77	623	AX132
	522	AU139	556	AW105	590	BD80	624	AX136

	625	AX137	659	BG274	693	AW33	727	BG504
	626	AX143	660	BG276	694	AW36	728	BG510
	627	AX146	661	AX12	695	AW47	729	BG511
	628	AX51	662	AX17	696	AW49	730	BG513
5	629	AX55	663	AX256	697	AW52	731	BG516
	630	AX56	664	AX30	698	AW60	732	BG518
	631	AX60	665	AX32	699	AW66	733	BG526
	632	AX65	666	AX34	700	AW76	734	BG528
	633	AX78	667	AX49	701	AY241	735	BG552
10	634	AX80	668	AX6	702	AY259	736	BG553
	635	AX81	669	AX8	703	AY268	737	BG556
	636	AX92	670	AZ180	704	BA123	738	AX309
	637	AX97	671	BG191	705	BA134	739	AX315
	638	AX98	672	BG193	706	BA170	740	AX318
15	639	AX99	673	BG199	707	BA176	741	AY186
	640	AZ109	674	BG201	708	BA178	742	AY190
	641	AZ114	675	BG219	709	BA179	743	AY200
	642	BF286	676	BG220	710	BA216	744	AY208
	643	BF290	677	BG221	711	BA233	745	AY211
20	644	BF314	678	BG225	712	BD372	746	AY283
	645	BG236	679	BG228	713	BD375	747	AY289
	646	BG237	680	BG442	714	BD379	748	AY304
	647	BG240	681	BG449	715	BD380	749	AY307
	648	BG241	682	BG457	716	BD403	750	AY318
25	649	BG248	683	BG458	717	BD407	751	AY333
	650	BG249	684	BG461	718	BD409	752	AY334
	651	BG250	685	BG465	719	BD413	753	AY342
	652	BG251	686	BG467	720	BD414	754	AY358
	653	BG255	687	BG471	721	BG481	755	AY362
30	654	BG260	688	BG59	722	BG482	756	BF190
	655	BG267	689	AW12	723	BG492	757	BF191
	656	BG271	690	AW22	724	BG494	758	BF193
	657	BG272	691	AW24	725	BG495	759	BF197
	658	BG273	692	AW32	726	BG503	760	BF208

	761	BF211	795	BG373	829	BD174	863	BI17
	762	BF216	796	BG374	830	BD176	864	BI2
	763	BF221	797	BG379	831	BD177	865	BI24
	764	BF227	798	BG386	832	BD178	866	BI25
5	765	BF228	799	BG388	833	BD183	867	BI3
	766	BF245	800	BG389	834	BE50	868	BI36
	767	BF250	801	BG391	835	BE64	869	BI37
	768	BF258	802	BG393	836	BE89	870	BI39
	769	BF259	803	BG396	837	BG490	871	BI40
10	770	BF263	804	BG409	838	BG491	872	BI41
	771	BF270	805	BG411	839	BG501	873	BI46
	772	BF273	806	BG414	840	BG502	874	BM1
	773	BG280	807	BG420	841	BG512	875	BM17
	774	BG283	808	HW105	842	BG532	876	BM4
15	775	BG284	809	BB54	843	BK162	877	BM41
	776	BG288	810	BD101	844	BK165	878	BM46
	777	BG296	811	BD104	845	BK167	879	BM69
	778	BG305	812	BD107	846	BK171	880	BM88
	779	BG306	813	BD109	847	BK179	881	BM90
20	780	BG309	814	BD119	848	BK180	882	BA106
	781	BG324	815	BD121	849	BK183	883	BA12
	782	BG327	816	BD127	850	BK186	884	BA32
	783	BG329	817	BD128	851	BK194	885	BA38
	784	BG332	818	BD132	852	BK200	886	BA40
25	785	BG334	819	BD136	853	BK206	887	BA71
	786	BG335	820	BD137	854	BK216	888	BA79
	787	BG350	821	BD140	855	BK231	889	BA8
	788	BG356	822	BD144	856	BK232	890	BA88
	789	BG357	823	BD151	857	BK236	891	BA90
30	790	BG363	824	BD154	858	BK237	892	BA91
	791	BG365	825	BD164	859	BK241	893	BA98
	792	BG366	826	BD165	860	BK243	894	BK15
	793	BG368	827	BD169	861	BK246	895	BK17
	794	BG372	828	BD170	862	BK253	896	BK24

	897	BK257	931	AY428	965	BK146	999	BG139
	898	BK26	932	AY437	966	BK155	1000	BG140
	899	BK260	933	AY440	967	BK158	1001	BG141
	900	BK265	934	AY442	968	BK75	1002	BG142
5	901	BK270	935	AY449	969	BK78	1003	BG145
	902	BK271	936	AY457	970	BK92	1004	BG148
	903	BK280	937	AY470	971	BK93	1005	BG151
	904	BK284	938	AY487	972	BK95	1006	BG156
	905	BK286	939	AY489	973	BK96	1007	BG158
10	906	BK29	940	AY511	974	BM101	1008	BG160
	907	BK291	941	BE153	975	BM117	1009	BG168
	908	BK295	942	BF327	976	BM124	1010	BG170
	909	BK296	943	BI64	977	BM139	1011	BG171
	910	BK299	944	BI66	978	BM154	1012	BG172
15	911	BK304	945	BI75	979	BM155	1013	BG173
	912	BK307	946	BI80	980	BM158	1014	BG93
	913	BK308	947	BI81	981	BM94	1015	BG95
	914	BK339	948	BI82	982	AY102	1016	BI102
	915	BK34	949	BI86	983	AY107	1017	BI103
20	916	BK343	950	BI87	984	AY122	1018	BI107
	917	BK40	951	BI88	985	AY131	1019	BI110
	918	BK41	952	BI91	986	AY137	1020	BI114
	919	BK48	953	BI92	987	AY140	1021	BI117
	920	BK49	954	BK102	988	AY147	1022	BI120
25	921	BK57	955	BK105	989	AY157	1023	BI122
	922	BK59	956	BK107	990	AY160	1024	BI124
	923	BK61	957	BK112	991	AY183	1025	BI126
	924	BK68	958	BK114	992	AY93	1026	BI127
	925	BL341	959	BK115	993	BG102	1027	BI129
30	926	AY398	960	BK117	994	BG104	1028	BI133
	927	AY406	961	BK120	995	BG112	1029	BI139
	928	AY407	962	BK130	996	BG125	1030	BI150
	929	AY408	963	BK134	997	BG132	1031	BI164
	930	AY421	964	BK142	998	BG137	1032	BI97

	1033	BI98	1067	BQ58	1101	BO71	1135	BL209
	1034	BI99	1068	BD189	1102	BO87	1136	BL210
	1035	BS1	1069	BD194	1103	BO9	1137	BL211
	1036	BS54	1070	BD199	1104	BD235	1138	BL219
5	1037	BS58	1071	BD200	1105	BD240	1139	BL220
	1038	BS81	1072	BD201	1106	BD241	1140	BL229
	1039	BS89	1073	BD208	1107	BD244	1141	BL230
	1040	BH100	1074	BD209	1108	BD247	1142	BL243
	1041	BH106	1075	BD213	1109	BD251	1143	BL247
10	1042	BH111	1076	BD214	1110	BD257	1144	BL249
	1043	BH123	1077	BD222	1111	BD260	1145	BL255
	1044	BH131	1078	BH19	1112	BD262	1146	BL257
	1045	BH157	1079	BH195	1113	BD265	1147	BL271
	1046	BH297	1080	BH2	1114	BD268	1148	BL274
15	1047	BH306	1081	BH227	1115	BD522	1149	BL30
	1048	BH309	1082	BH272	1116	BD538	1150	BL67
	1049	BH316	1083	BH276	1117	BD544	1151	BL73
	1050	BH323	1084	BH281	1118	BD548	1152	BL89
	1051	BH339	1085	BH41	1119	BD561	1153	BD420
20	1052	BH365	1086	BH51	1120	BL147	1154	BD423
	1053	BH389	1087	BH66	1121	BL15	1155	BD426
	1054	BH392	1088	BH7	1122	BL152	1156	BD427
	1055	BJ54	1089	BH87	1123	BL156	1157	BD428
	1056	BJ62	1090	BH90	1124	BL160	1158	BD438
25	1057	BJ66	1091	BJ20	1125	BL178	1159	BD441
	1058	BJ67	1092	BJ27	1126	BL179	1160	BD445
	1059	BJ69	1093	BJ29	1127	BL183	1161	BD473
	1060	BJ70	1094	BJ38	1128	BL185	1162	BD486
	1061	BJ75	1095	BJ39	1129	BL186	1163	BD489
30	1062	BJ76	1096	BJ9	1130	BL187	1164	BD492
	1063	BJ78	1097	BO11	1131	BL194	1165	BD512
	1064	BJ87	1098	BO20	1132	BL196	1166	BL106
	1065	BQ20	1099	BO4	1133	BL201	1167	BL310
	1066	BQ3	1100	BO52	1134	BL205	1168	BN1

	1169	BN107	1203	BD351	1237	BN351	1271	BP22
	1170	BN12	1204	BN189	1238	BN354	1272	BP24
	1171	BN130	1205	BN201	1239	BN365	1273	BP25
	1172	BN132	1206	BN212	1240	BN422	1274	BT99
5	1173	BN133	1207	BN280	1241	BN425	1275	BP28
	1174	BN139	1208	BN284	1242	BN439	1276	BP3
	1175	BN141	1209	BN329	1243	BN460	1277	BP4
	1176	BN153	1210	BN331	1244	BN461	1278	BP43
	1177	BN156	1211	BN591	1245	BN463	1279	BP47
10	1178	BN171	1212	BO153	1246	BN472	1280	BP504
	1179	BN174	1213	BO157	1247	BN473	1281	BP506
	1180	BN180	1214	BO159	1248	BO100	1282	BP508
	1181	BN246	1215	BO166	1249	BO107	1283	BP521
	1182	BN267	1216	BO178	1250	BO114	1284	BP528
15	1183	BN268	1217	BO189	1251	BO121	1285	BP530
	1184	BN33	1218	BO194	1252	BO126	1286	BP532
	1185	BN40	1219	BO210	1253	BO133	1287	BP537
	1186	BN48	1220	BO212	1254	BO137	1288	BP544
	1187	BN5	1221	BO213	1255	BO398	1289	BP545
20	1188	BN563	1222	BO218	1256	BO399	1290	BP55
	1189	BN65	1223	BO226	1257	BO401	1291	BP567
	1190	BN69	1224	BO279	1258	BO432	1292	BP569
	1191	BN81	1225	BO301	1259	BO528	1293	BP57
	1192	BN97	1226	BO323	1260	BO535	1294	BP590
25	1193	BN99	1227	BO358	1261	BO538	1295	BP61
	1194	BD286	1228	BO365	1262	BO549	1296	BP70
	1195	BD288	1229	BO385	1263	BO551	1297	BP71
	1196	BD297	1230	BO250	1264	BO93	1298	BP780
	1197	BD316	1231	BO254	1265	BP101	1299	BP783
30	1198	BD317	1232	BO256	1266	BP118	1300	BP784
	1199	BD321	1233	BO260	1267	BP121	1301	BP791
	1200	BD327	1234	BO261	1268	BP15	1302	BP797
	1201	BD335	1235	BO273	1269	BP19	1303	BP806
	1202	BD339	1236	BN342	1270	BP21	1304	BP809

	1305	BP810	1339	BV243	1373	CC71	1407	BR572
	1306	BP813	1340	BV248	1374	CC76	1408	BR559
	1307	BP814	1341	BV250	1375	CC78	1409	BR538
	1308	BP815	1342	BV259	1376	CC81	1410	BR537
5	1309	BP820	1343	BV273	1377	CC89	1411	BR533
	1310	BP84	1344	BV275	1378	CD124	1412	BR500
	1311	BP919	1345	BV49	1379	CD128	1413	BR48
	1312	BP925	1346	BV51	1380	CD140	1414	BR475
	1313	BQ115	1347	BV66	1381	CD145	1415	BR436
10	1314	BQ129	1348	BV70	1382	CD146	1416	BR434
	1315	BS116	1349	BV71	1383	CD173	1417	BR4
	1316	BT101	1350	BV72	1384	CD194	1418	BR346
	1317	BT133	1351	BV73	1385	CD31	1419	BR342
	1318	BT139	1352	BV88	1386	CD50	1420	BR338
15	1319	BT33	1353	BW345	1387	CF50	1421	BR333
	1320	BT4	1354	CB25	1388	CF62	1422	BR332
	1321	BW13	1355	CB3	1389	CF78	1423	BR212
	1322	BW18	1356	CB30	1390	CF85	1424	BR195
	1323	BW2	1357	CB37	1391	CF89	1425	BR194
20	1324	BW51	1358	CC144	1392	BR814	1426	BR19
	1325	BW61	1359	CC145	1393	BR782	1427	BR141
	1326	BW83	1360	CC149	1394	BR778	1428	BR122
	1327	BV185	1361	CC153	1395	BR77	1429	BR107
	1328	BV195	1362	CC162	1396	BR767	1430	BR1010
25	1329	BV200	1363	CC25	1397	BR758	1431	BR101
	1330	BV202	1364	CC31	1398	BR733	1432	BR1008
	1331	BV204	1365	CC322	1399	BR719	1433	BQ135
	1332	BV206	1366	CC39	1400	BR711	1434	BP913
	1333	BV210	1367	CC397	1401	BR71	1435	BP911
30	1334	BV212	1368	CC403	1402	BR63	1436	BP897
	1335	BV227	1369	CC46	1403	BR616	1437	BP895
	1336	BV238	1370	CC50	1404	BR610	1438	BP894
	1337	BV239	1371	CC59	1405	BR607	1439	BP893
	1338	BV241	1372	CC69	1406	BR595	1440	BP884

	1441	BP883	1475	BU65
	1442	BP875	1476	BU68
	1443	BP870	1477	BU76
	1444	BP859	1478	BV106
5	1445	BP837	1479	BV112
	1446	BP833	1480	BV123
	1447	BP499	1481	BV124
	1448	BP492	1482	BV126
	1449	BP488	1483	BV128
10	1450	BP484	1484	BV131
	1451	BP483	1485	BV133
	1452	BP481	1486	BV134
	1453	BP475	1487	BV135
	1454	BN418	1488	BV138
15	1455	BN415	1489	BV139
	1456	BN405	1490	BV140
	1457	BN394	1491	BV141
	1458	BN390	1492	BV145
	1459	BN387	1493	BV15
20	1460	BN379	1494	BV158
	1461	BN377	1495	BV160
	1462	BR84	1496	BV172
	1463	BR853	1497	BV180
	1464	BR854	1498	BV21
25	1465	BR884	1499	BV27
	1466	BT160	1500	BV29
	1467	BU165		
	1468	BU29		
	1469	BU44		
30	1470	BU45		
	1471	BU53		
	1472	BU57		
	1473	BU6		
	1474	BU60		

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selectin "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification
5 and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that
10 the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making
15 suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the
20 polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions,
25 most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table 1 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 1

	Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) ²	Hybridization Temperature and Buffer ¹	Wash Temperature and Buffer ¹
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	< 50	T _B *; 1xSSC	T _B *; 1xSSC
	C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	< 50	T _D *; 1xSSC	T _D *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
10	F	RNA:RNA	< 50	T _F *; 1xSSC	T _F *; 1xSSC
	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	< 50	T _H *; 4xSSC	T _H *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	< 50	T _J *; 4xSSC	T _J *; 4xSSC
15	K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	< 50	T _L *; 2xSSC	T _L *; 2xSSC
	M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	< 50	T _N *; 6xSSC	T _N *; 6xSSC
	O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
20	P	DNA:RNA	< 50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	< 50	T _R *; 4xSSC	T _R *; 4xSSC

∴ The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

∴ SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log [Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. ~~The isolated~~ polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* **19**, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* **185**, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control

sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

5 A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

10 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any
15 bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

20 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art,
25 as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting
30 expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA

Sephacrose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

- and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 -
- 5 Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

- Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in:
- 10 *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun.
- 15 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988..

Immune Stimulating or Suppressing Activity

- A protein of the present invention may also exhibit immune stimulating or immune
- 20 suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may
- 25 be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course,
- 30 in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other
5 conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune
10 response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from
15 immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), *e.g.*, preventing
20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys
25 the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-T, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the
30 molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

5 The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci
10 USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating
15 autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B
20 lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of
25 well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

30 Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient
5 by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding
10 a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably
15 B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor
20 cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection
25 *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation
signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or
30 which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected
5 with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured
10 by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-
15 3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa
20 et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching
25 (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.c.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

30 Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnoli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad. Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162. Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

5 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

10 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma
15 induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of
20 progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the
25 protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein
30 may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or
5 progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural
10 cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized
15 neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from
20 chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

25 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of
30 fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured
5 by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

10 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

15 Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention,
20 alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may
25 be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale

et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

5 A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide
10 particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can
15 stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

20 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one
25 cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et
30 al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A
5 protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

10 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

15 Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors
20 involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.
25 A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those
30 described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med.

169:149-160 1989; Stoltenborget et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

5 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or
10 suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality,
15 arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

20 In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor
25 precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

30 A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the

5 fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent

10 behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for

15 example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

20

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

5 The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, 10 diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

15 As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, 20 administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a 25 mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either 30 simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 mg to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also
5 optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and
10 cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices
15 for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such
20 as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

25 Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

30 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

Table 3

Sel.	Species	Tissue	Cell Type
AA	Human	Kidney	19-23wks., M/F pool of 5
AB	Human	Fetal Lung	Fetal Lung
AC	Human	Placenta	26yrs., 1 specimen
AD	Murine	Embryo	Fetal ES cells
AE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine	Fetal Thymus	Fetal Thymus
AI	Human	Blood	Adult PBMC/TH1or2
AJ	Human	Testes	10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
AT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
AV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
AY	Human	Retina	16-75yrs., pool of 76
AZ	Human	Colon	Caco-2 Adenocarcinoma
B	Human	Blood	PeripheralBloodMononuclearCell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1or2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	10-61yrs., pool of 11
BM	Human	Muscle	N/A
BN	Human	Placenta	26yrs., 1 specimen
BO	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
BX	Human	Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1or2
BZ	Human	Kidney	19-23wks., M/F pool of 5
C	Human	Blood	PeripheralBloodMononuclearCell
CA	Murine	Embryo	Fetal ES cell embryoid bodies
CB	Human	Brain	19-23wks., M/F pool of 5
CC	Human	Brain	N/A
CD	Human	Brain	19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	26yrs., 1 specimen
CG	Human	Testes	10-61yrs., pool of 11
CH	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CJ	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61yrs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	SalivaryGland	N/A
CQ	Human	Heart	13-73yrs., pool of 3
CR	Human	Testes	10-61yrs., pool of 11
CS	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	PeripheralBloodMononuclearCell
DA	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD	Human	Testes	10-61yrs., pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ	Human	Placenta	26yrs., 1 specimen
DK	Human	Fetal Kidney2	Fetal Kidney

DL	Human	Brain	N/A
DM	Human	Brain	N/A
DN	Human	Brain	19-23wks., M/F pool of 5
DO	Human	Testes	10-61yrs., pool of 11
DP	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DU	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	PeripheralBloodMononuclearCell
EI	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	26yrs., 1 specimen
EK	Human	Brain	19-23wks., M/F pool of 5
EL	Human	Testes	10-61yrs., pool of 11
EM	Human	Fetal Kidney2	Fetal Kidney
EN	Human	Brain	19-23wks., M/F pool of 5
EO	Human	Adrenal Gland	Adult Adrenal Gland
EP	Human	Placenta	26yrs., 1 specimen
EQ	Human	Testes	10-61yrs., pool of 11
ER	Human	Brain	19-23wks., M/F pool of 5
ES	Human	Placenta	26yrs., 1 specimen
ET	Human	Testes	10-61yrs., pool of 11
EU	Human	Kidney	Adult Kidney
EV	Human	Stomach	Adult Stomach
EW	Human	Placenta	26yrs., 1 specimen
EX	Human	Testes	10-61yrs., pool of 11
EY	Human	Brain	19-23wks., M/F pool of 5
EZ	Human	Fetal Kidney2	Fetal Kidney
FA	Human	Brain	19-23wks., M/F pool of 5
FB	Human	Placenta	26yrs., 1 specimen
FC	Human	Testes	10-61yrs., pool of 11
FD	Human	SalivaryGland	N/A
FE	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA

FG	Human	Brain	N/A
FH	Human	Brain	19-23wks., M/F pool of 5
FI	Human	Small Intest	Adult Small Intestine
FJ	Human	Lung CA	Adult Lung CA
FK	Human	Kidney	Adult Kidney
FM	Human	Brain	N/A
FN	Human	Brain	19-23wks., M/F pool of 5
FO	Human	Brain	N/A
FP	Human	Placenta	26yrs., 1 specimen
FQ	Human	Testes	10-61yrs., pool of 11
FR	Human	Placenta	26yrs., 1 specimen
FS	Human	Testes	10-61yrs., pool of 11
FT	Chicken	Fetal Lung	Fetal Lung
FU	Chicken	Limb Bud	Fetal St. 23 Limb Bud
FV	Human	Testes	Adult NCCIT TeratoCA
FW	Human	Testes	Adult NCCIT TeratoCA
FX	Human	Brain	19-23wks., M/F pool of 5
FY	Human	Placenta	26yrs., 1 specimen
FZ	Human	Placenta	26yrs., 1 specimen
G	Human	Blood	PeripheralBloodMononuclearCell
GA	Human	Testes	10-61yrs., pool of 11
GB	Human	Placenta	26yrs., 1 specimen
GC	Human	Testes	10-61yrs., pool of 11
GD	Human	Placenta	26yrs., 1 specimen
GE	Human	Brain	N/A
GF	Human	Brain	19-23wks., M/F pool of 5
GG	Human	Fetal Kidney2	Fetal Kidney
GH	Human	Placenta	26yrs., 1 specimen
GI	Human	Retinoblastoma	Adult Retinoblastoma Y79
GJ	Murine	Spleen	Adult Spleen
GK	Human	Fetal Kidney2	Fetal Kidney
GL	Murine	Lymph Node	Adult Lymph Node
GM	Human	Uterus	N/A
GN	Human	Blood	PeripheralBloodMononuclearCell
GO	Human	Adrenal Gland	Adult Adrenal Gland
GP	Human	Ovary	PA-1 Teratocarcinoma
GQ	Human	Pineal Gland	N/A
GR	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
GS	Human	Retina	16-75yrs., pool of 76
GT	Human	Brain	N/A
GU	Human	Fetal Kidney2	Fetal Kidney
GV	Rat	Retina	Newborn Retina
GW	Chicken	Limb Bud	Fetal St.26 Limb Bud
GX	Human	Brain	N/A
GY	Human	Testes	10-61yrs., pool of 11
GZ	Human	Brain	19-23wks., M/F pool of 5
H	Human	Blood	PeripheralBloodMononuclearCell

HA	Human	Testes	Adult NCCIT TeratoCA
HB	Human	Fetal Kidney2	Fetal Kidney
HC	Human	Brain	19-23wks., M/F pool of 5
HD	Human	Brain	N/A
HE	Human	Testes	10-61yrs., pool of 11
HF	Human	Brain	19-23wks., M/F pool of 5
HG	Human	Fetal Kidney2	Fetal Kidney
HH	Human	Brain	N/A
HI	Human	Testes	10-61yrs., pool of 11
HJ	Human	Brain	N/A
HK	Human	Brain	19-23wks., M/F pool of 5
HL	Human	Fetal Kidney2	Fetal Kidney
HM	Human	Testes	Adult NCCIT TeratoCA
HN	Human	Fetal Kidney2	Fetal Kidney
HO	Human	Brain	N/A
HP	Human	Brain	19-23wks., M/F pool of 5
HQ	Human	Testes	10-61yrs., pool of 11
HR	Human	Brain	N/A
HS	Human	Brain	N/A
HT	Human	Brain	19-23wks., M/F pool of 5
HU	Human	Fetal Kidney2	Fetal Kidney
HV	Human	Testes	10-61yrs., pool of 11
HW	Human	Brain	N/A
HX	Human	Brain Hippoca	Adult Brain Hippocampus
HY	Human	Trachea	Adult Trachea
HZ	Human	Brain Thalamus	Adult Brain Thalamus
I	Human	Blood	PeripheralBloodMononuclearCell
IA	Human	Thyroid	Adult Thyroid
IB	Human	Embryonal CA	Fetal NT2-D1
IC	Human	WER1-Rb1 line	Adult Retinoblastoma
ID	Human	Muscle	N/A
IE	Human	Brain	19-23wks., M/F pool of 5
IF	Human	Uterus	N/A
IG	Human	Testes	10-61yrs., pool of 11
IH	Human	Muscle	N/A
II	Human	Brain	N/A
IJ	Human	Blood	PeripheralBloodMononuclearCell
IK	Human	Retinoblastoma	Adult Retinoblastoma Y79
IL	Human	Retina	16-75yrs., pool of 76
IM	Human	Various	Various
IN	Human	Prostate	Adult Prostate
IO	Human	Brain	19-23wks., M/F pool of 5
IP	Human	Fetal Kidney2	Fetal Kidney
IQ	Human	Prostate	Adult Prostate
IR	Human	Brain Hippoca	Adult Brain Hippocampus
IS	Human	Trachea	Adult Trachea
IT	Human	Brain Thalamu	Adult Brain Thalamus

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth
McCoy, John
LaVallie, Edward
Racie, Lisa
Merberg, David
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael
- (ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
- (iii) NUMBER OF SEQUENCES: 1500
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy Disk
 - (B) COMPUTER: IBM PC Compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A.
 - (B) REGISTRATION NUMBER: 32,724
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 498-8224
 - (B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

GTCGACCCCA TCCCATCCAA TAGTCCCAT CTCTTCTCAG CTCTCTCTGT AGTTTCTCTT      60
CCTCCGCCTG CCTTTAAGT TAGTGTTTCC CAGGACAGAG GTGACTCAGT TGTATCCAGA      120
COGCTCTGTG ACTGAACACC CACTTCTTT TCCTTTTCCA ATAAATATAT GTAACATACA      180
TGTCAACTAG GAACAAAACA GTATCTCAGG AATCCACCAT CCAGTTAAAA ATGGACCCTT      240

```

ACCCTTACCG TGCCCCTGCA GAGACCCCAA TACAGCGCAT TTCCCTCATT CTTTGTCTTT 300
TCTCAAGTTT TACCACGGCC TCTTTGGCCC TCGAG 335

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCGGCC AAAGAGGCCG TTGACCATTG ATAGAACACA GGCATACACA GGAAGATACA 60
TTCACAGAAG AGCTTCCTGC ACAAAGTAAG CCACCAGCGC AACATGACAG TGAAGACCCT 120
GCATGGCCCA GCCATGGTCA AGTACTTGCT GCTGTCGATA TTGGGGCTTG CTTTCTGAG 180
TGAGGCGGCA GCTCGGAAAA TCCCCAAAGT AGGACATACT TTTTCCAAA AGCCTGAGAG 240
TTGCCCGCCT GTGCCAGGAG GTAGTATGAA GCTTGACATT GGCATCATCA ATGAAAACCA 300
GCGCGTTTCC ATGTCACGTA ACATCGAGAG CCGCTCCACC TCCCCCTGGA ATTACTGT 360
CACTTGGGAC CCCAACCGGT ACCCTCGGA AGTTGTACAG GCCCAGTGTA GGAACCTGGG 420
CTGCATCAAT GCTCAAGGAA AGGAAGACAT CTCCATGAAT TCCGTTCCCA TCCAGCAAGA 480
GACCTGTGCG ACGGCCTCTT TGGCCCTCGA GACA 514

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCGACCCTC CACCTGCAA TCCACTGTCC ATACCCTTGG ATTGGTTGAA GAGCCTTTGG 60
TCATACTGAA CTTCAATTGA AGTCCGAGGA TTAGGAACAC CGAGAGCAAT AACTTCACTG 120
ATATCCCGAT TTTCAATTTCT CTGAAGTTTC GACCTCTTAT CAGGAGCTGC CTTGGAAAGA 180
TTCCGGTCAT GCTGTCTCTC TTTTCGCCTG TCATGCCGGA TTTCACTCCT CTCACGTGGC 240
TCCCCATCCT CTTTTCAC ATGAGTTTGG ATCCAGCTC TTCTCTCCCT GGCCTTCTGG 300
GCCATTTCTC TAAGTTTCTC TNCANGTNTN NCCTTTTCTT TCTGAGCCAT TTTCTCTCT 360
ACTTGGGCGT CGACGGCCTC TGGGGCCCTC GAG 393

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCGACCAGG CATAACAGG AAGATACATT CACAGAAAGA GCTTCCTGCA CAAAGTAAGC 60
CACCAGCGCA ACATGACAGT GAAGACCCTG CATGGCCAG CCATGGTCAA GTACTTGCTG 120

CTGTCGATAT TGGGGCTTGC CTTTCTGAGT GAGGCGGCAG CTCGGAAAAT CCCCAAAGTA	180
GGACATACTT TTTTCCAAAA GCCTGAGAGT TGCCCGCCTG TGCCAGGAGG TAGTATGAAG	240
CTTGACATTG GCATCATCAA TGAAAACCAG CGCGTTTCCA TGTCACGTAA CATCGAGAGC	300
CGCTCCACCT CCCCCTGGAA TTACACTGTC ACTTGGGACC CCAACCGGTA CCCCTCGGAA	360
GTTGTACAGG CCCAGTGTAG GAACTTGGGC TGCATCAATG CTCAAGGAAA GGAAGACATC	420
TCCATGAATT CCGTTCCCAT CCAGCAAGAG ACCCTGGTCG TCCGGAGGAA GCACCAAGGC	480
TGCTCTGTTT CTTTCCAGTT GGAGAAGGTG CTGGTGACTG TTGGCTGCAC CTGCGTCACG	540
TCAACGGCCT CTTTGGCCCT CGAG	564

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTGCACCTTC AGTTGCCTCA GACCCCAAGTA ATACAACGGT CACCACCATG AAACCTACAG	60
CGGCATCTAA TACAACAACA CCAGGGATGG TCTCAACAAA TATGACTTCT ACCACCTTAA	120
AGTCTACACC CAAAACAACA AGTGTTCAC AGAACACATC TCAGATATCA ACATCCACAA	180
TGACCGTAAC CCACAATAGT TCAGTGACAT CTGCTGCTTC ATCAGTAACA ATCACAACAA	240
CTATGCATTC TGAAGCAAAG AAAGGATCAA AATTTGATAC TGGGAGCTTT GTTGGTGGTA	300
TTGTATTAAAC GCTGGGAGTT TTATCTATTC TGTCACGGC CTCTTTGGCC CTCGAG	356

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTACTGCTGC ACGGACTCTG GAACCATGAA CATATTTGAT CGAAAGATCA ACTTTGATGC	60
GCTTTTAAAA TTTTCTCATA TAACCCCGTC AACGCAGCAG CACCTGAAGA AGGTCTATGC	120
AAGTTTTGCC CTTTGTATGT TTGCGGCGGC TGCAGGGGCC TATGTCCATA TGGTCACTCA	180
TTTCATTGAG GCTGGCCTGC TGTCTGCCCT GGGCTCCCTG ATATTGATGA TTTGGCTGAT	240
GGCAACACCT CATAGCCATG AACTGAACA GAAAAGACTG GGAATTCTTG CTGGATTTGC	300
ATTCCTTACA GGAGTTGGCC TGGGCCCTGC CCTGGAGTTT TGATTGCTG TCAACCCAG	360
CATCCTTCCC ACTGCTTTCA TGGGCACGGC AATGATCTTT ACCTGCTTCA CCCTCAGTGC	420
ACTCTATGCC AGGCGCCGCG GCTACCTCTT TCTGGGAGGT ATCTTGATGT CAGCCCTGAG	480
CTTGTTGCTT TTGTCGACGG CCTCTTTGGC CCTCGAGACA	520

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCGACGTAC	CACCAGCAAC	CATCAATCCC	GTCTCCTCCT	GCCTCCTCTC	CTGCAATCCA	60
CCCCGCCACG	ACTATCGCCA	TGGCAGCCCT	GATCGCAGAG	AACTTCCGCT	TCCTGTCACT	120
TTTCTTCAAG	AGCAAGGATG	TGATGATTTT	CAACGGCCTG	GTGGCACTGG	GCACGGTGGG	180
CAGCCAGGAG	CTGTCCTCTG	TGGTGGCCTT	CCACTGCCCC	TGCTCGCCGG	CCCGGAACATA	240
CCTGTACGGG	CTGGCGGCCA	TCGGCGTGCC	CGCCCTGGTG	CTCTTCATCA	TTGGCATCAT	300
CCTCAACAAC	CACACCTGGA	ACCTCGTGGG	CGAGTGCCAG	CACCGGAGGA	CCAAGAACTG	360
CTCCGCCGCC	CCCACCTTCC	TCCTTCTAAG	CTCCATCCTG	GGACGTGGGG	CTGTGGCCCC	420
TGTCACCTGG	TCTGTCTCT	CCCTGCTGCG	TGGTGAGGCT	TATGTCTGTG	CTCTCAGTGA	480
GTTCGTGGAC	CCTTCCTCAC	TCACGGCCTC	TTTGGCCCTC	GAGACA		526

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCACTGTG	CAGCGGAGTT	TGACTTTATG	GAAAAAGAGA	CTCCACTGAG	ATACACAAAG	60
ACATTATTGC	TTCCAGTTGT	TCTTGTAAGT	TTTGTGCTA	TTGTTAGAAA	GATTATTAGT	120
GATATGTGGG	GTGTCTTAGC	TAAACAACAG	ACACATGTAA	GAAAACACCA	GTTTGATCAT	180
GGAGAGCTGG	TTTACCATGC	ATTGCAATTG	TTAGCATATA	CAGCCCTTGG	TATTTTAATT	240
ATGAGACTAA	AACTCTTCTT	GACACCATAC	ATGTGTGTTA	TGGCATCACT	GATCTGCTCA	300
AGACAGCTAT	TTGGATGGCT	CTTTTGCAAA	GTACATCCTG	GTGCTATTGT	GTTTGTATA	360
TTAGCAGCAA	TGTCAATACA	AGGTTCAACA	AATCTGCAAA	CCCAGTGGA	GTGACGGCC	420
TCTTTGGCCC	TCGAGACA					438

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCGACCCTA	CACCATGTTT	TTCTCCACGT	TCTACCACGC	CTGCGACCAG	CCCGGGGAGG	60
CGGTGCTGTG	CATCCTCAGC	TACGACACGC	TGCAGTACTG	CGACTTCTTG	GGCTCCGGGG	120
CGGCATCTG	GGTCACCATC	CTGTGCATGG	CACGGCTCAA	GACAGCCCTG	AAATACGTGC	180
TGTTTCTTCT	GGGTACACTG	GTCATCGCCA	TGTCCTTGCA	GCTGGACCGC	AGGGGCATGT	240
GGAACATGCT	GGGGCCCTGC	CTCTTTGCCT	TCGTGATCAT	GGCCTCCATG	TGGGCTTACC	300
GCTGCGGGCA	CCGGCGCCAG	TGCTACCCCA	CCTCGTGGCA	GCGCTGGGCC	TTCTACCTCC	360
TGCCCCGGCGT	CTCTACGGCC	TCTTTGGCCC	TCGAG			395

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTCGACAGAM	WNCAACCTC	AGACGCCACA	TCCCCTKACA	AGCTGMCAGG	CAGGTTCTCT	60
TCCTCTCACA	TACTGACCCA	CGGKTCCACC	CTCTCTCCCC	TGGAAAGGAC	ACCATGAGCA	120
CTGAAAGCAT	GATCCGGRAC	GTGGAGCTGK	CCGAGGAGGN	GYTCCCCAAG	AAGACAGGGG	180
GGRCCAGGG	CTCCAGGCGG	GGGTTTGTTT	CTCAGWCTCT	TCTCCTTCCT	GATCGNGGGA	240
GGGGGCACCA	CGCTCTTCTG	TCTGCTGGAC	TTTGGAGTGA	TCGNNCCCCA	GAGGGAAGGA	300
GTTCCCCCAGG	GGAACCTCTC	T				321

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTCGACGGCC	GAGAWGGACA	TGAAGCAATA	TCAAGGCTCC	GGCGGCGTCG	CCATGGATGT	60
GGNACGGAGT	CGTTCCCTCT	ACTGCGTGGT	GTGGACGCCC	ATCCCGGTGN	TCACGTGGTT	120
TTTCCCATC	ATCGGCCACA	TGGGCATCTG	CACATCCACA	GGAGTCATTC	GGGACTTCGC	180
GGGCCCCCTAC	TTGTCTCAG	AGGACAACAT	GGCCTTTGGA	AAGCCTGCCA	AGTACTGGAA	240
GTTGGACCCT	GCTCAGTCT	ATGCTAGCGG	GCCCAACGCA	TGGGACACGG	CTGTGCACGA	300
CGCCTCTGAG	GAGWACAAGC	ACCGCATGCA	CAATCTCTGC	TGTGACAACT	GCCACTCGCA	360
CGTGGCATCG	GCCCTGAATC	TGATGCGCTA	CAACAACAGC	ACCAACTGGA	ATATGGTGAC	420
GCTCTGCTTC	TTCTGCCTGC	TCTACGGGAA	GTACGTCAGC	GTTGGGGCCT	TCGTGAAGAC	480
CTGGCTGCCC	TTCATCCTTC	TCCTGTGAC	GGCCTCTTTC	GCCCTCGAGA	CA	532

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTGTACACCA	AGATGATGAC	CAAGAAGCCG	GGCATGTTCT	TCAACCCCGA	GGAGTCGGAG	60
CTGGACCTGA	CCTACGGNAA	CAGATACAAN	AAOGTGAAGC	TCCCTGACGN	CTACGAGCGC	120
CTCATCCTGG	ACGTCTTCTT	TGGGAGGCAG	ATGNACTTCG	TGCGCAGGGA	CGANCTCCNT	180
GAGGNCTGGC	GTATTTTCA	CCCCACTGNT	GTACCANATT	GAGCTNGAGA	AGGCCAAGCC	240
TCCAGGAACA	CATGTGGGGT	CATTACCAAA	CAGGGTCCAT	CCACATGATG	GTGAACATCA	300
ANCTTTGGGC	GGACAANGAT	TGCTGGGAAT	GGGAATCCTG	TTCACTGGGG	AGCTCTGGGA	360
GTTCTTGAGC	TTTGCTGAAA	GGTACCCTGC	CATCATCTAT	AACATCCTGC	TCITTGGGCT	420
GACCAAGTCC	CTGGGTCAGA	GCWTCATCTT	TATGAOGATT	GTGTATCTTG	GTCCCCTGAC	480
CTGCTCCATC	ATCACTACAA	CTCGAAAGTT	CTTCACAAAW	KTGCCCCGCTG	TGATCCTCTT	540
CGCCAATCCC	ATGTCGACGG	CCTCTTTGGC	CCTCGAGACA			580

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

GTCGACACTA CTTATGCGGC TACTTGTCC AGGGCACAAA ATGCCGTGGC AGTATCTAAC      60
TAAACCCCA CAAAACTGCT TAATAACAGT TTKGRATGTG AGAAATTTAG ATAATTTAAA      120
TATAAGGTGC AGGTTTAAAT TTCTGAGTTT CTTCCTTTCT ATTTTATTA AAAAGAAAAT      180
AATTTTCAGA TTTAATTGAA TTGGAAAAAA CAATACTTCC CACCAGAATT ATATATCCTG      240
AAAATTGTAT TTTTGTATA TAAACAACTT TTAAGAAAGA TCATTATCCT TTTCTCTACC      300
TAAATATGAG GAGTCTTAGC ATAATGACAA ATATTTATAA TTTTCAATT AATGGTACTT      360
GCTGGATCCA CACTAACATC TTTGCTAATA ATCTCATTGT TTCTTCGTCA ACGGCCTCTT      420
TGGCCCTCGA GACA                                     434

```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

GTGGACGTTT TTTTTTCTT TTTCTTTTTT TTAAGAAAAA CCCATTTTTT TCCTTAAGGA      60
CTTACTAGCC AAAATTTCTT AAACCTCGAG GACTCTACTA GCCATGGCCG AGCCATTCTT      120
GTCAGAATAT CAACACCAGC CTCAACTAG CAACGTGACA GGTGCTGCTG CTGTCCAGGA      180
AGAGCTGAAC CCTGAGCGCC CCCCAGGCGC GGAGGAGCGG GTGCCCGAGG AGGACAGTAG      240
GTGGCAATCG AGAGCGTTCC CCCAGTTGGG TGGCCGTCCG GGGCCGGAGG GGAAGGGAG      300
CCTGGAATCC CAACCACTC CCTTGCAGAC CCAGGCCTGT CCAGAATCTA GCTGCCTGAG      360
AGAGGGCGAG AAGGGCCAGA ATGGGGACGA CTCGTCCGCT GCGGCGGACT TYCCGCCGCC      420
GGCAGAAGTG GAACCGACGC CCGAGGCCGA GCTGCTCGCC CAGCCTTGTC ATGACTCCGA      480
GGCCAGTAAG ATGGGGTCGA CGGCCTCTTT GGCCCTCGAG ACA                          523

```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

GTCGACCCTC ANTGTTCTGG AACTGGTCTT GGAAGGGATN GTTTATNCTG AGTACACCTG      60
GGAAGTATTT GGGTACTGTC ANGAGCTGGA GTTGNCTNG NATTACCNTC TTCTGCCNCA      120
TCTGTTGGTA GGGGTAAACC NG                                     142

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

GTCCACCCGG GCCGCCCTC GCCGCCGGG CTCTTCGCGG GCTGCTCTTT GTCTCCCCGA      60
CCTCGATCCC TGCCTCTCCG GCGGCGTGCG GGCTCGTCTG AGGCTTCCCG CATCTCCCCG      120
CTGGAACTCC TGCCTCCCGG GGGTTAGAGG AGGGTTCGTT CGAGGGCTGG AAGCGGAAA      180
GCGGGGCGGA AGGACTGGGC TCATCGCCTC CTGATTAAC TGTGTCTTT ACTTAAATG      240
ACTTTTCCC CACTTTGTCA AACTTGAGAA CTGTSTGTG TGTGTGTGT TCCTTGAGTC      300
TCTAGCTTCA AAATTAAGAG TAGGCGCTAC CGCTGCGATT GTGGGCAGTT GTGTGGTTGG      360
CGGCTGCGTT TGGAGCTCTG AGTTGAAAAG ATGTACGTGA ATGTATGGTT TAGATTTTGT      420
TCTTTTTTTT GCGATTGTC GATTGGGAGT ACTTTTCCTT TCGGAAATGG GCGAATTGG      480
TTTTCTTTTT GTTCATTGAG AACTGGGTCG ACGGCCTCTT TGGCCCTCGA GACA          534

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

GTTCMCGAAG GGAAGAAGAA GATGAACAAG AACAAATGCCA AGGCTCTGAG CACCTTGCGT      60
CAGAAGATCC GAAAATACAA CCGTGATTTT GAGTCCCATC TCACAAGCTA CAAGCAGAAC      120
CCCGAGCAGT CTGCGGATGA AGATGCTGAG AAAAGTGAGG AGGATTCAGA AGGCTCTTCA      180
GATGTGGATG AGGATGAGGA CGGAGTCAGT GCTGCAACTT TCTTGAAGAA GAAATCAGAA      240
GCTCCTTCTG GGGAGAGTCG CAAGTTCCTC MAAAAGATGG ATGATGAAGA TGAGGACTCA      300
GAAGATTCCG TAGATGATGA AGACTGGGAC WCAGGTTCCA CATCTTCCGA CTCCGACTCA      360
GAGGAGGAAG AAGGGAACA AACC GCGCTG GCCTCAAGAT TTCTTAAAAA GGCACCCACC      420
ACAGATGAGG ACAAGAAGGC AGCCGAGAAG AAACGGGAGG ACAAGCTAA GAAGAAGCAC      480
GACAGGAAAT CCAAGCGCCT GGATGAGGAG GAGGAGGACA ATGAAGGCGG GTTCACGGCC      540
TCTTTGGCCC TCGAGACA

```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

GTTGACGGCC AGCTTGCTGT CTAACTTTC ACATCGGAGA AGCTCCTTGG CCTGGGAGGA      60
CTTCTCGTG CTTTCCCCCT TCCCAGAGAT GCCCCTGTCT AGGGAGTGGC AGAGACCATC      120
CTGGAGGGTG CCAGGAGCGG GGGCCCGTCT GAAGTCCCG CCACCCTGGC GGTGCTCCGC      180
AGGCACCGGG CCATCCGACA TGCACCCTC GCTGGCGCGC ACGCTGGCCT GCTTGTGAAG      240

```



```

AGCATCCTTC AGCAGGCTGC CCAGCGGTGG CGCCTCCTGC ATAGACGCTT TGTTTTCAAA 300
AGTACTTGAC CTTTCCACAG CCTTCGGATA GACTTTCTTC TCTCTCTCTT CCAGCTTAAA 360
CAGAGCAAAG TTTTCCAAAT CACTCCCGGG TCCATGGGAT TTCTGGTGGG ATTCCTGTTT 420
CTCTGGGAAG CCGTCTGGTC GACGGCCTCT TTGGCCCTCG AGACA 465

```

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 694 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

GNNNTCGTTG TTCCAGAACT TGATGAGGGG ATCTCGGAAC AACACNGAAA CTTTTCCTC 60
CCTCANTNAC GCACCNGAC TCTCTATTGA GCCAACGGNA ANNCGGCCCT TCCCTCCAAG 120
TAACTTTGNA TTGAAAATA AAAAAAAG NTGCTGTCC TTGCTATCCA AGAATAAATA 180
GACCTNCAAN TATTAATCTT TTGTTCCCT CGTCATTGTT CTCGTTCCCT TTCTNCCTTG 240
TTTCTTTTTC TGACAATAT ATCAAGCNAT ACCAAGCATA CAATCAAAC CCAAGCTCGG 300
AATTCGGCCA NAGAGACCGT CGACGGAAGA AATTGNCTGG AAACCTTGTT ATGGTGATAT 360
ATACCGTCCN CCAAGAAAAG GGATGCTGCT ATCAGTCTTT CTAGGATCCG GGACACAGAT 420
ATTAATTATG ACCTTTGTGA CTCTATTTT CGCTTGCCTG GGAGTTTGT CACCTGCCAN 480
CCGAGGAGCG CTGATGACGT GTGCTGTGGT CCTGTGGGTG CTGCTGGGCA CCCCTGCAGG 540
CTATGTTGCT GCCAGATTCT ATAAGTCTT TGGAGGTGAG AAGTGGAAAA CAAATGTTTT 600
ATTAACATCA TTTCTTTGTC CTGGGATTGT ATTTGCTGAC TTCTTTATAA TGAATCTGAT 660
CCTCTGGTCA ACGGCCTCTT TGGCCCTCGA GACA 694

```

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 473 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

AGACTCGTCT CAGACCACTT GCAGCCTTCT CAACCCAAAC GCCGACCAAG GAAAACTCA 60
CTACCATGAG AATTGCAGTG ANTTGCTTTT GCCTCCTAGG CATCACCTGT GoCATACCAG 120
NTAAACAGGC TGATTCTGGA AGTTCTGAGG AAAAGCAGCT TTACAACAAA TACCCAGATG 180
CTGTGNCCAC ATGGCTAAAC CTTGACCCAT CTCAGAAACA GAATCTCCTA GCCCCACAGA 240
CCCTTCCAAG TAAGTCCANC GAAAGCCATG ACCACATGGA TGATATGGAT GATGAAGATG 300
ATGATGACCA TGTGGACAGC CAGGACTCCA TTGACTCGAG CGACTCTGAT GATGTAGATG 360
ACAoCTGATGA TTCTCACCAG TCTGATGAGC CTCACCATTC TGATGAATCT GATGAACCTGG 420
TCACTGATTT TCCCACGGAC CTGCCGTCGA CGGCCTCTTT GGCCCTCGAG ACA 473

```

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGAAGCTGTG ATCTTCAAGA CCATTGTGTC CAAGGAGATC TGTCTGATCC CAAGCAGAAG	60
TGGGTTTCAGG ATTCCATGGA CCACCTGGAC AAGCAACCCA AAACCTCCGAA GACGTGAACA	120
CTCACTCCAC AACCCAAGAA TCTGCAGCTA ACTTATTTTC CCCTAGCTTT CCCCAGACGT	180
CGACGCCTCT TTGCCCTCGA GACA	204

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTCCACACAC GCCGACCACG GAAAACTCAC TACCATGAGA ATTGCAGTGA TTTGCTTTTG	60
CCTCCTAGGC ATCACCCTGTG CCATACCACT TAAACAGGCT GATTCTGGAA GTTCTGAGGA	120
AAAGCAGCTT TACAACAAAT ACCCAGATGC TGTGGCCACA TGGCTAAACC CTGACCCATC	180
TCAGAAGCAG AATCTCCTAG CCCACAGAA TGCTGTGTCC TCTGAAGAAA CCAATGACTT	240
TAAACAAGAG ACCCTTCCAA GTAAGTCCAA CGAAAGCCAT GACCACATGG ATGATATGGA	300
TGATGAAGAT GATGACGACC ATGTGGACAG CCAGGACTCC ATTGACTCGA ACGACTCTGA	360
TGATGTAGAT GACACTGATG ATTCTACCA GTCTGATGAG TCTCACCATT CTGATGAATC	420
TGATGAACTG GTCACGTATT TTCCGTCGAC GGCCTCTTTG GCCCTCGAGA CA	472

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCGACTGAA AATTAACCT CAGACGCCAC ATCCCTGAC AAGATGCCAG GCAGGTTCTC	60
TTCTCTCAC ATACTGACCC ACGGGTCCAC CCTCTCTCCC CTGGAAAGGA CACCATGAGC	120
ACTGAAAGCA TGATCCGGGA CGTGGAGCTG GCCGAGGAGG NNTTNCCAA GAAGACAGGG	180
GGGGCCAGG GGTCCAGNG GNGCTTGTC CTCAGACTCT TCTCCTTCCT GATCGTGGGA	240
GGNGNACCA CGCTCTTCTG NCTGNTGNAC TTTGGAGTGG ATCCGGGCCC CAGAGGGAAG	300
AGTTCCCCCA GGGGACTCTT CTCTAATCNA GNCCTCTTGG	340

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

GTCGACGCGC GCCGGTAAAA ATGGCGAAAT GGGGGTAGGC GCGCTGGAC CTGAAGAGAT      60
GGGGCGCGCA GGTGGGGCGG TTGTCAGAGC CCCCTGACGT GGGCGCCGGG CTTTATCGG      120
CGATTGATC TGGCGACCTC GGGCCGCGC CTAAGAGGTC AGACTGCGGA GCCTGCGGGT      180
CGCCAGCGGC CCCGCCGAGT GCCGGAGGCA ATGGATGAAC AGAGCGTGA GCGCTGKCTG      240
WCAGAGCAGA GAGCTCAATG TCCTCATTCC CGTGCTCCAC TCCAGCTACG AGAACTAGTA      300
AATTGTCGTT GGGCAGAAGA AGTAACACAA CAGCTTGATA CTCTTCAACT CTGCAGTCTC      360
ACCAAACATG AAGAAAATGA AAAGGACAAA TGTGAAAATC ACCATGAAAA ACTTAGTGTA      420
TTTTGCTGGA CTTGTAAGAA GTGTATCTAC CATCAGTGTG CACTTTGGGT CGACGGCCTC      480
TTTGGCCCTC GAGACA                                     496

```

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

AGACACATAG ACCAACCGGG GAGATATGTT TGAATNTGAT GAAGATGAGA TGTTCTATGT      60
GGATCTGNAC AAGAAGGAGA CCTCTGTCAT CTGGAGGAGA NTGNCCAACC CTTTCTCTTT      120
GAGNCTCAGG GNGGGCTGTC TAACATTGCT ATANTGAACA ACAACNTGAA TACCTTGATC      180
CAGCGTTCCA ACCCACTCA GNCCACCAAC GATCCCCCTG AGGTGACCGT GTTCCCAAG      240
GTCACGGCCT CTTTGGCCCT CGAGACA                                     267

```

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 451 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

GTCGACCTTG AAGATGTTTT CTAAAGAATC AAAAATGCTA CAAAGAAGTA TATCATTTC      60
AAATATGGCT TTATCGTCTT GTTTACTTTT ACCAGGAGAT GCCACTGTCA TAACTTCTTC      120
ATGGGATAAT AATGTCTATT TTTATTCCAT AGCATTGGA AGACGCCAGG ACACGTTAAT      180
GGGACATGAT GATGCTGTTA GTAAGATCTG TTGGCATGAC AACAGGCTAT ATTCTGCATC      240
GTGGGACTCT ACAGTGAAGG TGTGGTCTGG TGTTCTGCA GAGATGCCAG GCACCAAAAG      300
ACACCACTTT GACTTGCTGG CCGAGCTGGA ACATGATGTC AGTGTAGATA CAATCAGTTT      360
AAATGCTGCA AGCACACTGT TAGTTCCGG CACCAAAGAA GGCACAGTGA ATATTTGGGA      420
CCTCACAACG GCCTCTTGG CCCTCGAGAC A                                     451

```

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTTGACGCAA GTTGCTGGGC TGGTGGGGGC CTGTCAAGTG AGGCCTGGTG GAGAAAGGTT	60
GAATTTGGAG GGCCAGGAAC AAGCTGGGAT GCAGGGGAGG CTTTCTAAAC TCTACAGTGC	120
TTCTAGAGAT GACGAGGAGG TAGGGAGTAG AAGAGAGCCG GACAGATTAG GGAGCTCCCA	180
GGGTGAGCTT GTGGGCAGSC CTSCAGAGGA GAAGAGGCTC TTCCCTAGGA GCTCAGAGGG	240
ACTTGTTCTG GAAGACTGAT GGGAGATGTA TGCAGCTGTT TAGAGGCTGC TTTGGAGAAC	300
AAATGAACAT GGTTCCTGGT GTGCAAGCAG TTACTGTGGT TCTTTTGTCT CATATATCTT	360
CCAATAAAGA CATTGAGCGA GGAGAGTTGA TACCGTCATG TTTTGGAGC TTAAGCACAG	420
ACTGGCAGGT CGACGGCCTC TTTGGCCCTC GAGACA	456

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTGCACAGAA TTCACAACAT CCCAAGATTC CACCTCNCAA GATGTTTCT AAAGNAATCA	60
AAAATGCTAC AAAGAAGTAT ATCATTTCCTA AATATGGCTT TATCGTCTTG TTTACTTTTA	120
CCAGGAGATG CCACTGTCTAT AACTTCTTCA TGGGATAATA ATGCTCTATT TATTCCATA	180
GCATTTGGAA GACGCCAGGA CACGTTAATG GGACATGATG ATGCTGTTAG TAAGGATCTG	240
TTGGCATGAC AACAGGCTAT ATTCTGCATC GTGGGACTCT ACAGTGAAGG TGCGGTCTGG	300
TGTTCCCTGC AGAGATGCCA GGCACCAAAA GACACCACTT TGGCTTGNTG GCCGAGCTGG	360
ACATGATGTC AGNGTNGGTA CAATCAAGNT TANNA	395

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGGNCCGAG ATAGAGGAGG CTTCCTCCA AGAGGACCCC GNGTTCCCG AGGGAACCCC	60
TCTNGAGGAG GAAACGTCCA GCACCGAGCT GGAGACTGGC AGTGTCCTCA TCCGGGTGT	120
GGAAACCAGA ACTTCCCCTG GAGAACAGAG TGCAACCAGT GTAAGGCCCC AAAGMCTGAA	180
GGCTTCCTCC CGCCACCTT TCCGCCCCCG GGTGGTGATC GTGRCAGAGR TGGCCCTGST	240
GGCATACGGG GAGGAAGAGR TGGCCTCATG GATCGTGGTG GTCCCGGTGG AATGTTTCTA	300
GRGGGCGTK GTGGAGACAG AGRTGKCTTC CGTGTGGCC GGGGCATGGA CCGAGGTGKC	360
TTTGGTGGAG GAAGACNAGG TGTCCCTGGG GGCCCCCTG NTCCTTTGAT GGAACAGATG	420
GGAGGAAGAA GAGGAGGACG TGGGTCGACG NCCTCTTTGT CCCTCGAGAC A	471

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTCGACCGTC TACGCCTACA CCATGTTCTT CTCCACGTTT TACCACGCCT GCGACCAGCC	60
CGGGGAGGCG GTGCTGTGCA TCCTCAGCTA CGACACGCTG CAGTACTGCG ACTTCTTGGG	120
CTCCGGGGCG GCCATCTGGG TCACCATCCT GTGCATGGCA CGGCTCAAGA CAGTCCTGAA	180
ATACGTGCTG TTTCTTCTGG GTACACTGGT CATCGCCATG TCCTTGACAGC TGGACCGCAG	240
GGGCATGTGG AACATGCTGG GGCCTGCCT CTTTGCCTTC GTGATCATGG CCTCCATGTG	300
GGCTTACCGC TCGGGGCACC GCGCCAGTG CTACCCACC TCGTGGCAGC GCTGGGCCTT	360
CTACCTCCTG CCCGGCGTCT CTACGGCCTC TTTGGCCCTC GAGACA	406

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 448 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCGCCAGC AAGTGAGCAG ATCCTCCGAG GCACCAGGNN ACTCCAGCCC ATGCCATGGC	60
GGATTCTGAG CGCCTCTCGG CTCCTGGCTG CTGGGCGGCC TGCACCAACT TCTCGCGCAC	120
TCGAAAGGGA ATCCTCCTGT TTGNTGAGAT TATATTATGC CTGGTGATCC TGATCTGCTT	180
CAGTGNCTCC ACACCAGGCT ACTCCTCCCT GTCGGTGAYT GAGATGATCC YTSCTCSCTA	240
TCTTTCCTYT GTTGTCTACA TGTGTGACCT GCACCACCAA GATACCATTG ATCAACTGSS	300
CCTGGAGTGA TTTCTTCCGA ACCCTCATAG GGGSAATCCT CTACCTGATC AMCTCCATTG	360
TKGTCTKGT TGAGAGAGGA AACCACCCCN TNAATCGTTC GTAGGGGTAC TGGGCCTAAT	420
CGCTACGGCC TCTTTGGCCC TCGAGACA	448

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTNCAATCNC CGATCCCCAT CACGAATGGG GGGCACCGGG TTACCCCCC CCTCCCGCCG	60
TAGGGTAGGC ACACNCTGAG CCAGTCAGTG TATCGCGCGT GCATCCCCG ACATCTAAGG	120
GCATCAGAGA CCTGTNTTG NTCATCTCG GGTGGNTGN CGCCACTTGT CNCTCTAAGA	180
ANATGGGGGA CGCCGNCCG TCGGGGGTNG CGTAACTAGN TAGNATNCCA GAGTCTCGTT	240
CGTTATCGGA AGTAACCAGA CANATCGCTC CNCCAATAA GANNGGCCAT NCACCACCAC	300
CCACGGAATC GAGANAGAGC TATCAATCTG TTGTAGGACA TAACCCGGCT TCTTGGTCAT	360
CATCNTGGTG TACNCGNCT CTTTGNCCCT CGAGACA	397

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TCCTGCCTGC	TGGGCCGCCT	TNCACCAAC	TTCTCGCGCA	CTCGAAAGGG	AATCCTCCTG	60
TTTGCTGAGA	TAAATANTAT	NCCTGGTGAT	CCTGATCTGC	TTCAGTGCCT	CCACACCAGA	120
CNACTCCTCC	CTGTCCGTGA	TTGAGATGAT	CCTTGCTGCT	ATTTTCTTTG	TTGTCTACAT	180
GTGTGACCTG	CACACCAAGA	TACCATTCTAT	CAACTGGCCC	TGGAGTGATT	TCTTCCGAAC	240
CCTCATAGCG	GCAATCCTCT	ACCTGATCAC	CNCCGTGTGT	GTCCTTGTG	AGAGAGGAAA	300
CCACTCCTAC	AATCGTCGCA	GGGGTACTGG	GCCTAATCGC	TACGGCCTCT	TTGGCCCTCG	360
AGACA						365

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTCGACGACA	CGCTGTCTTC	ACTACCTGAT	TGCCCAGAAG	ATCCACACTG	TCTACACTAC	60
CTGCCTGGCC	AGTAGATCCA	CGGTATCTAC	ACTACCTCCC	TGGCCAGCAG	ATTCACCCAG	120
TCTACACTAA	CCGCTTGTC	AGCAGGTCCA	CCCTGTCTAC	ACTACGTGCC	TGCCAGCAGA	180
TCCAAGCTGT	CTACACTCCC	TGCCTGGCCA	GATAGTCCAT	GCTATCTCCA	CTACCTGCCT	240
ATCCAACTGA	TCCACCCTCT	CTTTACTACC	TTCTGTCCG	GCAGATTGAC	CCTCTCTACT	300
CTACCTGCCT	GGCCAGCAGA	TCCACGCTAT	CTACACTACC	TGACTTACCA	GATCCACCCT	360
GTCTACACTA	CATGCTGTG	CAGCAGGTCC	ACCCTGTCTA	CACTACCTGC	CTCTCCAGAA	420
GATCCACGTC	AACGGCCTCT	TTGGCCCTCG	AGACA			455

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGANTTNGG	CCCAAAGAGC	CCGTTTGAGT	NAACCNAAGA	AGTCAAGATT	GGCCCNAAGT	60
TCCAGANATG	TTTTGAAGAC	CTGGAGAACT	GTTACAGTGN	AAATGAAGAA	GACAGTTCCT	120
CCATTGATCA	TCTGTCTCTG	AATCAGAAAT	CCTTCTATCA	TGTAAGCTAT	GGCCCACTCC	180
ATGAAGGCTG	CATGGATCAA	TCTGTGTCTC	TGAGNATCTC	TGAAACCTCT	AAAACATCCA	240
AGCTTACCTT	CAAGGAGAGC	ATGGTGGTAG	TANCANCCAA	CGGGAAGGTT	CTGAAGAAGA	300
GACGGTTGAG	TTTAANCCAA	TCCATCACTG	ATGATGACCT	GGAGGCCATC	GCCAATGACT	360
CAGAGGAAGA	AATCATCAAG	CCTAGGTCAT	CACCTTTTAG	CTCCCCGAGC	AATGTGAAAT	420
ACAACCTTAT	GAGGATCATC	AAATACGAAT	TCATCCTGAA	TGACGCCCTC	AATCAAAGGT	480
CGACGGCCTC	TTTGGCCCTC	GAGACA				506

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGTAACGCN GTTNTCCTNA GGCGAGCTCA GGGAGNACAA GAAACCCTCC CGTGAGCAA	60
GAANGCCACA AGCTCNCTTG ATCTTGATTA TCAGGACGAA AACAGACCGT GAAAGCGGGG	120
CCTCACGATC CTTCTGACCT NNTGGGTNTT AAGCAGGAGG TGTCAGAAAA GTTNCCACAG	180
GGATAACTGN CTTGTGNCGN CCAAGCGNTC ATAGCGACGT CGCTTTTGA TCCTTCGATG	240
TCGGCTCTTC CTATCATTGT GAAGCAGAAT TCACCAAGCG TTGGATTGTT CACCCACTAA	300
TAGGGAACGT GAGCTGGGTT TAGACCGTCG TGAGACAGGT TAGTTTTACC CTACTGATGA	360
TGTGTGTTG CCATGGTAAT CTGCTCAGT ACGAGAGGAA CCGCAGGTTC AGACATTTGG	420
TGTATGTGCT TGGCTGAGGA GCCAATGGTC GACGGCCTCT TTGGCCCTCG AGACA	475

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTTGACCCCA TGGAGGAGGA GGAGGTTGAG ACGTTOGCCT TTCAGGCAGA AATTGCCCG	60
TTGATGTCAT TGATNCATCA ATACTTTCTA CTCGANCAAA GAGATCTTTC TGAGAGAGCT	120
CATTTCAAAT TCATCAGATG CATTGGACNC AATCCGGTAT GAAAGCTTGA CAGATCCCAG	180
TAAATTAGAC TCTGGGAAAG AGCTGCATAT TAACCTTATA CCGAACAAAN AAGANCGAAC	240
TCTCACTATT GTGGATACTG GAATTGGAAT GACCAAGGCT GACTTGATCA ATAACCTTGG	300
TACTATCGCC AAGTCTGGAC CAAAGCGTTC ATGGAAGCTT TGCAGGCTGG TGCAGATATC	360
TCTATGATTG GCCAGTTCGG TGTGTTT TATTCTGCTT ATTTGGGTGC TGAGAAAGTA	420
ACTGTGATCA CCGTCGACGG CCTCTTTGGC CNGCGAGACA	460

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCAAGCAATA CCCAAGCAAA CAATCNACTC CAANCTCGGA ANTCGNCCNA AGAGACCGTC	60
GACCCCGTGT TCACNATGGT AGNNACGCCG NCTACCATCG ANAGTTGATA GGGCAGACGT	120
TCGNGTGGGT CGTCTCCCCC CCGGGGGGCG TGCGATCGCC CCGAGGTAT CTAGAGTCAC	180
CACACCCGCC GGCGCCCNCC CCCCNCNCGN NAAAAAAGA GGGGCTGTCTN GGGNTGGTTT	240
TGNTNTGATA AATANACGCA TCCCCCCCC GNNGGGGNN AGCGCCCGTC GGCATGTATT	300
ANCTCTAGAA TTACCACAGT TATCCAAGTA GGAGAGGAGC GAGCGNCCAN AGGANCCATA	360
NCTGATTAA TGAGCCATTC NCAGTTTCNC TGTTCCGNCC GTGCGTACGN AACGACCTCT	420
TTGTNCNTAA AGNCG	435

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

GTGACCACA CTGCTGCTCA CGCTCAGCAA CCTCATGTTT CTGGCCCCCA TCGCCGTCTC      60
AGTGCGGCGA TTCTTCCTGG TGGAGGCCTC CGTCTACGCC TACACCATGT TCTTCTCCAC      120
GTTCTACCAC GCCTGCGACC AGCCCGGGGA GCGGTGCTG TGCATCCTCA GCTACGACAC      180
GCTGCAGTAC TGCAGCTTCT TGGGCTCCGG GCGGCCCATC TGGGTACCA TCCTGTGCAT      240
GGCAGCGCTC AAGACAGTCC TGAAATACGT GCTGTTTCTT CTGGGTACAC TGGTCATCGC      300
CATGTCCTTG CAGCTGGACG GCAGGGGCAT GTGGAACCTG CTGGGGCCCT GCCTCTTTGC      360
CTTCGTGATG ATGGCCTCCA TGTGGGCTTA CCGCTGCGGG CACCGGCGCC AGTGCTACCC      420
CACCTCGTGG CAGCGCTGGG CTTCTACCT CCGCCCGGC GTCTCTACGG CCTCTTTGGC      480
CCTCGAGACA

```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

CGTCTCAGGC CAGTTNCANC CTTCTCANN CAGAAGCGGN CCCAAGGAAA ANCTCACTAC      60
CATGAAGAAT TGCAGTGATT TGCNTTTGCC TCCTAGGCAT CACCTGTGCC ATACCAGNTA      120
AANCAGGCTG ATTCTGGAAG TTNCTGAGGG AAAAAGCAGC TTTACAACAA ATACCCAGAT      180
GCTGTGGCCA CATGGCTAAA CCCTGANCCA TCTCAGAAGC AGAATCTCCT AGCCCCACAG      240
AATGCTGTGT CCTCTGAAGA AACCAATGAC TTAAACAAG AGACCCAAAC AAGTNAGTCC      300
NACGAAAGCC ATGACCACAT GGATGATATG GATGATGAAG ATGATGATGA CCATGTGGAC      360
AGCCAGGACT CCATTGACTC GNNCGACTCT GATGATGTAG ATGACTGA TGATTCTCAC      420
CAGTCTGACG AGTCTACCA TTCTGATGAA TCTGATGAAC TGGTCACTGA TTTCCACG      480
GACCTGCCGT CGACGGCCTC TTGACCCTC GAGACA

```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

GCCAAGACTC GTCTCAGNCC AGTTGCAGCC TTCTCANCCA AACNCCGACC CAAGGANAAC      60
TCCCCTACCA TGAGAATTGC AGTGATTTCG TTTTGCTTCC TAGGCATCAC CTGTGCCATA      120
CCAGTTAAAC AGGCTGATTC CTGGAAGTTC CTGAGGAAAA GCAGCTTTAC AACAAATACC      180

```


CAGATGCTGT GTCCACATGG CTAAACCCTG ACCCATCTCA GAAGCAGAAT CTCCTAGCCC	240
CACAGAATGC TGTGTCTCTT GAAGAAACCA ATGACTTTAA ACAAGAGANN CANCCAAGTA	300
AGTCCANCGA AAGCCATGAC CACATGGATG ATATGGATGA TGAAGATGAT GATGACCATG	360
TGGACAGCCA GGACTCCATT GACTCGANCG ACTCTGATGA TGATAGATGAC ACTGATGATT	420
CTCACCAGTC TGACGAGTCT CACCATTCTG ATGAATCTGA TGAAGTGGTC ACTGATTTTC	480
CCACGGACCT GCCGTCGACG GCCTCAATGN CCCTCGAGAC G	521

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GCAAGCAANC AATCCAACCC AAGNTNGGGA NTCGNCCNAA GAGNCCGTTG ANCAGAAGCC	60
ANTNATGGAT GANCAAGCGG ACCTTATCTC CAACAATGAG CAACTGNCCA TNCTGGGNCC	120
GGNCGCCCTG GGGCNC CGGA GAGCAAGTGC ANCCGCGGAG CCCTGTACAC AGGCTTTTCC	180
ATCCTGGTGA CTCTGCTCCT CGCTGGCCAG GCCACCACCG CCTACTTCCT GTACCAGCAG	240
CAGGNCCGGC TGGACAACT GACAGTCACC TCCCAGAACC TGCAAGTGA GAACCTGGCG	300
ATGAAGCTTC CCAAGCCTCC CAAGCCTGTG AGCAAGATGC GCATGNCCAC CCGCTGCTG	360
ATGCAGGCGC TGCCCATGGG AGCCCTGCCC CAGGGGCCCA TGCAGAATGC CACCAAGTAT	420
GGCAACATGA CAGAGGACCA TGTGATGCAC CTGCTCCAGA ATGCTGACCC CCTGAAGGTG	480
TACCGCCGT CGACGGCCTC TTTGGCCCTC GAGACA	516

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TGCTATCCNA GNATAAATA AGACCCTGCA ANTATTAATC TTNTTTGTTT CCTCGTCATT	60
GTTCTCGTTC CCTNTCTTCG TTGTTTCTNN TTCTGCACAA TATNTTCAAG CTATACCGAG	120
CATACAATCA AACTCCAAGC TCGGAATTGC NCCAAAGAGG CCGTCGAGCC GAATTCTCCA	180
CNAGAATAGC ATTTCTGCTC ATCTGCATGG TCGCAGTCAC GAGCCAGATG NCCTGNITTN	240
CCACAGTTGT AGCAGCATTG CTCTCGCTCT CTCTGGGCT CCTTGCAATG CTGGCAATG	300
TGGCCGCTC TACCGCAGTT ATAGCAGGCA TCCTCCTGAA GATCACAATC CTTGGCAAGA	360
TGACCAGACT CACCACAGCG ATAACAAATA TCTGGAAGAG ACGAGGAAAC AAAGTGGAAA	420
CCTCTATCCG AGGTAAACC ACCTCTGCCA CGGCTTCTCA TTCCACGACC ACGGCCTCTT	480
TGGCCCTCGA GACA	494

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCTCCANATN	ANCTTTNTTC	CTCTCATTGT	NTCGTCCCTC	CTCCTTGTTT	TTTNTGCCCC	60
AAAATCCANC	AAANCCAACA	ACCATCCNCN	CCACCTGGAA	GTNGCCCAAA	GAGGCCGNAC	120
CAAGAAGTGT	CGATTCCCTT	GTNTGNAGGA	GCGACCAGGA	ACATCTACGG	TTGAGAAGAA	180
AGAAAGANTG	CCTTCGTCTGA	TGTCTTCCTG	TGTGAANTTT	CCAGACATAG	CCCAGTCGAC	240
CAGCCTTCCC	CACNAGACTG	GAGCGTCTCT	ATTGTATNTG	GGTCCCTGTA	AGAGTAGAAG	300
GGTGAAAATC	CCANTGTGTC	TGAGTNTTGC	GCCNCCACCA	TAAACACCGC	CTTTTCTCG	360
AATTTCTGTA	TNCAAGAAAN	TGTCAGTCAT	CACACGTGCA	AGGATNTTAA	GACTGNCATG	420
ATCTGGGNCC	GTGTAGGGGN	CAGNTCGGAT	NCATTCACCC	ACGTAATTCA	CCGGGANGGG	480
CATCAGGAAG	TGAGTCTTCA	TCTCCCAGGG	CGTGNAGGTG	GGTNCCATGA	CCAGCTTCCT	540
AATGACCTGG	GAGCCATGGG	GAACGTGGGC	ATCTCCACCA	GAGCTACTGG	GCACAGGTTT	600
CTCGACCGTG	TGTGGNCGCA	CAGACCGTCG	ACGGCCTCTT	TGNCCCTCGA	GACA	654

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTGACCTGA	GAATCTGGAA	AAATTGGAGA	AGTTGGGTAT	GAGCTCAGAC	CTGGTGAGCA	60
GGCTGCCTAC	CATTTATAGA	AATGCACATG	ACATCAAGAA	TAAGAGCTCT	GCCCCAGCA	120
GAGTGCCTCC	TCTTTTGTG	CCACAGGGGA	CTTCTGAAAG	AAAAGACAGT	TCAGGTTCTG	180
TGTCCCCAMA	CACTCTTAGC	CAGGAGGAGG	GTGATCAGAT	CTGTTTGTC	CATATCCGGA	240
AAAGTTGTAG	CTTTCAGAT	AAGTGCCATA	GAGTTCATT	CCATTGCGC	YATCGATGGC	300
AATTCCTGGA	TAGAGGCAAA	TGGGAGGATT	TGGACNACAT	GGAACNTATT	GTAGAGNCAT	360
ATTGCAATCC	CCCCATAGAA	AGGATCCTGT	GCTCTGAGTC	AGCCAGTACC	TTTCACTCTC	420
ATTGTCTGAA	CTNTAACGCC	ATGACTTACG	GTGCTACCCA	GGCTCGCCGC	CTCTCCACGG	480
CCTCTTTGGC	CCTCGAGACA					500

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTGACACAA	ATGTTTCCTT	GGATAATCCA	GCTTTACATG	GTGAGAACCA	TGCTAGAGTC	60
CCTCATTGCA	GACAAAAGTG	GTTCCAAGAA	AACCTTGAGA	AGTAGCCTTG	AGGGGCCAC	120
CATATTGGAC	ATAGAAAAAT	TTCATCGAGA	GTCATTCTTC	TACACTCACT	TGATAAATTT	180
CAGTGAAACG	CTGCAGCAGT	GCTGTGACCT	TTCCGAGCTG	TGGTTCCGAG	AGTTCTTCCT	240
GGAGCTGACC	ATGGGCAGGA	GGATCCAGTT	CCCCATTGAG	ATGTCGATGC	CCTGGATCCT	300
GACGGACCAC	ATCCTGGAGA	CCAAGGAGGC	ATCGATGATG	GAGTACGTGC	TCTACTCCCT	360
GGACCTGTAC	AATGACAGCG	CCCACTACGC	GCTCACCAGG	TTCAACAAGC	AGTTCTCTTA	420
CGACGAAATT	GAGGCCGAGG	TCACGGCCTC	TTTGGCCCTC	GAGACA		466

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

GTCGACGGAA GTTGATTTT AATGATAAAG TACAATGAAG GGAGGGCAGA GGGGCTAAGC      60
CTAGCTGTCT GGGGTGCTGT GGTGGTGGTA GACTGGCTAC ACAAACTGTT GCTGCTGCTG      120
CTGCTTCTTG GTGGCCGCCT TGCTGGCGAG GTCCTTGGCC TTCTCTGTAG CTGCCAGTGC      180
CGTCTCCTTT GCCTTCTCCT TGGCTTCCTT GGCTGTCTCA ACAAGTGTTT TGAAGGGGC      240
CTCGCCTTGC AGCTTAGCCA AGATATATTC AAAACCCCTC ATAGTCTTGG TCACGTTGCT      300
TTTGAACCGG GCAAGACCAA ATTCCTGGAC AGCTCTGGCT ACACAACTG TTGCTGGTCA      360
ACGGCCTCTT TGGCCCTCGA GACA                                     384

```

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

GTGACGGGAC AAAAATCTAG GGAGGCACCA ATCCTGAAAG AGTTTAAGGA AGAAGGGGAA      60
GAGATACCTA GAGTAAAACC AGAGGAGATG ATGGATGAGA GACCCAAAAC AAGATCCCAG      120
GAACAGGAGG TGTTAGAGAG AGGAGGGAGA TTTACAAGAT CCCAGGAAGA GGCTAGAAAA      180
AGTCATCTGG CCAGACAGCA GCAGGAGAAG GAAATGAAAA CAACATCTCC CTTGAGGAG      240
GAAGAAAGAG AAATAAAATC TTCACAAGGC TTAAGGAAA AATCGAAGTC TCCTTCCCT      300
CCTCGACTGA CTGAAGATCG AAAGAAGGCC CCACCTGTAG CGCTGCCAGA GCAAAGTCC      360
AGCGAGGAGG AGACTCCTCC ACCTTTACTA ACAAGGAAG CATCTTCTCC ACCACCTCAT      420
CCACAGCTCC ATAGCGAAGA AGAAATAGAG CCCATGGAAG GCCCAGCCCC CCCTGTCTC      480
ATTCAGTTAT CTCCTCTTAA TACAGATGCT GACACCAGGT CGACGGCCTC TTTGGCCCTC      540
GAGACA                                     546

```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

GTCGACGTCG GTGGTGCGAG CGGCGGCGGC GCGGTTCCA GCATGAAGAG GAGAGCTGGC      60
CTGGGGGGCA GCATGAGGTC AGTGGTGGGC TTCTTGTCCT AGCGGGGCTC GCATGGGGAC      120
CCCTGCTCA CTCAGGACTT TCAGAGGAGA CRCCTGCGGG GCTGCAGAAA CCTCTACAAG      180
AAGGACCTCC TCGGCCACTT CGGCTGTGTC AATGCCATTG AATTCTCCAA CAATGGAGGC      240
CAGTGGCTGG TCTCAGGAGG AGATGACCGC CGGGTTCTGC TATGGCACAT GGAACAAGCC      300
ATCCACTCCA GGTCAAGCC CATACAGCTG AAAGGAGAGC ACCATTCCAA CATTTTTCG      360

```

CTGGCTTTCA ACAGTGGGTA CACTAAAGTG TTCTCTGGAG GCAATGATGA GCAAGTTATC	420
CTCCATGATG TTGNAAGCAG TGAGACATTG GACGTGTTTG CTCATGAAGA TGCAGTATAT	480
GACTTGCTCG TGGTCNGCGC CCTCTTTGGC CCTCGAGACA	520

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTCGACTCCA GACACACCCC CCAGTCGAGC CCTGCAGCCA AACAGAGCCT TCACAACCAG	60
CCACACAGAG CCTGCCTCAG CTGCTCGCAC AGATTACTTC AGGGCTGGAA AAGTCACACA	120
GACACACAAA ATGTCACAAT CCTGTCCCTC ACTCAACACA AACCCCAAAG CACAGAGAGC	180
CTGCCTCAGT ACACTCAAAC AACCTCAAAG CTGCATCATC ACACAATCAC ACACAAGCAC	240
AGCCCTGACA ACCCACACAC CCCAAGGCAC GCACCCACAG CCAGCCTCAG GGCCCAAGG	300
GGCACTGTCA ACACAGGGGT GTGCCAGAG GCCTACACAG AAGCAGCGTC AGTACCCTCA	360
GGATCTGAGG TCCCAACACG TGCTCGCTCA CACACACGGC CTGTTAGAAT TCACCTGTGT	420
ATCTCACGCA TATGCACACG CACAGCCCTC AACGGCCTCT TTGGCCCTCG AGACA	475

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCTGCCACAA TAATNTCCNA AGCCTAAAAC CCGAGCAATA CAANCNAACC CAAGCTCGGA	60
AATCGGGCCA AAGAGACCGT TCTTAGNTGG TGGAGCGATT TGTCTGGTTN ATTCCGATAA	120
ACGAACGAGA CTCTGGCATG CTAAGTAGTT ACGCGACCCC CGAGCGGTGCG GCGTCCCCCA	180
ACTTCTTAGA GGGACAAGTG NCGTTCANCC CACCCGAGAT TGAGCAATAA CAGGTCTGTG	240
ATGCCCTTAG ATGTCCGGGG CTGCACGCGC GCTACACTGA CTGGCTCAGC GTGTGCCTAC	300
CCTACGCCGG CAGGCGCGGG TAACCCGTTG AACCCCATTC GTGATGGGGA TCGGGGATTG	360
CAATTATTCC CCATGAACGA GGAATTCCCA GTAAGTGCGG GTCATAAGCT TCGGTTGATT	420
AAGTCCCTGT CGACGGCCTC TTTGGCCCTC GAGACA	456

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTGCCRCAA SMTYTYTMMA CTGTGGNGGG GCTCTACCCN TGAGGGCCTG GCCGCARCNT	60
------------------------------------------------------------------	----

GGCTGSGGGC	TGWCAGTAT	GAACAGRTCG	AGAAMGTGKN	CGATTACTAC	CCGGAGTACA	120
AGCTRCTCTY	CGAGGGTGCA	GGTAGGCAAC	CCTGGAGACA	TGACKCTGGA	GGGMCGATTA	180
CTTTGAGYAC	GAGGTAAARC	TGAACAAGTT	GTSCCTCCTG	ANACAGTWCC	ACCTTGGTGT	240
CTTCTATRCC	TTCGTGAAGC	TCAAGGAGCA	GGAGTGTCKC	AACATCGTGT	GGATCGCTGA	300
ATGTATCTRC	CAACGCMSS	GCRMMYCSMA	MSWCAWCCWY	ATTCTSTRTC	CTKSYAASGT	360
CWCAMTGAAN	CWAGCCCTCT	CAATTGCACT	GCACTGTGTG	TGTGTGTGTG	TGTGTTGTGC	420
GTGTGTGTG	CGTGTGTGTG	TATGTGGTCT	GTGACAAGCC	TGTGGCTCAC	CTGGTCGACG	480
GCCTCTTTGG	CCCTCGAGAC	A				501

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCNCCGTTTG	TTGTNNTGCA	CCAAANANCC	NCNAATTGNC	CANANAAAAT	TGATGGGAAG	60
ACCACTTAAA	GGGGGGGNAN	TTAGGCGGGN	CAAAGACAAG	GCACCCNACA	AGATGTCGTT	120
TGTTCCAGAG	CTGATTGAGG	GGTATCTCGG	AAGNAACACN	GAAACTTTTT	TCCTTCCTTC	180
AATTCAACGC	ACACTACTCT	CTAATGAGCN	NCGGAATACG	GCCTTCCTTC	CAGTTACTTG	240
AATNTGAAAT	AAAAAAAAGT	TTGCTGTCTT	GCTATCCAAG	TATAAATAGA	CCTGCAATTA	300
TTAATCTTTT	GTTTCCTCGT	CATTGTTCTC	GTTCCCTTTC	TTCTTGTTT	CTTTTTCTGC	360
ACAATATTTT	AAGCTATACC	AAGCATACAA	TCAACTCCAA	GCTCGGAATT	CGGCCAAAGA	420
GGCGTCGAC	GAACCACCGG	CTGAAAATTG	GCTTCTTCAA	CCAGCAGTAT	GCAGAGCAGC	480
TGCGCATGGA	GGAGACGCCC	ACTGAGTACC	TGCAGGGGGG	CTTCAACCTG	CCCTACCAGG	540
ATGCCCGCAA	GTGCCTGGGC	CGCTTTGGCC	CTCGAGACA			579

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCTGCNCCAA	NANTTCCNAA	CCNAATAACC	CAANAANACC	AATCCNNNCT	CCANCTGGGG	60
AATTCGGNCC	NAAGAGACCG	TTGTNTTGAT	GACAAGTCGA	AGCCAANAAT	ACCATNCAAC	120
CTGCTCCCAA	TCATGCAGGN	TNCNGCCACT	GCTGCCCTTG	CCGTCCCTCC	TCTGCACCAT	180
GGCTNCTCCT	GCAACCAGGT	CCTCTCTGCA	CCACTTGCTG	CTGANACGCC	GACCGCCTGC	240
TGCTTCAGCT	ACACCTCCCG	ACAGATTCCA	CAGAATTTCA	TAGCTGACTA	CTTTGAGACG	300
AGCAGCCAGT	ACTCCAAGCC	CAGTGTCTATC	TTCCTAACCA	AGAGAGGCCG	GCAGGTCTGT	360
NNTGACCCCA	GTGAGGAGTG	GGTCCAGAAA	TACGTCAAGT	ACCTGGAGCT	GAGTGCCAGA	420
GGGGTCCAGA	AGCTTCGAGG	CCCAGCGACC	TCAGTGGGCC	CAGTGGGGAG	GAGCAGGAGC	480
CTGANCTTGG	GGAACATGCG	TGTGACCTCT	ACAGCTACCT	CGTCGACGGC	CTCTTTGGCC	540
CTCGAGACA						549

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GTGACCTCC	CAGGTCATTA	GGAAGCTGGT	CATGGAACCC	ACCTTCAAGC	CCTGGCAGAT	60
GAAGACTCAC	TTCTGATGC	CCTTCCCGGT	GAATTACGTG	GGTGAATGCA	TCCGAACGTG	120
CCCCTACACG	GACCCAGATC	ATGCCAGTCT	TAAAATCCTT	GCACGTTTGA	TGACTGCCAA	180
ATTCTTGCAT	ACAGAAATTC	GTGAAAAAGG	CGGTGCTTAT	GGTGGAGGCG	CAAACTCAG	240
CCACAATGGG	ATTTTCACCC	TTTACTCTTA	CAGGGACCCA	AATACAATAG	AGACGCTCCA	300
GTCCTTTGGG	AAGGCTGTCG	ACTGGGCTAA	GTCTGGAAAA	TTACACACAGC	AAGACATCGA	360
CGAAGCCAAA	CTTTCTGTCT	TCTCAACCGT	AGATGCTCCT	GTGCTCCTT	CAGACAAAGG	420
AATGGACCAC	TTCTGTACG	GCCTCTTTGG	CCCTCGAGAC	A		461

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 511 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GTGACAATA	ATTCCACCTC	ACCAGGATAA	TACCCATCCT	TCAGCACCAA	TGCTCCACC	60
TTCTGTTGTG	ATACTGAATT	CAACTCTAAT	ACACAGCAAC	AGAAAATCAA	AACCTGAGTG	120
GTCAAGTGAT	AGTCATAACC	CTAGCACTGT	ACTGGCAAAC	CAGGCCAGTG	GTGAGCCAAA	180
CAAGATGCAG	ACTTTGACAC	AGGACCAGTC	TCAAGCCAAA	CTGGAAGACT	TCTTTGTCTA	240
CCCAGCTGAA	CAGCCCCAGA	TTGGAGAAGT	TGAAGAGTCA	AACCCATCTG	CAAAGGAAGA	300
CAGTAACCCCT	AATTCTAGTG	GAGAAGATGC	TTTCAAAGAA	ATCTTTCAAT	CCAATTCACC	360
GGAAGAATCT	GAATTGCGCG	TGCAAGCGCC	TGGGTCTCCC	CTAGTGGCTT	CCTCTTTATT	420
AGCTCCTAGC	AGTGGCCTTT	CAGTTCAAAC	TTCCACCAG	GGCTTTACTG	CAAAACAAGC	480
ACGGTCAACG	GCCTCTTTGG	CCCTCGAGAC	A			511

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

--- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTGACAGTC	CAAAGTCTCA	AGACAGTTAT	CCTGTTAGTC	CTGACCTTT	TAGTAGTCCA	60
AGTATGAGCC	CCAGCCATGG	AATGAATATC	CACAATTTAG	CATCAGGCAA	AGGAAGCACC	120
GCACATTTT	CAGGTTTTGA	AAGTTGTAGT	AATGGTGTA	TATCAAATAA	AGCACATCAA	180
TCATATTGCC	ATAGTAATAA	ACACCACTCA	TCCAACCTGA	ATGTACCAGA	ACTAAACAGT	240
ATAAATATGT	CAAGATCACA	GCAAGTTAAT	AACCTCACCA	GTAATGATGT	AGACATGGAA	300
ACAGATCACT	ACTCCAATGG	AGTTGGAGAA	ACTTCATCCA	ATGGTTTCCT	AAATGGTAGC	360
TCTAAACATG	ACCACGAAAT	GGAAGATTGT	GACACCGAAA	TGGAAGTTGA	TTCAAGTCAG	420
TTGAGACGCC	AGTTGTGTGG	AGGAAGTCAG	GCCGCGTCTA	CGGCCTCTTT	GGCCCTCGAG	480
ACA						483

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

GTCGACGAGG TGGTGATCAT GGAAGACGCC CCTGACTATT ATGCAGTGGA AGACATTTTC      60
AGCGAGATCT CAGACATTGA TGAGACAATT CATGACATCA AGATCTCTGA CTTTCATGGAG      120
ACCACCGACT ACTTCGAGAC CACTGACAAT GAGATAACTG ACATCAATGA GAACATCTGC      180
GACAGCGAGA ATCCTGACCA CAATGAGGTC CCCAACAACG AGACCACTGA TAACAACGAG      240
AGTGCTGATG ACCACGAAAC CACTGACAAC AATGAGAGTG CAGATGACAA CAACGAGAAT      300
CCTGAAGACA ATAACAAGAA CACTGATGAC AACGAAGAGA ACCCTAACAA CAACGAGAAC      360
ACTTACGGCA ACAACTTCTT CAAAGGTGGC TTCTGGGGCA GCCATGGCAA CAACCAGGAC      420
AGCAGCGACA GTGACAATGA AGCAGATGAG GCCAGTGATG ATGAAGATAA TGATGGCAAC      480
GAAGGTGACA ATGAGGTCAC GGCCTCTTTG GCCCTCGAGA CA                      522

```

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

GTCGACAGAT CATGTTGGAA GAGCCCCCAG TAGCAAAAGT GTTAGAGCCT TCAGAAACCC      60
TTGTGGTATC ATCAGAGACA CTTACTGAGG TGTACCCTGA GCCAAGCACA TCAACAACAA      120
TGATTTTCC AGAGTCATCT GCAATTGAAG CGCTAAGATT GCCAGAGCAG CCTGTAGACG      180
TACCATCGGA GATTGCAGAT TCATCCATGA CAAGACCGCA GGAGTTGCCG GAGCTGCCTA      240
AGACCACAGC GTTGGAGCTG CAGGAGTCGT CGGTGGCCTC AGCGATGGAG TTGCCGGGGC      300
CACCTGCGAC CTCCATGCCG GAGTTGCAGG GGCCCCCTGT GACTCCAGTG CTGGAGTTAC      360
CTGGGCCCTC TGCTACCCCG GTGCCAGAGT TGCCAGGGCC CCTTTCTACC CCAGTGCCTG      420
AGTTGCCAGG GCCCCCTGCG ACAGCAGTGC CTGAGTTGCC AGGGCCCTCT GTGACACCAG      480
TGCCACAGTT GTGCGAGGAA TTGCCGTCAA CGGCCTCTTT GGCCCTCGAG ACA                      533

```

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

CCACCAGACA TAAAGTACTG ACATGATCAG AGGAATCATC AGCAACTGCA TNTCCATTGC      60
TAAGCCAGTA ATCAGCATGC AAATCCAGTT AAAGAGGAGC ATGAATAAAT AGTCTGCTGG      120
CCTCCCATCA AAAGCTCCTG TTTCAAGTCG CGTAGAATAC TGATATAAGA AATATANATT      180

```

GACCAAATAA AGAAATCCAG TTCCTGGACC CACAGGGAAA TAAAAGGTGG CAGTGATTGN	240
CCTCCAAATC TGAAAGCGAT ANAGGAAGGC TTCGGGCCAG AGGAAGAGGT AGGCCGGGCT	300
GATGAGGCCG AGTTTGCCGA CCAAGGGCAC GGNACCGTG GCGGCGAACC AATAGCGCGT	360
GATCGCCGGG ATGCTCCTGA ACCAGTCTCC GATGTCCGAC ATCTTCGACC CACAGGTAGC	420
CAAGATGCAC AAGACGCCC GACTCCCCG GCGACCCCC TCACGACGCG GCCGGCTCCG	480
CGACTGTTAG GTGTCTAGGT GGAAGCCGCG TCGAC	515

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATNCNGGAGN CCCAGATGCT GTGGGCCATG ATCGCANNTT GNNTGAGAGA ATTGGCAGAA	60
NCAGANTACT CCTAGCNAGA NCAGTATNT GTGTNACTCT GGAGAATTNC AGTGATGNAA	120
AAAAANAGAC CNGTNCAAGT AAGTCCAGCG AAAAGCATGC CCACATGGAT GAANTGGATG	180
ATGAAGATGA TGCCNNCCNT GNGGNCAGCA GGAAGTCTN TNCTGCGNG NCNACTCNTG	240
NTGNTGTAGA TGANGCTGGT NAAGCNNANC AGTCTGNTGA GNCTCCTCGA GTCTGATGGA	300
TCTNATGAGC AGANCGNTGA TTCGTCNGCC GCGTNTCTCC TTNGAGCCCN CNAGACA	357

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTTGATAGATG GAGCGGGGAG NCAGACTNCT GGGNGCTGCG TGANTGCTGA CGTGAGATGG	60
ATTAATTAAT GGCNAGCAAG NATGGNGNCT NCGAGCCCT CCTGNNCGT NCCTNCCAGN	120
NGTGGCAATN GCGTACGTGG NCAGACTTCA GGNAGAAAAA AAAAAAANGG GNCNCGTAAG	180
CTGCTGCGGG NNCAGCAGCT TGAGACTGNC AAGTACTCA GATGCAGAGT CAGACTNTCG	240
GGCTAGCTCT AACAACTCCN CCGTCTCAA CACCAGCACC GAGGGCTTCG GGGACATCAT	300
GTCTTTGACC AGCAGCCTCT ATCGGAACCA CAGTACCAGC TTCAGTCTTT CAAACCTCAC	360
ACTNCCGTCG NCGGCCTCNT TGGCCTTTNG AGGCGA	396

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTGACCCCA GATGAAATGT CATGGCAAAT TTGATAAAAA CCAAGAGGGA GTGAAACTGA	60
------------------------------------------------------------------	----

CGCTGGGGGA GGAAGGGTC AAGTCGAGGG AAGGTGAAAC CAAAAGGCAC TGAGCATGCG 120
 TGGTGGGGCA GGAAGGACA CCATCACTCC AGAGACAGTA TGGTAACAAA GGGACAGGAA 180
 TGGTCCAGGC CAGCTTCAGG CTCTTCAGAA GCCAGAGAGA TGTCCAAGTC TACCAAACCG 240
 AGTTCTCCAA GGCTTTTCAA GAAATGGGAT TTGCTTGCAA GATGAATGAG GGAGGAGGTC 300
 CCATGGCTTC TAAGAGATCA ACCCAAGTCT TCCAATACTC ACTGCTAAGT CCCACCTGGG 360
 TCCCCCAGAG CCAGGAAGCT CCCTGGTGGC AGGTCCCCCT CTTGCCCTCA CGGCCTCTTT 420
 GGCCCTCGAG ACA 433

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTGCACAAA TAGTTCTGTT AAAGAATACC GAATGGAAGT TCCATCTCG TTTTCAGAAG 60
 ACATGTCAAA TATCAGGTCA CAGCATGCAG AAGAACAGTC CAACAATGGT AGATATGACG 120
 ATTGTAAAGA ATTAAAGAC CTCCACTGTT CCAAGGATTC TACCCTAGCT GAGGAAGAAT 180
 CTGGGTCCC TTCTACTTCT ATCTCTGCAG TTCTGTCTGA CTTAGCTGAC TTGAGAAGCT 240
 GTGATGGCCA AGCTTTGCCC TCCCAGGACC CTGAGGTTGC TTTATCTCTC AGTTGTGGCC 300
 GTTCCAGAGG ACTCTTTAGT CATATGCAGC AACATGACAT TTAGATACC CTGTGTAGGA 360
 CCATTGAATC TACAATCCAT GTCGTCACAA GGATATCTGG CAAAGGAAAC CAAGCTGCTT 420
 CTTGGTCAAC GGCCTCTTTG GCCCTCGAGA CA 452

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTNAAANTTA CCATCACAGT TNCTACAATC GGCTCTTTCC AATTTGGCNA CAACNCTGGG 60
 TCATCAATGC TCCTGAGAAG ATCATAAAGG AATTTATCAA TAAACTTTG TCGGACAAGG 120
 GAAATNCCCC ACCCTCTGAG GTGCTGCTCA CGTCTCTCTG TCCCTTGCT GTGACCATAT 180
 TTTCGTGGG GGGNATGATC GGCTCCTTTT CCGTCGGACT CTTCGTCAAC CGCTTTGGCA 240
 GGCGCAANNC AATGCTGATT GTCAACCTGT TGGCTGTAC TGGTGGCTGC TTTATGGGAC 300
 TGTGTAAAGT AGCTAAGTC GTTGAATGC TGATCCTGGG TCGCTTGTT ATTGGCCTCT 360
 TCTGCGGACT CTGGTCGAGC GCCTCTTTGG CCCTCGAGAC A 401

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTGAGAGCA	GCATGTTTTN	NCCACTGAAA	CTCATCCTGC	TGCCAGTGTT	ACTGGATTAT	60
TCCTTGGGCC	TGAATGACTT	GAATGTTTCC	CCGCCTGAGC	TAACAGTCCA	TGTGGGTGAT	120
TCAACTCTGA	TGGGATGTGT	TTTCCAGAGC	ACAGAAGACA	AATGTATATT	CAAGATAGAC	180
TGGACTCTGT	CACCAGGAGA	GCACGCCAAG	GACGAATATG	TGCTATACTA	TTACTCCAAT	240
CTCAGTGTGC	CTATTGGGCG	CTTCCAGAAC	CGCGTACACT	TGATGGGGGA	CATCTTATGC	300
AATGATGGCT	CTCTCCTGCT	CCAAGATGTG	CAAGAGGCTG	ACCAGGGAAC	CTATATCTGT	360
GAAATCCGCC	TCAAAGGGGA	GAGCCAGGTG	TTCAAGAAGG	CGGTGGTACC	GCATGTGCTT	420
CCAGAGGAGC	CCAAAGAGCT	CATGGTCCAT	GTGGGTGGAT	TGATTTCAGAT	GGGATGTGTT	480
TTCCAGAGCA	CAGAAGTGAA	ACACGTGACC	AAGGTAGAAT	GGATATTTTC	GTCGACGGCC	540
TCTTTGGCCC	TCGAGACA					558

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GTGGAGAAAA	TTGCTGCTGA	GAAGGACATT	TTGAAGGTTT	TGTTGGCTGA	AAAAGCTGTT	60
TCTGGAATCA	CCCCTAGATC	TTTCTTGAAG	ACTTGAATTA	GATTACAGCG	ATGGGGACAC	120
AGAAGGTCAC	CCCAGCTCTG	ATATTTGCCA	TCACAGTTGC	TACAATCGGC	TCTTTCCAAT	180
TTGGCTACAA	CCTGGGGTC	ATCAATGCTC	CTGAGAAGAT	CATAAAGGAA	TTATCAATA	240
AAACTTTGAC	GGACAAGGGA	AATGCCCCAC	CCTCTGAGGT	GCTGCTCAGC	TCTCTCTGGT	300
CCTTGCTCTGT	GGCCATATTT	TCCGTCGGGG	GTATGATCGG	CTCCTTTTCC	GTCGGACTCT	360
TCGTCAACCG	CTTTGGCAGG	CGCAANTCAA	TGCTGATTGT	CAACCTGTTG	GCTGTCACTG	420
GTGACTGCTT	TATGGGACTG	TGTAAAGTAG	CTAAGTCGGT	TGAAATGCTG	ATCCTGGGTC	480
GCTTGGTTAT	TGGCCTCTTC	TGCGGACTCT	GGTCGACGGC	CTCTTTGGCC	CTCGAGACA	539

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GTTGACCCCA	TTTTCCACCA	CCAAGCAAGC	AGAGCCTGTT	GTTTTGTCCA	AAATCAAAAC	60
ATGCACATCCA	CAGAGCAGAG	ATCTCAAAGA	TTATGCGAGA	ATGTCAGGAA	GAAAGTTTCT	120
GGAAGAGAGC	TCTGCCTTTT	TCTCTTGTA	GCATGCTTGT	CACCCAGGGA	CTAGTCTACC	180
AAGGTTATTT	GGCAGCTAAT	TCTAGATTG	GACCATTGCC	CAAAGTTGCA	CTTGCTGGTC	240
TCTTGGGATT	TGGCCTTGGA	AAGGTATCAT	ACATAGGAGT	ATGCCAGAGT	AAATTCCATT	300
TTTTTGAAGA	TCAGCTCCGT	GGGGCTGGTT	TTGGTCCGTC	GACGGCCTCT	TTGGCCCTCG	360
AGACA						365

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GTCGACCTCG	GTAAATGCCT	CAGTTCCCCT	CCCAGATGGA	GGCATCGTTG	TGAGAGTCTG	60
ATTGGGAGGG	GAATATGAAA	ATGTTTTCGG	AAGATAAAAG	TACTACACAG	ATGTGAGGTG	120
GTTTTCCTT	GGAAGAAAGT	GTCCTTAGA	TGTGTCTGGA	TGTTATGCAG	AGTGATCGTG	180
GCGTGTCAAT	CTTTCTTTTG	GGTGTTTTGC	AGCCTGAGAC	ATAAGGTAAT	TGTCAGAAAA	240
GGGAGACGTA	GAAGTGTTGA	TCTGTGGAAG	CTCACTCTTA	ACAAGAATTC	TAAGATGCAC	300
ATTTAAGTAC	TTGCCATGAC	GTGAGGTGTT	GTACACGTC	AACCTGAGA	TGCTGTCAGT	360
GTCCCAGGGG	ACTTGACATT	TATGTTACCC	AGGAATGACT	GTGTAAATGT	GCAGGTGCAG	420
GCCGGGCGCC	GTGGCTCAGT	GCCTGTAATC	CCAGCACTTT	GGGAGCCCCG	TCGACGGCCT	480
CTTTGGCCCT	CGAGACA					497

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTAGACANCA	NTAGAAAAAC	AAAAATCTCA	TAATGCAAAA	GCATCAAGTG	TTTGA CTCTG	60
AGAAGCGCCT	TGTATGCCCA	GTTACTCTCG	TTCTCCCTCA	GCTCTTGCTT	GTGCTTCTCC	120
ACCTGCCATT	CCACTTTGGC	CTGGTACTGC	CTGTAGTCTT	CCTGGCAGGC	CCCAGCTCCA	180
GTTCTTTGGA	GCAGCTGGGC	ATCCAAGAAG	AGGTCAATTG	TGTGGAAGGA	GCCCTCTCGC	240
TCCCTCCCA	GCCTCTCAAT	CACAGCCAGG	AGCTCTGCCT	GCTGCTGCCT	CTGCTCCTCC	300
ACAGAGCCCC	AGTTGTTGAA	GGCACAGTAC	CTTCTCTCAC	ACTCCCGCGC	CAGGTCTTTC	360
AGGCTGCAGT	TGTCCGTGTT	TGCTACATAG	TCATCCAGGG	CCTGGCCCCG	TCGACGGCCT	420
CTTTGGCCCT	CGAGACA					437

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CCTGCNCNAA	ANNANTCCAA	GCNAANNCCC	AAACAATCCC	AATNCCNACC	CCAAGCTNNG	60
GAGTTTCGCC	CAAAAGAGGC	CCNCGAACG	TAGATTNCAG	TGAGCCAAGA	TCGTNCCACT	120
GCACNCCAAG	CCNGGGCANC	CAAGAGCGAA	ACTCCGTCNC	CNCNNANAA	AGAGAAAATT	180
AGCCGGGCGT	GGTGGCGTTA	ATCCCANCTA	CTGTGTAGGN	TAAGGGAGGA	GAATTGCTTG	240
AACCCAGGAG	GCAGAGGTTG	CAGTGAGCTG	AGATCACGCC	ATTGCACTCC	AGCCTGGGCC	300
ACAAGAGCAA	GACTCCATCT	CCCAAAAAA	AAAAAATAG	CGTCAGAAAA	ATGTCCTTGT	360
ATGCCATTTT	CTCCATTTTA	TTGACATTTT	GCCOGACTTT	TGTCTTTGTT	TCAGGGAAAT	420
CGTGGAACAC	ATGGTCCAGC	ACTTTAAAC	ACAGATCTTT	GGGGATCGGA	AGCCCGTGTT	480
TGACGGCAGG	GTCAACGGCC	TCTTTGNCCC	TCGAGACA			518

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

AAACCAAAAC TCATGTTGCT TGNCCCCCA TCGTCGTCTC AAGTGNNGGC GANNACTTTC      60
CTGGTTGGAG CCCTCCGTCC NAACNNCTAA CACAATGTTT TTTCNCAAAC GTTCTACNAA      120
CGCCTGCGAC NAGNCCAGGG AGGGGGTGCT GTGNATCCTC AGCNACGACA CGCTGCAGTA      180
CTGCGACTTC TTGGGCTCCG GGGCGGCCAT CTGGGTCACC ATNCTGTGNA TGGCACGGCT      240
CAAGACAGTC CTGAAATACG TGCTGTTTCT TCTGGGTACA CTGGTCATCT CCATGTCCTT      300
GCAGCTGGAC CGCAGGGGCA TGTGGAACAT NCTGGGGCCC TCCCTCTTTG CCTTCGTGAT      360
CATGGCCTCC ATGTGGGCTT ACCGCTGCGG GCACCGGCGC CAGTGCTACC CCACCTCGTG      420
GCAGCGCTGG GCCTTCTACC TCCTGCCCCG CGTCTCTACG GCCTCTTTGN CCCTCGAGAC      480
A                                                                                   481

```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

GACCCCTCCAN TAATAANCCT TTTGTTTCCC TCGTCNNTGT TNGTCCGTTT CCCTTTCCTN      60
CCCTTGTTTC NNTNTCCTGC ACCAATATTT CCAANCTAAT ACCCAAGCAA NACAATCCNA      120
ACTCCAAGCT CGGGAATTCC GCCCAAAGAG ACCGTAGGCC GAAACCCACC GGANGGAACC      180
ATCTCACTGT GTGTAAACAT GACTNCCAAG CTGNCCGTGG CTCTCTTGCC AGCCTTCCTG      240
ATTTCTGCAG CTCTGTGTGA AGGTGCAGTT TTNCCAAGGA GTGCTAAAGA ACTTAGATGT      300
CAGTGCATAA AGACATACTC CAAACCTTTC CACCCCAAAT TTATCAAAGA ACTGAGAGTG      360
ATTGAGAGTG GACCACACTG CGCCAACACA GAAATTATTG TAAAGCTTTC TGATGGAAGA      420
GAGCTCTGTC TGGACCCCAA GGAAACTGG GTGCAGAGGG TTGTGGAGAA GTTNTTGAAG      480
AGGGCGTCGA CGGCCTCTTT GGCCCTCGAG ACA                                       513

```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

CAANTAATAA ANCTTTTGTT TCCTCGNCA TTGTNNTGTT TCCCCTGTCC NGCCTTGTTT      60
CCNNGTCTCT GCACCAATAT TTCAAACCN AATACCCAAG CATACAATCC NNACTCCAAG      120
CTNNGAATTC GCCCANAGAG ACCGTCGNGG GAAGAANTTG NCTGGAAACT TGTTTCATGGT      180

```

GATATATACC	GTCTCCAAG	AAANGGGATG	CTGCTATCAG	TCTTTCTAGG	AGCCGGGANA	240
CAGATATTAA	TTATGACCTT	TGTGACTCTA	TTTTTCGCTT	GCCTGGGAGT	TTTGTACCT	300
CCCANCCGAG	GAGCGTGAT	GACGTGTGCT	GTGGTCCTGT	GGGTGCTGCT	GGGCACCCCT	360
GCAGGCTATG	TTNCTGCCAG	ATTCTATAAG	TCCTTTGGAG	GTGAGAAGTG	GAACAACAAAT	420
GTTTTATTAA	CATCATTTCT	TTGTCCTGGG	ATTGTATTTG	CTGACTTCTT	TATAATGAAT	480
CTGATCCTCT	GGTCAACGGC	CTCTTTGGCC	CTCGAGACA			519

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CGGGCCCCAA	GACANGCANN	CCNACAAGAT	GTGTTGTTC	CAAGAAGCTG	ATNGAGGGGT	60
ATCTCGGAAG	CACACGGAAA	CTTTTCCTT	CCTTCAATTC	NACGCACACT	AACTCTCTAA	120
TGAGCAANCG	GTATACGGCC	TTCTTCCAG	TTACTTGNAT	GTGAAATAAA	AAAAAGTTTG	180
CTGTCTTGCT	ATCAAGTATA	AATAGACCTN	CAATTATTAA	TCTTTTGTTC	CCTCGTCATT	240
GTTCTCGTTC	CTTTTCTTCC	TTGTTTCTTT	TTCTGCACAA	TATNTCAAGC	TATACCAAGC	300
ATACAATCAA	CTCCAAGCTC	GGAATTCGGC	CNAAGAGGCC	GTCGACCGTT	CGTTATCGGA	360
ATTAACCAGA	CAATCGCTC	CACCAACTAA	GAGCGNCCAT	GCACCACCAC	CCACGGAATC	420
GAGAAAGAGC	TATCAATCTG	TTGAAGAACA	TGCCCCGGCTT	CTTGGTCATC	ATCATGGTGT	480
ACACGNCCTC	TTGNCCCTC	GAGACA				506

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTCTTGTTT	CCTTTTCCT	NCCCCAATAT	TTCCAAGCTA	ATACCCAAGC	AATACAATCC	60
NACTCCAANC	TCGGGAATTC	GGCCACAGA	GACCGNTGAC	CNTGTAAATG	AGTGAGGCAG	120
GAGTCCCGNG	GAGGTTAGTT	GTGTCAATAA	AAATGATTAA	GGATACTAGT	ATAAGAGATC	180
AGGNTCGTCC	TNTAGTGTG	TGTATGGNTA	TCATTTGTTT	TGAGGNTAGT	TTGATTAGTC	240
ATTGTTGGGT	GGTGATTAGT	CGGTTGTTGA	TGAGATATNT	GGAGGTGGGG	ATCAATAGAG	300
GGGGANATAG	AATGATCAGT	ACTCCGNCAG	GTAGGCCTAG	GATGTGGGG	GCAATGAATG	360
AAGCGAACAG	ATTTTCGTTT	ATTTTGGTTC	TCAGGGTTTG	TTATAATTTT	TTATTTTAT	420
GGNCTTTGGT	GAGGGAGGTA	GGTGGTAGTT	TGTGTTTAAT	ACAAAAAGTT	GGGTCGACGN	480
CCTCTTTGNC	CCTCGAGACA					500

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AACCGGATTC	GGNCCNAAAG	AGACCGGTTG	CCCAAACTT	TCTGCTGAGA	AGGACATTTT	60
GGAGGGGNTT	TGTTGGGCTG	AAAAAAGCT	GTTTCCTGGG	AATNNAACCC	CCNAGANCTT	120
TCTTGAAGAC	NTTGAATTAA	GATTACCAAN	CGATGGGGGA	CACAGGAAGG	TCCACCCCCA	180
NGCTCTGATA	TNTGCCATCA	CAGTTGCTAC	AATCAGCTCT	TTCCAATTTG	GCTACCAACA	240
CTGGGGTCAT	CAATGCTCCT	GAGAAGATCA	TAAAGGAATT	TATCAATAAA	ACTTTGACGG	300
ACAAGGGAAA	TGCCCCACCC	TCTGAGGTGC	TGCTCACGTC	TCTCTGGTCC	TTGTCTGTGG	360
CCATATNTTC	CGTCGGGGGN	ATGATCGGCT	CCTTTTCCGT	CGGACTCTTC	GTCAACCGCT	420
TTGGCAGGCG	CAATTCAATG	CTGATTGTCA	ACCTGTTGGC	TGCTACTGGT	GGCTGCTTTA	480
TGGGACTGTG	TAAAGTAGCT	AAGTCGGTTG	AAATGCTGAT	CCTGGGTCGG	TTGGTTATTG	540
ACCTCTTCTG	CGGGTCGACG	ACCTCTTTGG	CCCTCGAGAC	A		581

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GTCAACCTGG	GAGGCTCTCC	CCACCTTCT	TTCAATCTCT	TCTCAAACCTC	TGCTATCCTCA	60
GAGGGGCCTT	GCCTGATTGG	CCTTCTTAAA	ATGGATCTGC	CCCACCCAC	TTTGTAATTG	120
CTGTGCCCTC	TGCTTTCAGG	CGTGTCTCA	AACAGGATCT	CAACAAGGCC	TCCCCTGACC	180
ACACTTTAAA	ACTGCATGCC	CTATATATAC	CCCATCTCTC	TTATTTTAT	TTGTCTCCCT	240
AATGCTTATC	CCCAGTATAC	TCTGTTTATT	GTCTGTCTCT	CCTCACTACA	AAATAAACTC	300
CCCAAGGCCT	AGAGTTTITT	CTGTCTTGTC	CCTGCTATAT	ACCAAGTCTT	AGAACAGCGC	360
CCTGCACAGA	ATAGAGGCC	AATTCAATAT	GGATTGCTA	CCACTACATC	CTATTGTTT	420
CCTTCCCATC	ACTTTTCGAA	CACTCATCTA	TTCAGCTCTG	CTGACCTGTT	TCACATCTGG	480
ATCCTGTATA	GCAACGTCGA	CGGCCTCTTT	GGCCCTCGAG	ACA		523

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GTNGACTGAT	ACTCGAGTAC	CTGGATCAGC	GGCTGAAAGC	TGCAGAGAAC	AAGTTTGCCA	60
AGTGCCTCAT	GACCTGTCTC	AAATGCTGCT	TCTGGTGCCT	GGAGAAGTTC	ATCAAATTCC	120
TTAATAGGAA	TGCCTACATC	ATGATTGCCA	TCTACGGCAC	CAATTTCTGC	ACCTCGGCCA	180
GGAATGCCTT	CTTCCTGCTC	ATGAGAAACA	TCATCAGAGT	GGCTGTCCTG	GATAAAGTTA	240
CTGACTTCCT	CTTCCTGTTG	GGCAAACCTC	TGATCGTTGG	TAGTGTGGGG	ATCCTGGCCT	300
TCTTCTTCTT	CACCCACCGT	ATCAGGATCG	TGCAGGATAC	AGCACCACCC	CTCAATTATT	360
ACTGGGTTCC	TATACTGACG	GTGATCGTTG	GCTCCTACTT	GATTGCGTCG	ACGGCCTCTT	420
TGGCCCTCGA	GACA					434

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GAGGCCCTC AANTTCTGCC ATTTTATTTT ATTTTTTTGA NCTGGAGTNT TGCTCTGTAT	60
CCCAGGCTGG AGTGCACTGG CGCAATCTCG GCTCACTGCA AGNTCCTCCT CCCGGGTTC	120
CGCACATTCT CCTGCTTCAG CCTCCCTAGT AGCTGGGACT ACAGGAGCCC GCCACCACGN	180
CTTGTTAATT TTTTGTAT TTTTAGTAGA GACAGGNTT CACTNTNTTA GTCAGGATGG	240
TCTATTNTT CTGANGTCAT GATCCGCCCA CCTCGGCCTC CCAAAGTGCT GGGAKTACAG	300
GMGCGARCCA CCGCGCCCGG CCTATTTTTT GGKGGTTTNA WWTCTGGGTG ACTTGTGAGC	360
AGGAAGTTTT TGTTKTTTTT TTTCCANTGA AAAGATCTGG CCANAATAGT GGGNNTGTCA	420
AAGTATCTCT TTGCAGNTTT AATTGTCATT TTCCANTGA CTAAGATGAT GTTGTGCAAT	480
TTTTTCAGAN ACTGTNTGCT ATCTGTATAT CATCTCTTT TTTTTTTTC TTTTGGAAAT	540
GGATCCGGTN CGNCTCTTT GCCCTCGAG ACA	573

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GAANCCCCAT CCACTTCNCG GGAGGGGGGA GAGCGGGNG ACGGGTCTCG CTCCCTCGGC	60
CCCGGGATTC GGCGGGTGCA GNTGCCGGAT CCTTCAGCGT CTGNATCTCG GCGTCGCCCC	120
GCGTACCGTC GCCCGGCTCT CCGCCGCTCT CCCGGGGGTT CGGGGCACCT GGGTCCCACA	180
GTCTGGTCCT GCTTCACCTT CCCCTGACCT GAGTAGTCRC CATGGCACAG GTTCTCAGAG	240
GCACTGTGAC TGACTTCCTT GGATTTGATG AGCGGGCTGA TGCAGAACT CTTCGGAAGG	300
CTATGAAAGG CTTGGGCACA GATGAGGAGA GCATCCTGAC TCTGTTGACA TCCCGAAGTA	360
ATGCTCAGCG CCAGGAAATC TCTGCAGCTT TTAAGACTCT GTTTGKCAGG GATCTTCTGG	420
ATGACCTGCG GAAGTGGATC CGGTTCGGCC TCTTTGCCCC TCGAGACA	468

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAACCGGATC CACTTCGGG AAAACCTCGG ATTAGCAAGC AATAAAAACA TGACCTCACT	60
CTTCTCAAA GGAGCCCTG GTCTTCCTG TGTGACTCAG TTCTTTCCAT CTGTTGTGCC	120
CGCTGCAAGC CTCTTTCTGC GCTGACTGTG ACATCGGAAC GTGGCCTTCC TGTACCCCC	180
TCGTCGCCAC GCACTGAAGG CCACCCCCC CCACCTGGGA AACTAAGAAC TGGATATTTT	240
GCCTCATTCA CTTGTACTGT AACAAATGTAT ATAATTGGT TGGTATTTCA CTATTTAATT	300
TTTAAGAAGC CTATTTTACT AGTGTTTTAT ATGAACAAAG TACTGCAGAA GTTAAACCTG	360

TGTTGTATTT TTTCTGAGAT GTTTTGCTTT AAGAGATACT TTTTGCTCAG TTTTATATG 420
CCAGGAAGTG GATCCGGTTC GGCCTCTTTG GCCCTCGAGA CA 462

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGCCCGATNC ACTTCCGTGG NAAGAGCCTG CAATCCCNCC TACTCAGGAG GCTGAGGCAG 60
GAGAATCGCC CGAACCCGAA AGGTGGAGGT TGCAGTGAGC TGAGAATGTG CCACCGCACT 120
CCAGCCTGGG TGACAGGCGG AGACTCTCTC AAAGTAAATA AATTAAAAAA ATTTAANAAG 180
ATCATCAAAG AACAAACGAA ATTTTGTAT TTCAGTAAGT CAATTTAAAC AATAGAAGCC 240
AATTCTACCA CCAGAGGARC RMMATAAAT CTCATTATTA ATTGAGGGTG GCTTCTCTMC 300
CAGGTGRRAA ATTCTATAGR CAGGTATTTT GKTACTACT GACAGGTAAT AAGATTGTTT 360
CTWAGGTAAA GGTAACCCA GCAACACAAC ATTCTTCACT TTTGTTTAAAT GAACCTCNAN 420
ATTCATCATA TTACTIONTAT TTGCTAGCAT GCTTTTGTG GAAGTGGATC CGGTCGGCC 480
TCTTTGGCCC TCGAGACA 498

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CGASCCGGAT CCACTTCCCC CTTACGTATC ATTTGTCACA CAGGCCTCAG CCTGAAAAAA 60
AATTCAGTT TTTGTGTATT GCAGTCCCG TATGCTATTG TCAACCAACA GTTCCGTGA 120
TCCTTGTAGT CTAATGAGTT TGGATGCATC TATGTTCTA CTGGATCCAC TGTCCCGTCT 180
CGGCAGCTCT TCCTCACTGC TGCTACTCTT TTCTGGACAC TCCTTTTTTT CCATTGTGCA 240
AATGTGGTAT TTATGTCTTT ACTGTATCTT TTTTACCCAT GTGAGTTTCA GGAGCCCCAG 300
GGTGACAGAA GGAGGAGCGG AGGCTTGTG CTTGGACACT GCCAGGCTGC TCTGTGTTCT 360
GTTCTCTTG GRAAGTGGAT CCGGTTGGC CTCTTTGGCC CTCGAGACA 409

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAACCGGATC CACTTCCGAA GAGAAGGTCA GAGCGCACTG CAGGCAGCGC GGCTCTGGGA 60
AGAACTTAC GGAGCCCCTT CTTAGAGCAG GGAGGGGGCT TTCTCAGTGA AATGTTTGGT 120

TTTCTGCTGC CTCCTCTGCC CCAGGCCCCC CTCCAGGGTA CTGCCTATCC CAGATAGGTC	180
AGTGCACCAG GGACCCGGCC GCCAGCACCG CCGACCCCTC CCAGAGTGAC GCCCTTGTTT	240
ACTGACAAAG AGACCTGTCC CAGGAGTGTC CTCCACCGAG CCGGTGAGCT GTGGGTGGTT	300
TTCCTGTTAC GACGCTCAGT AGCCTGTAGC AATAACAAAC TCGTGGCTAT GAATGCAGAT	360
GCAGTGTCT CATAGAATAA CTGTTCTGTC ACTTTTACAG ACAAATCTAC GACAAAAAAA	420
AAGATCAACT TTTTTTTTCC GAACAACAAA AAAAATGAAT GATTACAATA GGAAAGGGAA	480
AAATTAAATA GCTACATATC ATTAACAAAT TAATGTTCTT CAAAAAATAC CTACAAATTT	540
CTCTGTACAT TCTTTACGCA CAGCGTAACG ATGGAAGTGG ATCCGGTTCG GCCTCTTTGG	600
CCCTCGAGAC A	611

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAACCGGATN CACTTCCCCT CCACGTAGTT GGNAGGGGAA CCAGCCAACC CGGCCATAGA	60
TCTCCCCTCG CCACCAGCCT TGGTGTCCTT TCTTGTTAAG GATCTTGATG ATGTCACCCT	120
CCTTGAGCGA CAGCTCTGAT CGGTCTCGGG CGCAGAAGTC ATAGCGGGCT TTGGGTGTGC	180
CAAATACTT TGTGCTTCCC ACTGNTGGNC TGCTGATGGT TCTCTTTTCA NGCTCCTTGA	240
AGGGGAACTG CAANGTGGTG TCCAGAGACT TGAAGCAATC CNTTAGAGAG TTCTGNTGGT	300
AAAACCTCCAC CAGNTCCGTA AGCCCCNGA AAGNCTTTT CTCTGTGATC CGGTACAGAA	360
CCTTCTTCTG TCA	373

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTTGACCGCC CACGATGATC TTGCCGCCAC GCTTGCTGGT CTTCTCCACT GACAAGGCAG	60
TGCTCAGGCC CTGCTCATGC TTCCCAGAC CCTGGCCCTC CCGGAAGCCG NACTTCTGCA	120
TGATCTTGTC CGCCACCGTG CCCCCATGT TAGCGAGGAA GGAGTTGCTA GGTCGGTTG	180
GAGATCTCGG TCTGTCTTGT TCCTCGTACA CTGGGGGAGG AATGGCTGCT TTGGAAGACT	240
GTGATCGAGG TCTTGAGTCC TCTCATAAG GAAAATCTCG GGGTAACTCT TTGTCTTTCT	300
CTACCAAGAG AGTGGGTGGG GCAATGGCAG CTCGCCCAT ACTTCTCTTC CTCCTCTCTC	360
GCTCATAATC TTCATCTTCA TCAGAATCTG GATCTGGTCT CTTTGCAAAC CCACTTGCTT	420
CATGTCTGTC TTTACGCCTT TTTCCCTTT CTCTATTTC CGTCGACGGC CTCTTTGGCC	480
CTCGAGACA	489

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GACGACTTTG	TGGGTATTAA	TTTTTGTTTA	AGTTTAAAT	AAAAGTAAAG	ATTCAATTTG	60
GATATCAGTT	GAAACCCCTT	AGTAACTCAG	TTTCTGTTAT	TCTTGTTCTC	ATTTCCTTTA	120
AATACACTTG	TTCTTGGCTT	TTGCCATTTT	GATTCTGTGA	AGTAGGCAGG	AGCAGGGATT	180
AATTTATACA	GTATTCCTGT	TCTGAACAAA	ACCAGAAAAG	TCACTGTATA	AACTTGACTT	240
AAAATAGTAT	CTTTCTCTTY	TCATGTATTT	TCATTGGGGG	GAAAAAAAT	CTCTTTAATT	300
GTAACCTGAA	TTCAAGCTGT	ACCCCTCCAT	GGTCCTACAC	TCTAGAGCTA	ATCTGGTTGG	360
GCAGAAAGGC	AGAAGGATGG	TATATTGTCC	CATTGTGCCT	ATAATGTATT	TTAAATTGGT	420
CATTCCACCT	TACCTAATGG	AAATTCTTGC	AGCTTTCCTA	GTGCTCATCA	GCGGTTTTAG	480
GAATTCACTA	ACGTCGACGG	CCTCTTTGGC	CCTCGAGACA			520

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTTGACGGCG	TGGTGGCGGG	TGCCTGTAAT	TCCAGCTACT	CAGGAGGCTG	AGGAAGGAGA	60
ATCATTTGAA	CCTGGGAAGT	GGGGGTTGCA	GTGAGCCAAA	ATCGTGCCAT	TGCACTCCAG	120
CCTGGGCAAC	AAGAGTGAAA	CTCCATCTCA	GAAAAAATAA	AAAAAATAAG	AAAAAATAAG	180
GAAGGAACCG	GTGGGGCAAG	CAGAGTTAAG	ATGCTTTGCT	AAGTTAAAAA	GTCTACTAAC	240
TACCAAAATCT	TGCTGTGGYT	TATCCAGAGC	TCTCAAAATG	CTGCCAATCT	ATTTTAAAGA	300
AGACCTAAAT	CCTCATTITG	GCTTTTAGGA	CACTAGGATT	TGCCTTCAAC	CCATGTCTCC	360
AGTCATATAT	TTTCTTACTA	TTCTTCAAAC	ATACCTTTTT	CTCTTTTCTT	CACTCTTCAT	420
TATGCTGTTT	AAATCGTCGA	CGGCCTCTTT	GGCCCTCGAG	ACA		463

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GTACAAGAAG	TGGTCCATTG	CTTTGTCTGA	AGGAGCGACA	GGAGCATCTA	CGGTTGAGAA	60
GACAGAAAGT	TTGGCTTCGT	CGATGTCTTG	CTGTGTGAAT	TTTCCAGACT	TAGCCCACTC	120
GACAGCCTTC	CCAAAAGACT	GGAGCGTCTC	TATTGTATTT	GGGTCCCTGT	AAGAGTAAAC	180
GGTGAAAATC	CCATTGTGGC	TGAGTTTTCG	GCCTCCACCA	TAAGCACCGC	CTTTTCTCTG	240
AATTTCTGTA	TGCAAGAATT	TGGCAGTCAT	CAAAACGTGA	AGGATTTTAA	GACTGGCATG	300
ATCTGGGTCC	GTGTAGGGGA	CAGTTCGGAT	GCATTACCCC	ACGTTATTCA	CCGGGAAGGG	360
CATCAGGAAG	TGAGTCTTCA	TCTGCCAGGG	CTTGAAGGTG	GGTTCCATGA	CCAGCTTCCT	420
AATGACCTGG	GAGCCATGGG	GAACGTGGGC	ATCTCCACCA	GAGCTGCTGG	GCACAGGTTT	480
CTCGACCGTG	TGTGGGCGCA	CAGGCCGTGC	ACGGCCTCTT	TGGCCCTCGA	GACA	534

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

GTCGACCAGG ACTAGATTCT GTCTCTCCAA AGTGGCCCAA GCCCTGTTCT CTGTACTAGG      60
GAAGCCAGCT GTGTCTTTTC GAGGACAGTT GGTCCAGCCA GCAGGCTCAG TTCAGATACC      120
AGACAACCAT TCCAGCACGA GGGCTCAGCG CCCTGGCCCC GCGGTCGCT CCAGTGCCTG      180
TGTGCCACC AGCACATCCA TGAGGTAGTC CAATTCGGCC TCGTCCAGCT CCGGAGCTTC      240
CTCCTTGGCC GGCCCATCCT CAGGGCCTGG TTTGAGGCC TCAGAGGCTG GTGCCCCAAG      300
TTCATTGTCA TACATAGAGG TGTCAATATC CTCAAACAGG CCCTCAAGCC CATCGTCCAG      360
TAGACAGCCA GTGGCTGGGC CCAGCAGGTC CAAGGCACCC AGGCTGGGCG CTGCTCCCCC      420
GATGCTACGG CCTCTTGGC CCTCGAGACA                                     450

```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

GTCGACGGCG GYCATGGCAA AGCAGTACGA CTCGGTGGAG TGCCCTTTT TTGTGATGAA      60
GTYTCCCAA ATACGAAGAA GCTCGCCAAG ATCGGCCAAG GCACCTTCGG GGAGGTGTTT      120
AAGGCCAGGC ACCGCAAGAC CGGCCAGAAG GTGGCTCTGA AGAAGGTGCT GATGGAAAAC      180
GAGAAGGAGG GGTTCCTCAT TACASCCTTG CCGGAGATCA GGATCCTTCA GCTTCTAAAA      240
CAGGAGAAATG TGGTCAACTT GATTGAGATT TGTCGGAACC AAAGCTTCCC CCTTATAACC      300
GCTGCAAGGG TAGTATWTTA CCTGGTGTTC GACTTCTGCG AGCATGACCT TGCTGGGCTG      360
TTGAGCAATG TTTTGGTCAA GTTACGCTG TCTGAGATNC AAGAGGGTGA TGCAGATGCT      420
GCTTAACGGC CTCTTTGGCC CTCGAGACA                                     449

```

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```

GTCGACAAAA CATGGAGTTG TTCCTTTGGC CACATATATG CGAATCTATA AGAAAGGTGA      60
TATTGTAGAC ATCAAGGGAA TGGGTACTGT TCAAAAAGGA ATGCCCCACA AGTGTTACCA      120
TGGCAAACT GGAAGAGTCT ACAATGTTAC CCAGCATGCT GTTGGCATTG TTGTAAACAA      180
ACAAGTTAAG GGCAAGATTC TTGCCAAGAG AATTAATGTG CGTATTGAGC ACATTAAGCA      240
CTCTAAGAGC CGAGATAGCT TCCTGAAACG TGTGAAGGAA AATGATCAGA AAAAGAAAGA      300
AGCCAAAGAG AAAGGTACCT GGTTTCAACT AAAGCGCCAG CCGCTCCAC CCAGAGAAGC      360
ACACTTTGTG AGAACCAATG GGAAGGAGCC TGAGCTGCTG GAACCTATTC CCTATGAATT      420

```

CATGGCACAA TAGGTGTTAA AAAAAAAAAA TAAAGGACCT CTGGGGTCAA CGGCCTCTTT 480
GGCCCTCGAG ACA 493

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 437 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GTCGACGAGG GGGTCATGGY AGGCAGGGGC AGGTGCGTCA GAGATGGAGC GCAGGTCTCTG 60
 CATGGAGAAG CTCGCGAGCC TGCGGGCCAG CGCCCCCTGA CTCTTGGTGG CAGCCTGCAC 120
 AGCAGCGGAG GCGGCAATGT TGAGGCCCGG CTTCCCGAAG CTGAGCACGG TCTCGTAGCT 180
 GCGCTCCTTG GCCTGCACGA TGTACGCGTC GATCTCCTTC TCATGGCGGG ACAGGGACGG 240
 GTGGACAAAC TTGCGGTAAA GCAGGCTGGC GCCCTTGGTG TAGGGTGAGA GCAGCCACAG 300
 CACGAAGGCC ATCTTGATCT CATAGTAGAA AGGGAACCAG GAGATAAAAA TGTCTGTAAC 360
 GATCTCTGCT GCCATGAAGA GTGCARCMMA CTATCCAGTA CATCATCCAG TGGACGGCCT 420
 CTTTGGCCCT CGAGACA 437

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTCNACCGCC CTTCTTGTCT CCTCCTCAGT NGTACACCTG TGTGGTCTCC ACCACCTCAG 60
 ACTTNCTCCG CCCCTTTTCTAG TNGGAAGAAG GNGCAGGCCC GTCTCGGGGT CCTCCACGCA 120
 CCGNTCCAGA AGTTGCCTGT ACGTGAGGTT CTCATGCGTG TTGGGGTNAA AGAAGCCCTT 180
 GGTGTCGTG CTGGGGTCCG CCGGGACGCG GRTCATCTCC TCACTGAAAT AGCCCGCTG 240
 GTAGRSCAG TCCACAGACA CGCGGTGGTT GTGYACGGG TCGATGATRC CGCCCGTGGC 300
 GATCTGGGCC TCCAGNAGGN GGATNCCGTG CTGCNGGAGA ACCAGNCCCT TCTNNATGTC 360
 CTGGAAGAGN GAGATGGTCC CCCCCGAGTA GGGGTCTCTG TANC CGGTGA CGNCCTTCTC 420
 GACAGACAGC ATCTGCTCGT GAAGCTCGGG GCCCACCAG CCCGCCTTCA CGGCCTCTTT 480
 GGCCCTCGAG ACA 493

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 571 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGACCCAC GTTAGTACGG TTGGATAGGA TATGCTCTCA TGATAACGG TCCAAGTTGG 60

AATGGTCTTC	CAGTCTCCAT	GGNATCCACA	TGCTACTGGC	GTTAGTTCCA	GATCTTGAGG	120
AAGNTATCCC	AGGACCCTGT	CGCCACAGGC	ATGNATCGT	CANTCACGCC	CAGGCAGCTG	180
ACGCGTTGT	CATGNCCAGN	CAAGACAACT	GCCCCGTCGG	GTTTGNGTGC	ATCCCAGACG	240
TTGCAGTTGA	AGTCGTCGTA	CCCAGCAAGG	AGGAGGSGSC	CGCTCTTGGW	GAAGGAGACA	300
GAGKTGATCC	CCCAGATGAT	GTTGTCTATGG	GAGTAAGTCA	TGAGCTCCYG	GTCAGCACGA	360
AGGTCAAACA	GCCTGCNGGT	GGCGTCGTCT	GAGCCAGTGC	CAAATGCATT	GCCATTTGGA	420
AAGAANCAAA	TGNCATTGAT	GTGAGACTCG	TGCCCAGTGA	AGGTCTNCCG	GCACATGCCT	480
TCTCGCACAT	CCCAGAGTTT	GTCTGAAGCA	TCACAAGCAC	CAGAGACGAA	CAGTCTGGTG	540
TCAGTCGACG	GCCTCTTTGG	CCCTCGAGAC	A			571

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 526 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTCGACGTAC	CACCAGCAAC	CATCAATCCC	GTCTCCTCCT	GCCTCCTCTC	CTGCAATCCA	60
CCCCGCCACG	ACTATCGCCA	TGGCAGCCCT	GATCGCAGAG	AACTTCCGCT	TCCTGTCACT	120
TTTCTTCAAG	AGCAAGGATG	TGATGATTTT	CAACGGCCTG	GTGGCACTGG	GCACGGTGGG	180
CAGCCAGGAG	CTGTTCTCTG	TGGTGGCCTT	CCACTGCCCC	TGCTCGCCCG	CCCCGAACTA	240
CCTGTACGGG	CTGGGCGCCA	TCGGCGTGCC	CGCCCTGGTG	CTCTTCATCA	TTGGCATCAT	300
CCTCAACAAC	CACACCTGGA	ACCTCGTGCC	CGAGTGCCAG	CACCGGAGGA	CCAAGAACTG	360
CTCCGCGGCC	CCCACCTTCC	TCCTTCTAAG	CTCCATCCTG	GGACGTGCGG	CTGTGGCCCC	420
TGTCACCTGG	TCTGTCACT	CCCTGCTGCG	TGGTGAGGCT	TATGTCTGTG	CTCTCAGTGA	480
GTTCGTGGAC	CCTTCCTCAC	TCACGGCCTC	TTTGGCCCTC	GAGACA		526

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTTGACTTTG	TGGGTATTAA	TTTTTGTTTA	AGTTTAAAT	AAAAGTAAAG	ATTCAATTTG	60
GATATCAGTT	GAAACCCCTT	AGTAACTCAG	TTTCTGTTAT	TCTTGTTCTC	ATTTCCCTTA	120
AATACACTTG	TTCTTGGCTT	TTGCCATTTT	GATTCTGTGA	AGTAGGCAGG	AGCAGGGATT	180
AAATTTATACA	GTATTCCTGT	TCTGAACAAA	ACCAGAAAAG	TCACTGTATA	AACTTGACTT	240
AAAATAGTAT	CTTTCTCTTT	TCATGTATTT	TCATTTGGGG	GAAAAAAAT	CTCTTTAATT	300
GTAACCTGAA	TTCAAGCTGT	ACCCCTCCAT	GGTCCTACAC	TCTAGAGCTA	ATCTGGTTGG	360
GCAGAAAGGC	AGAAGGATGG	TATATTGTCC	CATTGTGCCT	ATAATGTATT	TTAAATTGGT	420
CATTCCACCT	TACCTAATGG	AAATTCCTGC	AGCTTTCCTA	GTGCTCATCA	GCGGTTTTAG	480
GAATCACTA	ACGTCGACGG	CCTCTTTGGC	CCTCGAGACA			520

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

GAATTCGGCC AAAGAGGCCG TTGACGGGGC TGGAGGAGGA AGAAGAGGTG GATCCCCGGA    60
TCCAGGGAGA ACTGGAGAAG TTAAATCAGT CCACGGATGA TATCAACAGA CGGGAGACTG    120
AACTTGAGGA TGCTCGTCAG AAGTTCGGCT CTGTTCTGGT TGAAGCAACG GTGAAACTGG    180
ATGAAGTGGT GAAGAAAATT GGCAAAGCTG TGAAGACTC CAAGCCCTAC TGGGATGCAC    240
GGAGGGTGGC GAGGCAGGCT CAGCTGGAAG CTCAGAAAGC CACGCAGGAC CTCCAGAGGG    300
CCACAGAGGT GCTCCGCGCC GCCAAGGAGA CCATCTCCCT GGCCGAGCAG CGGCTGCTGG    360
AGGATGACAA GCGGCAGTTC GACTCCGCTT GGCAGGAGAT GCTGAATCTC GCCACTCAGA    420
GGGTATGGA GCGGAGCAG ACCAAGACCA GGAGCGAGCT GGTGCATAAG GAGGTCGACG    480
GCCTCTTTGG CCCTCGAGAC A

```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

GTCGACCGTG TCCAGAGCCC ACCTCCCTCA CACCCACACA GCGCTTCCTA AAGGCAGGGA    60
CAGGAGCTGG CCTCCCTCGC CTGCTGGCAT GGGGCTGGAC ACAGGAGGAA GTGGCGTGGG    120
GGCTGCCTGA GGGGAGTGAG GCGGCAGGAT AGCTTCCCCA GCAGGTCTCT GGCTCAGGTC    180
CAGGTATCTC CTCCTCCCCA TACCTCTGCC TCTCGCCTCC GCTCAGAAAA GCAGGTGCCC    240
TTAAGAGCCA TCTCCACCCC CATGTAAACT GCACACAGGA AGGGAGAGGC CACTCCGACT    300
GCTCTGAGGT CCAGGTAGGA TGGTTTCCCC CAGTGTCTGG GTGGGGAGCA AGGAACTCCA    360
GGGGCGACCT TGTGCCACCG CATCACCTTC CTGCTCAGGG AAGGGGCCCG TGCTGCCGCT    420
TGGAGGGTGC CATGCCAGA GCCTCTGCCC CTAGCCTCAG CCTCGCCTAC TCACTGGGGG    480
CTCCAGCACC CCCGGCCGTC AACGGCCTCT TTGGCCCTCG AGACA

```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

GTCGACGCGA GTGGAGACCT GTGGTAGAGA AGCTCCTTTT GATGTCCTAC AGGCTTTCCA    60
CTGTGGTGTC TCCAGTCATT CAGAGCTCAT CCCCTGAAGG CCTCATCCCA ATGGACACTG    120
ATTGAGAGTC AGCAASCCGC TTACAGATGA TTCTGAATGA GATTCANCT CGAGATACTA    180
ATGATTATTT TAACCAAGCC AAAATATTGA AAGAACATGA TAGCTTTGAT ATGAAGGACT    240
TGAATGCTAG TGTGGTGAAT ATTGATACTT CTACAGAAAT CAAAGGTAAA GAAGTAAAAA    300
CATGTGATGT AACTGCGCAG ATGGTGCTGG TATGTTGTTG GAGAAGTATG AAGGAAGTTG    360
CTTTACTTTT AGGCATGTTG TGCCAGCTTC TGCCCATGTC AACGGCCTCT TTGGCCCTCG    420
AGACA

```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

GGGACGTAAT CAACCCAAGC TTATGACCCG CACTTACTGG GAANTCNTCG TTCATGGGGA      60
AGAANTGCAA TCCCCGATCC GCCATCACGA ATGGGGGGCA CCGGGTTANC CGCGCCTCCC      120
GGCGTAGGGT AGNCACACNC TGANNACAGC AGTGTATCGC GCGTGCATCN CCGGACATCT      180
AAGGGCATCA CAGACCTGTT NTTGNTCAAT CTCGGGTGGN TGNNGCCAC TTGTCNCTCT      240
AAGAANATGG GGGACGCCGC CCNCTCGGGG GTNGCGTAAC TAGNTAGNAT NCCAGAGTCT      300
CGTTCGTTAT CGGAAGTAAC CAGACANATC GCTCCCCCAN CTAAGANNGG CCATNCACCA      360
CCACCCACGG AATCGAGANA GAGCTATCAA TCTGTTGTTA GGACATGCCC GGCTTGCTTG      420
GTCATCATCT TGGGTACNC GACCTCTTTG NCCCTCGAGA CA                          462

```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

GTCGACAGAA ATCATTATTC TTTATTTGCA GNCATTCCAC CCCACCTATG TTTTCTTCTC      60
CTTCCTTCTT CTCTGTCAGG AGAGTTCTTG TCATGCTGAG CTTCTTCATT GTATGGCATT      120
TATATTTTAG CACTGTTTAA TTATTGCCCT CTGTATCAGC ATGTTCAACA TTTTCTTCAA      180
ATATAACACA GGTCCCTAGA GTGTCTTCAT ACTCCCCAGC AAAGACACAG CTGTCCACTT      240
GCAGAATGGG CCTCTCAGTG TCAATGCCCA AAACCTTGCA TTTATTTTCA CATTTTGAGA      300
GGAAGTCTGA ATCAATAATT CCTGATAATT CCACCAGAAC CAACTGCTCC TCCTCTTCCT      360
CGTCTTCTCC GTCCTCTGGA CTCCGCTCGT CCGCCGCCGC CGCCATGGTC CCGCGGGGGT      420
TGACGGCCTC TTTGGCCCTC GAGACA                          446

```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

GANTTCCAGT GAAGTTGCCT TTTTGCCNNC CCTAGNCATC CAACCTNTCN AAAACCAAGT      60
ANACNAGGCT GATTCTGGAA GTTCTTGAGG AAAAAGCAAG CTTTACAACC AAAATACCCA      120
GATGCTGTGN CCACATGGCT AAACCCTTGA CCCATCTCAG AAGCAGAATC TCCTANCCCC      180
ACAGAGTGCT GTGTCCTCTG AAGAAACCAA TGACTTTAAA CAAGAGACCC TNCCAAGTAA      240
GTCCANCGAA AGCCATGACC ACATGGATGA TATGGATGAT GAAGATGATG ATGACCATGT      300

```

GGACAGCCAG GACTCCATTG ACTCGANCGA CTCTGATGAT GTAGATGACA CTGATGATTG	360
TCACCACTCT GATGAGTCTC ACCATTCTGA TGAATCTGAT GAACCGGTCA CTGATTTTCC	420
CACGGACCTG CCANCAACGT CGACGNCCTC TTTGNCCTC GAGACA	466

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTGACAGCG ACCGCTCCTC CCTTCCTTCC TTGAATCAGA GCACGGTAGA AAGCTGCTGC	60
TCTATGCCGA AGTGTTCCGA AATTCTTGGC AGCTGCATAG ACCGCGGGGC TGTCCTTAA	120
CCTTTGCTCT TGTCGCCTCC TCCACCAGGA GGGCCCCCT CCCTGTACCC CAGCTTCCCA	180
CAGAGCTGCA GGCACAGCTT GGCTGCCTCC CGCTTCCAGA CCCCTATCTC CATCAGGTGG	240
GCCTGAGGCG GGGCTGACTC TTTCTTTAGG CCCCTCACAG GGACTAGAGC AGAATGGCAC	300
TCAGTAAGCA GGGGTGACAA CTAGAGGAAT GGCAGGGTGT GTTCAGCTGG GAGAACAGTT	360
ACCAGAGACG CTGTGATTCT TCAGGTGTGA GGGCAACTGT TACAAGACTT AAGTAGCAAC	420
AACAACCATG GTAGACGCTG CCTTCGATTG TGCCCTTGGG AGTCCCAGGC CTGGCACCAG	480
GCCCTACTCA TCCTTCATTT CTTTTCTTT TCTTTTGT TTGTTTTTT GGGTTTTTTG	540
GTCAACGGCC TCTTTGGCCC TCGAGACA	568

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATTCANTTT GGATATCAAG TTGNCNCCCC CNTAGTAACT CAGTTTCTGT TATTCTTGT	60
CTCANTTCC CNATAAAAAC ACTTGTTTCGT GGCNTTTGCC ANNTTGATTG TGTGAAGTAG	120
GCAGGAGCAG GGATTAATTN ATANAGTATT CCTGTTCTGA NCGCAACCAG AAAAGTCACT	180
GTATAAACTT GACTTAAAT AGTATCTNTC TCTTTTCATG TATANTCAGG TGGGGGGGNA	240
AAAATCTCTT TAATTGTAAC CTGAANTCAA GCTGTACCCC NCCATGGTCC TACACTCTAG	300
AGCTAATCTG GNTGGGCAGA AAGGCAGAAG GATGGTATAT TGTCCCATTG TGCCTATAAT	360
GTATNTTAAA NTGGTCATTC CACCTTACCT AATGGAAATT CTTGCAGCTT TCCTAGTGCT	420
CATCAGCGGT TTTAGGAAGT CACTAACGTC GACGCGCTCT TTGGCCCTCG AGACA	475

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CCTGAGTTGT GTCTAAGGNN CNCAAGACAA GTACCCAAGT TTCCTCTAGN TTTCTCTTT	60
AAGCTTCTCN AGTCATACAT TTNCAAGCGT CCTTTTGTC ACCATNCCAG TCNANATACA	120
TTATTTGTCC TCCAATGGNT GACTTGCCAG CATCTACGTG NCCAATGAAT ACTACATTTA	180
CATGCTCTTT CTAGGAGCA CCTGGCGGTG CAACCACAGA CTTAGGTNTT GGGATTTCCT	240
CTTCCTCCTC CATCATTTC TGGGCACTTT TCTCTGGCGG CCTTCCATCT CCAAGGAAC	300
CACCCCTGG CTCTGCTTCA CTTATTCTT CTTTGTGCTC CCATGATTCT TCTGGAGACA	360
TTTCTGTCTC TCCACTTCT ACAATAGGTT CTGAAAGTTC CATGCTAACA GCTGAATTTG	420
AACCTTCACA CAATGACTGT TCGTCGACGG CCTCTTGGC CCTCGAGACA	470

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAATTTCGGCC AAAGAGGCCT ACTCACAGTC ATCAATTATA GACCCACAA CATGCGCCCT	60
GAAGACAGAA TGTTCATAT CAGAGCTGTG ATCTTGAGAG CCTCTCCTT GGCTTTCCTG	120
CTGAGTCTCC GAGGAGCTGG GGCCATCAAG GCGGACCATG TGTCAACTTA TGCCGCGTTT	180
GTACAGACCC ATAGACCAAC AGGGGAGTTT ATGTTTGAAT TTGATGAAGA TGAGCAGTTC	240
TATGTGGATC TGGATAAAAA GGAGACCGTC TGGCATCTGG AGGAGTTTGG CCGAGCCTTT	300
TCCTTTGAGG CTCAGGGCGG GCTGGCTAAC ATTGCTATAT TGAACAACA CTTGAATACC	360
TTGATCCAGC GTTCCAACCA CACTCAGGCC GTCGAG	396

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GAATTTCGGCC AAAGAGGCCT ACCCGATTGC TAAATGGATT ATGAAAGCAA ATTGCTACTG	60
GGAGGTGATG GTCAAAAGCA AACTTAGATG GTTTTCACAC CATCTGTCAT CATGACTCAA	120
AGGGAAATGC TAGCCACACC ATTTTCCAGT GAAGCCACTG CTTTACACAG TAGATACACA	180
TAGCTTCCTA TTGTTATTTT CTTTCTAAT TATGTACATT TAGAAAAAA ATACAACACT	240
GTGTTAAACA GCAGGACAGC TAGCAATGGA ACATACAACA CTATGCTGAA AAACCACAAC	300
AGCTTGTTA AGCGGAGGAG AGAAACAGAG ATGGCCTTCA TGGAGTGAAG CTGTCAATGC	360
CTGCCATCTC CTTAGTCTGT GACGGATCTG CACTCTGAGG GCAGGCCTTC TGAGCGCCGC	420
CACTTTGCCA GGCGTGCTT AAACCATTTC TGGGTCTCCT CCTCGGAAAG GCCTGCCTCG	480
GCCGCGATGA GGCACAGCGT GGTGAATCC GGTGCTTGT CGAG	524

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GAATTCGGCC AAAGAGGCCT ATTTT TTTT TCTTTT TTA GGCATATGTA GTAATATTAG	60
AAACATTTAA TTTGGGAAAC TTTGATTCTT GAAAGAGAAA ACAAAGCAT GTGAATAAAC	120
TTTGAAGTGT TCACCTCAGT TTGGGACCAA ACTGCTTGGA TCTTTGTAAA AACCGGTTTT	180
GTATGTCAAG GAGGAGTTTA AGGCCTTTCC GACCACCTTG TGTCCCTT TTCTGCGCAG	240
CCATGTATCA CGTGGAGTTG CTCCTTACCA CACCTCACGT GCCCCTGAGC CCTATTTCTT	300
GATTCTTCT GGGCTGGACT TCCCCTTCT CCACCAGCAG CTCCAGTATC CCTGTTGAAT	360
TCTAGACCTG CGTCGAG	377

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAATTCGGCC AAAGAGGCCT AGCGGACAAG TTTGAGAGAC CTGGCCTTGG CCAAAGCCCT	60
CGATTCGCTG TGTCAGAAAA ACTGAGGTGA GAAGAGACCA CCACCCTCTC CACCACCCTC	120
TCAGTAGGAA AGCGGGATCA ACAGAGATCA GAAGGACAGC AACTCACAC CTGCACATGA	180
ACACACCATC TATGTCAGGA AATCCAGGGG AAGGGGAAGA GGGGTGGAGT GGCTCCGAG	240
GGCTGACCTG ACAGGGGACA GGAACACTCC CCTAGACCCA GGGAAGTCGC CCCAAATCCA	300
AAGCTCTGA AAGGAGGTAT GGCCTCGAAA CTCCAGAAGC CTCTTCTGCC AACGCACCGA	360
GGACCTGCAC CTCCATTCA GCACGCGTCG AG	392

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CAATTCGGCC AAAGAGGCCT ACAGCATTTT TACTCCTTCC AAGAAGAGCA GCAAAGCTGA	60
AGTAGCAGCA GCAGACCAG CAGCAACAGC AAAAAACAAA CATGAGTGTG AAGGCGATGG	120
CTATAGCCTT GGCTGTGATA TTGTGTGCTA CAGTTGTTCA AGGCTTCCCC ATGTTCAAAA	180
GAGGACGCTG TCTTTGCATA GGCCCTGGGG TAAAAGCAGT GAAAGTGGCA GATATTGAGA	240
AAGCTCCAT AATGTACCCA AGTAACAAC GTGACAAAAT AGAAGTGATT ATTACCCTGA	300
AAGAAAATAA AGGACAACGA TGCCTAAATC CCAAAGTCGA G	341

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GAATTCGGCC AAAGAGGCCT AGCAGTAGCA TGTGCAGCAA CCAATCAAGA TGGAGAACTA	60
TACCTGCACT CATTTGTGTG TTTGCATGTA TAGTTCTCTG CAGTAGCATG TGCAGCAACC	120
AATCAAGATG GAGAACTGTT CCATCGCAAA GCTCCCTCTT GCCACTTCTT TTTAGCCACC	180
CAATCCTCTC TGCTCCCGTC GAG	203

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAATTCGGCC AAAGAGGCCT ATGAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC	60
TTTGGACCTG ATCAGCTTGA TACAAGAACT ACTGATTTC AACTCTTTGG CTTAATTCTC	120
TCGGAAACGA TGAAATATAC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTTGGGT	180
TCTCTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAATAT	240
TTTAATGCAG GTCATTGAGA TGTAGCGGAT AATGGAACTC TTTCTTAGG CATTTTGAAG	300
AATTGGAAAG AGGAGAGTGA CAGAAAATA ATGCAGAGCC AAATTGTCTC CTTTACTTTC	360
AAACTTTTTA AAAACTTTAA AGATGACCAG AGCATCCAAA AGAGTGTGGA GACCATCAAG	420
GAAGACATGA ATGTCAAGTT TTTCAATAGC AACAAAAGA AACGAGATGA CTTGAAAAG	480
CTGACTAATT ATTCGGTAAC TGACTTGAAT GTCCAACGCA AAGCAATACA TGAATCATC	540
CAAGTGATGG CTGAACTGTC GCCAGCAGCT AAAACAGGGG TCGAG	585

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 361 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCGGCC AAAGAGGCCT ACTGGCGGCC GCGGAGACGC AGAGTCTTGA GCAGCGCGGC	60
AGGCACCATG TTCCTGACTG CGCTCCTCTG GCGCGGCCGC ATTCCCGGCC GTCAGTGGAT	120
CGGGAAGCAC CGGCGGCCGC GGTTCGTGTC GTTGCCCGCC AAGCAGAACA TGATCCGCCN	180
CCTGGAGATC GAGGCGGAGA ACCATTACTG GCTGAGCATG CCCTACATGA CCCGGGAGCA	240
GGAGCGCGGC CACGCCGCGG TGCGCAGGAG GGAGGCCCTT GAGGCCATAA AGGCGGCCGC	300
CACCTCCAAG TTCCCCCGC ATAGATTCAT TCGGACCAG CTCGACCATC TCAATGTGCA	360
G	361

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```

GAATTCGGCC AAAGAGGCCT AAACAAAATG GTTATCAACC ACTTGGAGAA GTTGTTTGTG      60
ACAAACGATG CAGCAACTAT TTAAAGAGAA CTAGAAGTAC AGCATCCTGC TGCAAAAATG      120
ATTGTAATGG CTTCTCATAT GCAAGAGCAA GAAGTTGGAG ATGGCACAAA CTTTGTCTCTG      180
GTATTTGCTG GAGCTCTCCT GGAATTAGCT GAAGAACTTC TGAGGATTGG CCTGTCAGTT      240
TCAGAGGTCA TAGAAGGTTA TGAAATAGCC TGCAGAAAAG CTCATGAGAT TCTTCCTAAT      300
TTGGTATGTT GTTCTGCAAA AAACCTTCGA GATATTGATG AAGTCTCATC TCTACTTCGT      360
ACCTCCATAA TGAGTAAACA ATATGGTAAT GAAGTATTTC TGGCCAAGCT TATTGCTCAG      420
GCATGTCGAG                                     430

```

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```

GAATTCGGCC AAAGAGGCCT AGAAGAAGAT GATCCTAAAC AAAGCTCTGA TGCTGGGGGC      60
CCTCGCCCTG ACCACCGTGA TGAGCCCTTG TGGAGGTGAA GACATTGTGG CTGACCAAGT      120
TGCTCTTAC GGTGTAACT TGTACCACTC TTACGGTCCC TCTGGCCAGT TCACCCATGA      180
ATTGTATGGA GACGAGGAGT TCTATGTGGA CCTGGAGAGG AAGGAGACTG TCTGGAAGTT      240
GCCTCTGTTC CACAGACTTA GATTTGACCC GCAATTTGCA CTGACAAACA TCGCTGTGCT      300
AAAACATAAC TTGAACATCC TGATTAAACG TCCTCACTCT ACCGCTGCTA CCAATGAGGT      360
TCCTGAGGTC GAG                                     373

```

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```

GAATTCGGCC AAAGAGGCCT ACTTAACCAG AATGACAGTC TTCCCTAT CTTCCTCTT      60
TATTCITATC TTCTATCTTT CCTCCCAA CTCTTTCCCC GACATAACAG AAAACATGAA      120
GGAATTAAAG GAGGCCAGGC CGCGCAAAGA TAACAGGCGT CCAGATCTGG AAATCTATAA      180
GCCTGGCCTT TCTCGGCTAA GGAACAAGCC CAAATCAAG GAACCCCTG GGAGTGAGGA      240
ATTCAAAGAT GAAATTGTTA ATGACCGAGA TTGCTCTGCT GTTGAAAATG GTACACAGCC      300
CGTCGAG                                     307

```

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GGAGCTGCAC ATGGTACTTT TGGAGAGCCT GGTGGAATC ATTTTGGTTG CTGTTTCAGCA	60
TGTGGATTAT AGTCTTCGAT GTGAGCAGGA TCCAGAGAAG AAAGCTTTTA TCAGACAGAA	120
TGCATCCTTT TTATATGAAA CAGTCCTCCC TGTGGTGGAG AAAAGGTTTG AAGAAGGTGT	180
GGGGAAACCT GCCAAGCAAC TCCAAGATCT GAGGAATGCA TCTAGACTTA TTCGTGTGAA	240
TCCTGAAGTC GAG	253

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAATTCGGCC AAAGAGGCCT ACACATATTG GAAAAATGAT CTTTTGGAG CACTGTTCTG	60
CTGCTTAGAC CCAGTACTCA CTATTGCTGC TAGTCTCAGT TTCAAAGATC CCATTTGTCA	120
TTCCACTGGG AAAAGAAAAG ATTGCAGATG CAAGAAGAAA GGAATTGGCA AAGGATACTA	180
GAAGTGATCA CTTAACAGTT GTGAATGCGT TTGAGGGCTG GGAAGAGGCT AGGCGACGTG	240
GTTTCAGATA CGAAAAGGAC TATTGCTGGG AATATTTTCT GTCTTCAAC ACACTGCAGA	300
TGCTGCATAA CATGAAAGGA CAGTTTGCTG AGCATCTTCT TGGAGCTGGA TTTGTAAGCA	360
GTAGAAATCC TAAAGATCCA GAATCTAATA TAAATTCAGA TAATGAGAAG ATAATTAAAG	420
CTGTCGAG	428

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GAATTCGGCC AAAGAGGCCT ACAAGACGTC ATTTACAAAA GTGCGCCATT CTGAGGATAT	60
GCAGTTTGCC TTCTCTTATT TTTATTATCT CATGAGTGCA GTGCAGCCAC TGAATATATC	120
TCAAGTCTTT GATGAAGTTG ATACAGATCA ATCTGGTGTC TTGTCTGACA GAGAAATCCG	180
AACACTGGCT ACCAGAATTC ACGAACTGCC GTTAAGTTTG CAGGATTGGA CAGGTCTGGA	240
ACACATGCTA ATAAATTGCT CAAAAATGCT TCCTGCTGAT ATCACGCAGC TAAATAATAT	300
TCCACCAACT CAGGAATCCT ACTATGATCC CAACCTGCCA CCGGTCACTA AAAGTCTAGT	360
AACAACTGT AAACCACTAA CTGACAAAAT CCACAAAGCA TATAAGGACA AAAACAAATA	420
TAGGTTTGAA ATCATGGGAG AAGAAGAAAT CGCTTTTAAA ATGATTGTA CCAACGTTTC	480
TCATGTGGTT GGCCAGTTGG ATGACATAAG AAAAAACCCT GTCGAG	526

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GGGTGGCAAT ATGGACTTCC TCTTTTCTGC CANCCCANAC CCATACATCG GGATTCCTAT	60
AATACCTTCG TTGGTCTCCC TAACATGTAG GTGGNGGNGG GGAGATATAC AATAGAACAG	120
ATACCAGACA AGACATAATG GGCTAAACAA GACTACACCA ATTACACTGC CTCATTGATG	180
GTGGNACATA ACGAGCTAAT ACTGTAGCCC TAGACTTGAT AGCCATCATC ATATCGAAGT	240
TTCCTACCC TTTTCCATT TGCCATCTAT TGAAGTAATA ATAGCGCAT GCAACTTCTT	300
TTCTTTTTT TTCTTTTCTC TCTCCCCGT TGTGTGCGAG	340

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAATTCGGCC AAAGAGGCCT ACGTCCTTTT AAATCTTAAT GAAATATCAT GGAATATTGT	60
ATGGTCTTCA TATCGTTCTA TATAATGCAA ATGGTGAACT GCTCTGTTCT TTGCTTTCCT	120
GAAAGCATCC ATCCGATCAG TAGCTTTCCC AATAGAAAAA CCTGCAGCTC CTTTCCGTT	180
CCCCACAGCC ACCAAGACAC GGATCGATTT CTTTCTTCCC TCTTTCGCAG TCATAGTGAA	240
AACGTTTCTT ACCTCAAGTA TCCTGGTATC AAAATCCTCA TATGTTTCTC CACAGTCGAG	300

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTCGGCC AAAGAGGCCT ACCAGCTTGT AGGTTGACCT GTTCTCTTT GTCTGCCTTC	60
CCAAACACC AGCCCCCAGG AAGACATTAA GCAGCCTTAA GCTTAAATTC CTACTCCCTC	120
TTCCAAATTT GGCTCACTTG CCTTAGATCC AAGGCAGGGA AAGGAAAAGA AGGGGGGTCT	180
CTGGCTTTAT TACTCCCTA AGTCTTIACT CTGACTTCCC CAAACCCAGA AAGATTTTCT	240
CCACAGTGTT CATTTGAAAG AGGAGTATTT TGTCCCATTT TCCCCTTCCT CATTATCAAA	300
CAGCCCCAGT CTTCTTGTC TCTGCTAAGA AAGTAGAGGC ATGATGATCT GCCTCTCAAC	360
TGCCCTAGTC GAG	373

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```

GAATTCGGCC AAAGAGGCCT ACGCAGATAC GGGCTTACAG ATACTTTTTA CACTCTTACA      60
AAATGTTGCA CAAGAAGAAG CTGCAGCTCA GAGTTTTTAT CAAACTTATT TTTGTGATAT      120
TCTCCAGCAT ATCTTTTCTG TTGTGACAGA CACTTCACAT ACTGCTGGTT TAACAATGCA      180
TGCATCAATT CTTGCATATA TGTTTAATTT GGTGGAAGAA GGAAAAATAA GTACATCATT      240
AAATCCTGGA AATCCAGTTA ACAACCAAAT CTTTCTTCAG AAATATGTGG CTAATCTCCT      300
TAAGTCGGCC TTCCCTCACC TACAAGATGC TCAAGTAAAG CTCTTGTGTA CAGGGCTTTT      360
CAGCTTAAAT CAAGATATTC CTGCTTTCAA GGAACATTTA AGAGATTTCC TAGTTCAAAT      420
AAAGGAATTT GCAGGTGAAG ACACTTCTGA TTTGTTTTTG GAAGAGAGAG AAATAGCCCT      480
ACGGCAGGCT GATGAAGAGA AACATAAACG TCAAATGTCT GTCCCTGGCA TCTTTAATCC      540
ACATGAGATT CCAGAAGAAA TGTGTGATTA AAATCCAAAT TCATGCTGTT TTTTCTCT      600
GCAACTCGTT AGCAGAGGAA AACAGCATGT GGGTATTTGT CGAG                        644

```

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```

GAATTCGGCC AAAGAGGCCT ACGTTATACT ATTAGATCCT TTCATTATCA ATCCCTTTTA      60
AAGGCAAGGA AACAGGTTCA GCAAGATCAG CTGACTTCTC TGTGTAAGTG GGACCTGAGA      120
TTTGAAAGTT GAGAGCAGCA TGTTTTGCCC ACTGAAATC ATCCTGCTGC CAGTGTTACT      180
GGATTATTCC TTGGGCCTGA ATGACTTGAA TGTTTCCCG CCTGAGCTAA CAGTCCATGT      240
GGGTGATTCA GCTCTGATGG GATGTGTTT CCAGAGCACA GAAGACAAAT GTATATTCAA      300
GATAGACTGG ACTCTGTCAC CAGGAGAGCA CGCCAAGGAC GAATATGTGC TATACTATTA      360
CTCCAATCTC AGTGTGCCTA TTGGGCGCTT CCAGAACCGC GTACACTTGA TGGGGGACAA      420
CTTATGCAAT GATGGCTCTC TCCTGCTCCA AGATGTGCAA GATGTCGAG                        469

```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```

GAATTCGGCC AAAGAGGCCT AGAGGGGACT CGCCGCCATC TCAGGTCTCT TGGCTTTGCC      60
AGGGCCACC GGAGAAACT GACGACCCGT TTCTGTAATC CTTATGGGAG ACCAACCTTG      120
TGCTCCGGG AGATCCACTC TCCACCTGG AAACGCACGG GAAGCCAAGC CTCAAAAAAA      180
GCGCTGCCCT CTCGCTCCGC GTTGGGATTA TCCGGAAGGA ACTCCCAACG GAGGTAGTAC      240
CACTCTACCC TCCGCACCTC CTCCTGCATC AGCCGGCCTG AAGTGCACC CTCCTCCTCC      300
GGAGAAGTAG AGAAATAAAT TTCTCCACC CTAAACCACT CTTTGAGTGA TTGCAGTATG      360
ACTCCATTTC CCTGGTGCAT TCATATAATA GTTCACCTGG TGAAAAAAT GAAGATTATT      420
TACAATGCTA CCGG                        435

```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
GAATTCGGCC AAAGAGGCCT AACCAAGCAG AAGCTGTACC ACAAGAAGAT CTTCCGGACT    60
GCCATGCTGT TCCAGTTTGT GAACGTGCTG CTCCAGGTCC TGGTCCACAA GTCCCATGAT    120
CTTCTGCAGG AGGAGATTGG CATCGCCATC TACAACATGG CCTCAGTCGA G            171
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
GAATTCGGCC AAAGAGGCCT AGTCATGACT CCCCTGATTT GGCTCCTAAT GTCACCTTATT    60
CCCTGCCCAG AACCAAAAGT GGTAAGCCC CAGAAAGAGC CTCTAGCAAG ACTTCTCCAC    120
ATTGGAAGGA GTCAGGAGCC TCCCATTTGT CATTCCCAA GAACAGCAA TATGAGTATG    180
ACCCTGACAT CTCTCCTCA CGAAAAAGC AAGCAAAATC CCATTTTGA GACAAGAAGC    240
AGCTTGATTC CAAAGGTGAC TGCCAGAAAG CAACTGATTC AGACCTTCT TCTCCACGGC    300
ATAAACAAAG TCCAGGGCAC CAGGATTCTG ATTCAGATCT GTCACCTCA CGGAATAGAC    360
CTAGACACCG GG                                372
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
GAATTCGGCC NAAGAGGCCT AGGGTGGGAC AAGAGAGTGA GACTAGAATA TAAATATCCG    60
TAAACAGCAT CTGAGCATTG GTCTTTAACA GGGAGGAGGA ACCACTGGTG TATATTAATT    120
TAGGACACAG GATCATTATA GGGGTNGGGC CAGCTGGTGT TAATGGCATG CAGGCATATG    180
TGATGCCAAC CATGAGGGCT GGAAGAACCA GAAGCCAAAG AAGAATATGA CGGCATCTAT    240
TCTAAAGCTA CTGTGGTGGT TTCTCATGCT TCAGAGTCTC GTAAGTCTCC TGGTTCCTGG    300
TGCTCAGGCC CGTGTAACA CCATCTGATT TCTCATAGCT GGTTATAGCT GCCTTTCGCA    360
CTTGGATCTT CAGTCGAG                                378
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GAATTCGGCC AAAGAGGCCT AGGTGCCGCG GTCCTGTCTT GCTGTGCCTG CGGCAGGGGC	60
TCGGAACCAA TTCATTCTTG CACGGCCTGG GGCAGGAGCC CTTCGAGGGA GTCGCGTCAC	120
TGTGTTGCAG GTCCTCGCCT AGAGACCTGC GAGATGGAGA AAGAGAGCAC GAGGCGGCAC	180
AAAGGAAAAGC CCCAGGAGCA GAGTCTTGCC CATCTCTCCC TCTGAGCATC TCGGACATTG	240
GGACTGGATG TCTTTCGTCA CTGGAAGAAC TCAGACTGCC GACGCTGCGG GAAGAGTCAT	300
CCCTTCGAGA GTCGAGGAC TCGAGCGGAG ACCAGGGCCG GTGCGGTCCC ACACACCAGG	360
GATCCGAGGA TCCTTCGATG CTCTCGCAGG CCCAGTCCGC TACCGAGGGT CGAG	414

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

AAGCGTGCTC GTGCCCCGAT TNCCNAGGGG NTCAGTCTGT NNCGCCANA GNCCAAGNCC	60
AAGCCCAAGN CCNAGNCCAA GGATCCANN C AAGGCCAG GCTGCAGCCC CAGCTTCAGT	120
TCCAGCTCAG GCTCCACAC GTACCCAGGC CCCCACAAAG GCTTCAGAGN AGATATCTCT	180
CCCAACATGA GGACAGAAGG ACTGGTCCGA CCCCCACCC CGCCCCCTGG GCTACCATCT	240
GATCGGGCT GGGTCCTCCT GTGCTATTG TACAAATAAA CCTGAGGCAG TCGAG	295

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ATGGACTTCC TCTTTTCTGC CANCCACAC CCATACATCG GGAGCCTATA ATACCCTTCG	60
TGNTCTCCC TAACATGTAG GTGGCGGAGG GGAGATATAC AATAGAACAG ATACCAGACA	120
AGACATAATG GGCNNAACAA GACNACACCA ATTACNTNC CTCATTGATG GTGGNACATA	180
ACGAGCTAAT ACTGTANCCC TAGACNTGAT AGCCATCATC ATATCGAAGT TTCCTACCC	240
TTTTTCATT TGCCATCTAT TGAAGTAATA ATAGGCGCAT GCAACTTCTT TTCTTTTTTT	300
TTCTTTTCTC TCTCCCCGN TGTGTCTCA CCATATCCGC AATGACGTCG AG	352

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAATTCGGCC AAAGAGGCCT ACGTTATCCG CGATGCGTTT CCTGGCAGCT ACATTCCTGC	60
TCCTGGCGCT CAGCACCGCT GCCCAGGCCG AACCGGTGCA GTTCAAGGAC TCGCGTTCGT	120
TGGATGGAGT TATAAAGGAA GTGAATGTGA GCCCATGCCC CACCCAACCC TGCCAGCTGA	180
GCAAAGGACA GTCTTACAGC GTCAATGTCA CCTTCACCAG CAATATTCAG TCTAAAAGCA	240
GCAAGGCCGT GGTGCATGGC ATCCTGATGG GCGTCCCAGT TCCCTTTCCC ATTCTGAGC	300
CTGATGGTTG TAAGAGTGGA ATTAAGTGCC CTATCCAAAA AGACGTCGAG	350

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GAATTCGGCC AAAGAGGCCT ATTGAATTCT AGACCTGCGT CGACCTCCCT TCCAGCCCCC	60
AGAAAGCTCG GTCACCTGAG TGTTCCTAG AATCCTGGGG TGCTCCCGGG CCGCTCTCAG	120
AGAAGTGGA GGTTCACGT TCAGCCGTGT GCGGATCGT GTGGCTTCCA AAGCCTTTTA	180
CAGCCCCGC CCCCATCCC GTGGTCTGTC TGCAGGAAGT CTCCGTCTG TGAGAAGCCT	240
CTTTCGAGT CGAG	254

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCGGCC AAAGAGGCCT ACTAGAGGGG TCAGTGGCCC CGCACGGTGG GGTGGCCGCT	60
CAGGGCCTAG GGAGCAGGTG GGAGGGGCTT GGAGGGCAGA ACAGAGGGCC TGGGGGCTGC	120
TCTGCTGGCC ACCACTGCTT TCTGGTTGAA CCAGATAAGT AGCTGGTGGT GACGCTGTG	180
GGCCCTGAGT CGGGGAGAA GAGGCAGAGG GAGCAGTGGG CTGGGCTAGT GGGGACATGA	240
GTGGGTGGTG ATCATGCCTG TGTCGGGGGA GCTGAGGCAG AGAGTGGGGC AGCGAGCATC	300
CCCTGAGGGC AGGAGGAGAG GGGTGGGGAC AGGGAAGGGT CGGGGGTGGT CCCAGCCCTG	360
AAGACAGGAG TGGCGAGGGC AGGTGTGGTC TAGGTGCTTG TCGAGGTGGA CAACATGGGT	420
CGAG	424

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GAATTCGGCC	AAAGAGGCCT	AATGGCGTCC	AGGTCTAAGC	GGCGTGCCGT	GGAAAGTGGG	60
GTTCCGCAGC	CGCCGGATCC	CCCAGTCCAG	CGCGACGAGG	AAGAGGAAAA	AGAAGTCGAA	120
AATGAGGATG	AAGACGATGA	TGACAGTGAC	AAGGAAAAGG	ATGAAGAGGA	CGAGGTCATT	180
GACGAGGAAG	TGAATATTGA	ATTTGAAGCT	TATTCCTAT	CAGATAATGA	TTATGACGGA	240
ATTAAGAAAT	TACTGCAGCA	GCTTTTCTA	AAGGCTCCTG	TGAACACTGC	AGAACTAACA	300
GATCTCTTAA	TTCAACAGAA	CCATATTGGG	AGTGTGATTA	AGCAAACGGA	TGTTTCAGAA	360
GACAGCAATG	ATGATATGGA	TGAAGATGAG	GTTTTTGGTT	TCATAAGCCT	TTTAAATTTA	420
ACTGAAAGAA	AGGGTACCCA	GTGTGTTGAA	CAAATTCAAG	AGTTGGTTCT	ACGCTTCTGT	480
GAGAAGAACT	GTGAAAAGAG	CATGGTTGAA	CAGCTGGACA	AGTTTTTAAA	TGACACCACC	540
AAGCCTGTGG	GCCTTCTCCT	AAGTGAAAGA	TTCATTAATG	TCCCTCCACA	GATCGCTCTG	600
CCCATGTACC	AGCAGCTTCA	GAAAGAACTG	TCGGGGGCAC	ACAGAACCAA	TAAGCCATGT	660
GGGAAGTGCT	ACTTTTACCT	TCTGATTAGT	AAGACATTG	TCGAG		705

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAATTCGGCC	AAAGAGGCCT	ACCCAGCTCA	GAATCTTGCT	GCTCGGCCCC	CAGGAGAGCA	60
ACAACACAAC	GGGAACGATG	TGGAAGGTGT	CAGCTCTGCT	CTTCGTTTTG	GGAAGCGCGT	120
CGCTCTGGGT	CCTGGCAGAA	GGAGCCAGCA	CAGGCCAGCC	AGAAGATGAC	ACTGAGACTA	180
CAGGTTTGGA	AGGCGGCGTT	GCCATGCCAG	GTGCCGAAGA	TGATGTGGTG	ACTCCAGGAA	240
CCAGCGAAGA	CCGCTATAAG	TCTGGCTTGA	CAACTCTGGT	GGCAACAAGT	GTCAACAGTG	300
TAACAGGCAT	TCGCATCGAG	GATCTGCCAA	CTTCAGAAAG	CCCAGTCGAG		350

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GAATTCGGCC	AAAGAGGCCT	AGTGGACAGG	AAGTAGAATT	TATTGGTGAG	TATTAAGAGG	60
GGGGCAGCAC	ATTGGAAGCC	CTCATGAGTG	CAGGGCCCGT	CACTTGTTCCA	GAGGGCCACG	120
ACTGGGGATG	TACTTGACCC	CACAGCCATC	TGGGATGAGC	CGCTTTTCAG	CCACCATGTC	180
TTCAAATTCA	TCAGCATTGA	ACTTGGTGAA	GCCCCACTTC	TTTGAGATGT	GGATCTTCTG	240
GCGGCCAGGA	AACTTGAACT	TGGCCCTGCG	CAGGGCCTCA	ATCACATGCT	CCTTGTTCTG	300
CAGCTTGGTG	CGGATGGACA	TGATAACTTG	GCCAAATGTGA	ACCCTGGCCA	CAGTGCCTTG	360
GGGCTTTCCA	AAGGCACCTC	GCATGCCTGT	TTGGAGCCTG	TCAGCCCCAG	CACAGGACAA	420
CATCTTGTTG	ATGCGGATGA	CGTGGTCGAG				450

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
GAATTCGGCC AAAGAGGCCT ATGAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC      60
TTTGGACCTG ATCAGCTTGA TACAAGAACT ACTGATTTCa ACTTCTTTGG CTTAATTCTC      120
TCGGAAACGA TGAAATATAC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTTGGGT      180
TCTCTTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAATAT      240
TTTAATGCAG GTCATTGAGA TGTAGCGGAT AATGGAACTC TTTTCTTAGG CATTTTGAAG      300
AATTGGAAAG AGGAGAGTGA CAGAAAAATA ATGCAGAGCC AAATTGTCTC CTTTACTTTC      360
AAACTTTTAA AAAACTTTAA AGATGACCAG AGCATCCAAA AGAGTGTGGA GACCATCAAG      420
GAAGACATGA ATGTCAAGTT TTTCAATAGC AACAAAAAGA AACGAGATGA CTTGCGAAAAG      480
CTGACTAATT ATTCGGTAAC TGACTTGAAT GTCCAACGCA AAGCAATACA TGAATCATC      540
CAAGTGNTGG CTGAAGTGC GCCAGCAGCT AAAACAGGGG TCGAG                          585
```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```
GAATTCGGCC AAAGAGGCCT ATTGGAGTTT GAGTATAGTA AATTATGATC CTAAATATT      60
TGAGAGTCAG GATGAAGCAG ATCTGCTGTA GACTTTTCAG ATGAAATTGT TCATTCTCGT      120
AACCTCCATA TTTTCAGGAT TTTTGAAGCT GTTGACCTTT TCATGTTGAT TATTTTAAAT      180
TGTGTGAAAT AGTATAAAAA TCATTGGTGT TCATTATTTC CTITGCCTGA GCTCAGATCA      240
AAATGTTTGA AGAAAGGAAC TTTATTTTTC CAAGTTACGT ACAGTTTTTA TGCTTGAGAT      300
ATTTCAACAT GTTATGTATA TTGGAAGTTC TACAGCTTGA TGCTCCTGC TTTTATAGCA      360
GTTTATGGGG AGTCACTTGA AAGAGCGTGT GTACATGTAT TTTTCTCTN GGCAAACATT      420
GAATGCAAAC GTGTATTTT TTAATATAAA TATATAACTT CCTGCGTCGA G                          471
```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 477 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```
GAATTCGGCC AAAGAGGCCT ATGTTTGGCA ACTGGGGTGA AGGGATTGCC CTCCCCCTGC      60
TGGGATCCCC CCAGCCCCTC CGGTCTGGCA GGAAGGGGGC AGCCTGCAAC CCCCAGGGGC      120
AGGTGTGGGG CTGCCAGATG CTCCAGGCAG GGGGCCAGAA GGGGCTCACA AAGGCTTGCC      180
CTCCAGGGAG ATGACGGCAC TGCCCCCAG CTTCTCTGCC AGGGTGCAGC GGTCTTGAC      240
CTCCTCGTAG CAGTTTGCTT GCAATTCATG CTTGATCCCT GTCAGCTTCT TCTTGATGGC      300
GTCCTTGAG CTGGCATAAA TCATTTTGCT CTTAAGGGGS GCAGACTCGG GGGCCCAGAA      360
GATAAACACC AGATCCTCCT TCTTGCTCTC CYTGGTCTCA TAGGTTGCAT CATAGAGGGC      420
```

ATAGCGGCAG TCCTTATCTG GCAGCATCTT GACAAAGGTG GCGTAGGGAT CGTCGAG

477

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GAATTCGGCC CAAAGAGGCC YMAAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC	60
TTTGGACTTG ATCAGCTTGA TACAAGAACT ACTGATTTC ACTTCTTTGG CTTAATTCTC	120
TCGGAAACGA TGAATATAC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTTGGGT	180
TCTCTTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAATAT	240
TTTAATGCAG GTCATTGAGA TGTAGCGGAT AATGGAATC TTTTCTTAGG CATTTTGAAG	300
AATTGGAAAG AGGAGAGTGA CAGAAAAATA ATGCAGAGCC AAATTGTCTC CTTTACTTTC	360
AAACTTTTAA AAAACTTTAA AGATGACCAG AGCATCCAAA AGAGTGTCTGA G	411

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 427 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GAATCGGCCC AAAGAGGCCT ACTGAAGATC AGCTATTAGA AGAGAAAGAT CAGTTAAGTC	60
CTTTGGACCT GATCAGCTTG ATACAAGAAC TACTGATTTC AACTTCTTTG GCTTAATTCT	120
CTCGGAAACG ATGAAATATA CAAGTTATAT CTGGCTTTT CAGCTCTGCA TCGTTTTGGG	180
TTCTCTTGGC TGTTACTGCC AGGACCCATA TGTAAGAGAA GCAGAAAACC TTAAGAAATA	240
TTTTAATGCA GGTCAATCAG ATGTAGCGGA TAATGGAATC CTTTCTTAG GCATTTTGAA	300
GAATTGGAAA GAGGAGAGTG ACAGAAAAAT AATGCAGAGC CAAATTGTCT CCTTTTACTT	360
CAAACTTTT AAAAATTTA AAGATGACCA GAGCATCCAA AAGAGTGTGG AGACCATCAA	420
GGTCGAG	427

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 598 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAATTCGGCC AAAGAGGCCT AGAGAAGATA AACTGGACA CTGGGGAGAC ACAACTTCAT	60
GCTGCGTGGG ATCTCCAGC TACCTGCAGT GGCCACCATG TCTTGGGTCC TGCTGCCTGT	120
ACTTTGGCTC ATTGTTCAAA CTCAAGCAAT AGCCATAAAG CAAACACCTG AATTACGCT	180
CCATGAAATA GTTTGTCCTA AAAAATTTCA CATTTTACAC AAAAGAGAGA TCAAGAACAA	240

```

CCAGACAGAA AAGCATGGCA AAGAGGAAAG GTATGAACCT GAAGTTCAAT ATCAGATGAT      300
CTTAAATGGA GAAGAAATCA TTCTCTCCCT ACAAAAAACC AAGCACCTCC TGGGGCCAGA      360
CTACACTGAA ACATTGTACT CACCCAGAGG AGAGGAAATT ACCACGAAAC CTGAGAACAT      420
GGAACACTGT TACTATAAAG GAAACATCCT AAATGAAAAG AATTCTGTTG CCAGCATCAG      480
TACTTGTGNC GGGTTGAGAG GATACTTCAC ACATCATCAC CAAAGATACC AGATAAAACC      540
TCTGAAAAGC ACAGACGAGA AAGAACATGC CGTCTTTACA TCTAACCAGG AGGTCCGAG      598

```

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 238 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

GAATTCGGCC AAAGAGGCCT AGAGCTAAGG CGAAGACCAA GACACGTGAC ATTCATGCTT      60
TGGTGTGGGG TCCAAAGCAC TCTTATTTAA CATAGATTCC AAACCTTTTA CACCCATGGG      120
GTCAATATATA CTCTTTATTT TACCCTTCAT TATTTTAAAA ATCACAACAT CACCCATTGC      180
CCCCGTGTCC AAAGGAATCG CTTGTAATAA ATCAGCAGGT CTAGAATTCA ATCGGGAG      238

```

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```

GAATTCGGCC AAAGAGGCCT AGAGCTAAGG CGAAGACCAA GACACGTGAC ATTCATGCTT      60
TGGTGTGGGG TCCAAAGCAC TCTTATTTAA CATAGATTCC AAACCTTTTA CACCCATGGG      120
GTCAATATATA CTCTTTATTT TACCCTTCAT TATTTTAAAA ATCACAACAT CACCCATTGC      180
CCCCGTGTCC AAAGGATTTC CTTGTAATAA ATCAGCAGGT CTAGAATTCA ATCGGGAGGT      240
TCTCCCTATA GTGAGTCGTA TTAATTTTCA AGGAGTATTT AGAAGAGAAG CTGAAGCTGT      300
CGAG                                     304

```

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```

GAATTCGGCC AAAGAGGCCT ACGACAGTTG GTGTAAGGA AAACCTTCTGA GTCCTGTCAG      60
TTCACCTGGT ACATTGGAAT TAAAGTGCTT GGATGTTTTT CCCCCACTTT AAAAAAACTT      120
TTGAGGTTTT TTTTTTTTTT TGTCTTTTAA AAACATCGTA ACATTAAAC ATGGCCGTTT      180
ACCGTCCCCC AGCGATGGGA GCTGGCCTGG GCCCCAGGGT CCTCCAGGAT CTTCATCAT      240

```

TCACAGTAAC GGTTCCTGACC AGTCCTCCAG GTCGCACGTG GATGCGACAG GGGTGGGGAG	300
GGAGGAGGAA GTGACTGTCC CACCTCTGCA GGACCATGGG AGTGGGCAAG GTGTTCTCCG	360
GGGCGCACCC CTGAACCCAG GGGTGTCTGCA GGACNTG	397

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 592 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GAATTCGGCC AAAGAGGCCT ATAAGAATT AAGATGCATT TTTGCATTG CTATATTTCT	60
TTAAATTCTA GATAGTTATT TTCAAGTGTT GGTAAACATA AATCTTAGGC TTAGGAACCA	120
TTGGATTAGT AACAGCATTG TGCTAATCAA AACTTTAAAA AAATGAGTTC AAAATTGTGA	180
TAATGTAATT TTATAGATT TCTTTTATCC TCAACCTGCA GAAGCCGGAA AGTGAGGCAC	240
ATAGCCCCAC ATAGGCAGAA ATTAAAGCCT AGGCAATAAC TTAGTGAAAA TGGAAATTTT	300
AGAACATTCC ACTTCTTGT TAGTACAATT TTATGGCCAT GGTGCTAGCT AATGGAAATG	360
GCTAGTATAC TATTTATAGG CCAGCAATAT TTTGGTGAAT TTAAGCGAAA CTATGCTCAG	420
TATCATTGAA ATGGGGGTGG GGTGGGCTTG AGACATGAAA TCAATCATAC AAAGTCAAAA	480
ACTATTTTAA CCCAGGAATA AGTTAAATTC CTGTCACCCA GTCGAGGTTC TCCCTATAGT	540
GAGTCGTATT AATTCAGAG GAGTATTAG AAGAGAAGCT GAAGCTGTCTG AG	592

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GAATTCGGCC AAAGAGGCCT AGATGATGAT ATGTTTAAACC ACCAAGTTCC TTATTTGTGG	60
CTGATTTACT GCCTTTGTCA TCCTCTTCAA TCAAGTATTA AAGAAACAGT GGAGGCATAT	120
GAGGCAGCAT TAGGGGTGGC TATGAGATGT GATATAGTAC AGAAGATATG GATGGATTAT	180
CTTGCTTTG CAAATAATAG AGCTGCTGGA TCCAGAAACA AAGTTCAAGA ATTCAAATTT	240
TTTACTGATT TAGTGAATAG ATGTTTGGTT ACAGNCCCTG CCCGATACCC CATTCTTTT	300
AGCAGNGCTG ATTACTGGTC CAACTATGAA TTTCATAATA GGGTCGAG	348

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAATTCGGCC AAAGAGGCCT ACAGAATTGA GAGTTTGTTC TTACACACAA GTTTAATGCC	60
-------------------------------------------------------------------	----

ACCTTCCTCT	GTCTGCCATG	GACCAACAAG	CAATATATGC	TGAGTTAAAC	TTACCCACAG	120
ACTCAGGCCC	AGAAAGTTCT	TCACCTTCAT	CTCTTCCTCG	GGATGTCTGT	CAGGGTTCAC	180
CTTGCCATCA	ATTTGCCCTG	AAACTTAGCT	GTGCTGGGAT	TATTCTCCTT	GTCTTGTTG	240
TTACTGGGTT	GAGTGTTTCA	GTGACATCCT	TAATACAGAA	ATCATCAATA	GAAAAATGCA	300
GTGTGGACAT	TCAACAGAGC	AGGAATAAAA	CAACAGAGAG	ACCGGGTCTC	TTAAACTGCC	360
CAATATATTG	GCAGCAACTC	CGAGTCGAGG	TTCTCCCTAT	AGTGAGTCGT	ATTAATTTC	420
GAGGAGTATT	TAGAAGAGAA	GCTGAAGCTG	TCGAG			455

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAATTCGGCC	AAAGAGGCCT	AAAAATCTCT	TATTAAAGGT	AGAACCTCTG	CTAGCCAGAC	60
AACTATATTA	TTTGTCTCAA	CAAAACAGTG	GACATTTCCT	GAGGGGCTAC	GATTTACCAG	120
AACACATCAG	CAATCCAGAA	GATTACCACA	GATCTATCCG	CCATTCTCT	ATTCAAGAAT	180
GAAAAATGTC	AAGATGAGTG	GTTTTCTTTT	TCCTTTTTTT	TTTTTTTTTT	TTTGTATACG	240
GGGATACGGG	GTCTTGCTCT	GTCTCCAGG	CTGGAGTGCA	GTGACACAAT	CTCAGCTCAC	300
TGTGACCTCC	GCCTCTGGG	TTCAAGAGAC	TCTCTGCCT	CAGTCGAG		348

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GAATTCGGCC	AAAGAGGCCT	ACCTTAAAGC	CGTATACTTA	TGAATTTAAA	GTGGAAAATT	60
TTTTTGTTGG	CCCTGGCCCC	CTTGCCAGAT	TCCAGCTGGC	CGTCAGTGCT	CGCGTGTCTC	120
TCTGAAGAGG	CTCTGCGGTT	CTGGTCCCTG	TGCCTGAGCT	CCAGGTGCCG	CCAGACATTA	180
TACAACGTGA	AGGCTGAGAT	CTTCCCCCT	TCGGGAATGG	AGTATTGCAG	AACAGGCTCC	240
CTCTGCTCCC	TGGAGGTTTT	GATCACGAGG	CTCTCAGACC	TCTTGAGGT	GGATAAAGAT	300
GAAGCACTGA	CTGAATCTGA	TGAGCATTTT	TCGACAAAGC	TTATGTATGA	AGTTGTCGAG	360

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GAATTCGGCC	AAAGAGGCCT	ACTCATCTTG	GGTCCAGCC	AGGCCCCCCC	AAAACCAAAG	60
------------	------------	------------	-----------	------------	------------	----

CCCCCTCAAG TCCTGGGGTC CCAGCCTGTG CCCCCAGCTT CCTGCCCCACC CAGCCCCGAG	120
CATTCTCACA CAGAGAAAGA ACAAGCAAGG GCTCCAGGGG GACAGGATGG GGCAGGGCAT	180
ACAGTGGGGG GTGGGGGGGC AGCTGGGAGG AGGGAGGGAC AAAACAAAAC ATTTTCCTTT	240
GGGTTTTTTT TTTCTTTCTT TTTTCTCCCC TTTACTCTTT GGGTGGTGTT GCTTTTCCTT	300
TCCTTTTCCC TTGAGATT TTTTGTGTT GTTTCCTTTT TGTATTTTAC TGATATCACC	360
AGGATAGTTT ACTCTCCTTC TAGCTTTCTG CTTACCGCAC ACTGGATAAC ACACACATAC	420
ACACCCACAA AAATGCTCAT GAACCCAATC CGGAGAAGGT TCCAGCAGGT CCCCCACCCT	480
CCCCTCCTCC TCCTACTTCT CCTCTTGACA GCGAGGACAG GAGGGGGACA AGGGGACACC	540
TGGGCAGACC CGCCGGCTCT CCCCCACCC CACCCGCTCG AG	582

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAATTCGGCC AAAGAGGCCT AGAAATAAAA CATTCTACAC CGTCTCCTAC CAAATATTCA	60
CTATCACCAA GTAAAAGTTA CAAGGTAAAC AGGAAAGAAT GGAATCATT CATTTGTGAAA	120
TTGTTTCTGT TCTAAGTGTT TTAAATGCTG TTTTGTATT TTTATTTTT TTTTCAGTAT	180
TCTCCGAAA CACCACCTCG ATGGACAGAA GATCGGAATT CTTTACTGAA TATGATTTCG	240
CAACAAGTAG AGGCCATGTC GAG	263

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GAATTCGGCC AAAGAGGCCT AATTCTCAG CTCCAAGCAT TAGGTAAACC CACCAAGCAA	60
TCCTAGCCTG TGATGGCGTT TGACGTCAGC TGCTTCTTT GGGTGGTGCT GTTTTCTGCC	120
GGCTGTAAAG TCATCACCTC CTGGGATCAG ATGTGCATTG AGAAAGAAGC CAACAAAACA	180
TATAACTGTG AAAATTTAGG TCTCAGTGAA ATCCCTGACA CTCTACCAA CACAACAGAA	240
TTTTTGGAAT TCAGCTTTAA TTTTTCCT ACAATTCACA ATAGAACCCT CAGCAGACTC	300
ATGAATCTTA CCTTTTGGGA TTAACTAGG TGCCAGATTA ACTGGATACA TGAAGACAT	360
TTTCAAAGCC ATCATCAATT AAGCACACTT GTGTTANCTG GAAATCCCCT GATATTCATG	420
GCAGAAACAT CGCTTAATGG GCCCAAGTCA CTGAAGCATC TTTTCTTAAT CCANNCGGGA	480
ATATCCAATC TCGAGTTTAT TCCAGTGAC AATCTGGAAA ACTTGAAAG CTGTATCTT	540
GGAAGCAACG TCGAG	555

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 414 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

```

GAATTCGCCC AAAGAGGCCT AGATGATGAT ATGTTTAACC ACCAAGTTCC TTATTTGTGG      60
CTGATTTACT GCCTTTGTCA TCCTCTTCAA TCAAGTATTA AAGAAACAGT GGAGGCATAT      120
GAGGCAGCAT TAGGGGTGGC TATGAGATGT GATATAGTAC AGAAGATATG GATGGATTAT      180
CTTGTCTTTG CAAATAATAG AGCTGCTGGA TCCAGAAACA AAGTTCAAGA ATTCAAATTT      240
TTTACTGATT TAGTGAATAG ATGTTTGGTT ACAGNCCCTG CCCGATACCC CATTCCCTTT      300
AGCAGNGCTG ATTACTGGTC CAACTATGAA TTTTATAATA GGGTCGAGGT TCTCCCTATA      360
GTGAGTCGTA TTAATTTTCA AGGAGTATTT AGAAGAGAAG CTGAAGCTGT CGAG          414

```

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 590 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```

GAATTCGGCC NAAGAGGCCT AAGCAGATGC TGATCTCATT ATGCTTGGCC TTGCCACACA      60
TGAACCGAAC TTTACCATTA TTAGAGAAGA ATTCAAACCA AACAAGCCCA AACCATGTGG      120
TCTTTGTAAT CAGTTTGGAC ATGAGGTCAA AGATTGTGAA GGTTTGCCAA GAGAAAAGAA      180
GGGAAAGCAT GATGAACCTG CCGATAGTCT TCCTTGTGCA GAAGGAGAGT TTATCTTCCT      240
TCGGCTTAAT GTTCTTCGTG AGTATTTGGA AAGAGAACTC ACAATGGCCA GCCTACCATT      300
CACATTTGAT GTTGAGAGGA GCATTGATGA CTGGGTTTTC ATGTGCTTCT TTGTGGGAAA      360
TGACTTCCTC CCTCATTTCG CATCGTTAGA GATTAGGGAA AATGCAATG ACCGTTTGGT      420
TAACATATAC AAAAATGTGG TACACAAAC TGGGGTTTAC CTTACAGAAA GTGGTTATGT      480
CAATCTGCAA AGAGTACAGA TGATCATGTT AGCAGTTGGT GAAGTTGAGG ATAGCATTTT      540
TAAAGAGAGA AAGGATGATG AGGACAGTTT TAGAAGACGA CAGGGTCGAG          590

```

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```

GAATTCGGCC AAAGAGGCCT AGACGGGCCT CGGTCAGCAG CACGGGGTGC TCCTCGGGAG      60
CCACACGCAG CTCATTGTAG AAGGTGTGGT GCCAGATTTT CTCCATGTCT TCCCAGTTGG      120
TGACGATGCC GTGCTCGATG GGGTACTTCA GGGTGAGGAT GCCTCTCTTG CTCTGGGCCT      180
CGTCGCCCAC ATAGGAATCC TTCTGACCCA TGCCCACCAT CACGCCCTGG TGCTTGGGGC      240
GCCCCACGAT GGAGGGGAAG ACGGCCCGGG GGGCATCGTC CCCCAGGAAG CCGGCCTTGC      300
ACATGCCGGA GCCGTTGTCT AG          322

```

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```
GGGTTGACAA ATATGGACTT CCTCTTTTCT GCCNNCCCAA ACCCATACAT CGGGATTCTCT    60
ATAATACCTT CGTTGGTCTC CCTAACATGT AGGTGGCGGA GGGGAGATAT ACAATAGANC    120
AAGATACCAG ACAAGACATA ATGGGCTAAA CAAGACTACA CCAATTACAC TGCCTCATTG    180
ATGGTGGTAC ATAACGAACT AATACTGTAG CCCTAGACTT GATAGCCATC ATCATATCGA    240
AGTTTCACTA CCCTTTTTC ATTTGCCATC TATTGAAGTA ATAATAGGCG CATGCAACTT    300
CTTTTCTTTT TTTTCTTTT CTCTCTCCCC CGTTGTTGTC TCACCATAG                349
```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```
GAATTGGGCC AAAGAGGCCT ACTATAAGAG AGATCCAGCT TGCCTCCTCT TGAGCAGTCA    60
GCAACAGGCT CCCCTCCTTG ACACCTCAGC CTCTACAGGA CTGAGAAGAA GTAAAACCGT    120
TTGCTGGGGC TGGCCTGACT CACCAGCTGC CATGCAGCAG CCCTTCAATT ACCCATATCC    180
CCAGATCTAC TGGGTGGACA GCAGTGCCAG CTCTCCCTGG GCCCCTCCAG GCACAGTTCT    240
TCCCTGTCCA ACCTCTGTGC CCAGAAGGCC TGGTCAAAGG AGGCCACCAC CACCACCGCC    300
ACCGCCACCA CTACCACCTC CGCCGCGGCC GCCACCACTG CCTCCACTAC CGCTGCCACC    360
CCTGAAGAAG AGAGGGAACC ACAGCACAGG CCTGTGTCTC CTGTGTATGT TTTTCATGGT    420
TCTGGTTGCC TTGGTAGGAT TGGGCCTGGG GATGTTTCAG CTCTCCACC TACAGAAGGA    480
GCTGGCAGAA CTCGAGAGT CTACCAGCCA GATGCACACA GCATCATCTT TGGAGAAGCA    540
AATAGGCCAC CCCAGTCCAC CCCCTGAAAA AAAGGAGCTG AGGAAAGTGG CCCATTTAAC    600
AGGCAAGTCC AACGTCGAGG TTCTCCCTAT AGTGAGTCGT ATTAATTCA GAGGAGTATT    660
TAGAAGAGAA GCTGAAGCTG TCGAGACA                688
```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```
GAATTGGGCC AAAGAGGCCT AATGATTTTG ATAGGAAGAA TGTGAGCCCA GGTTCCCATG    60
AACATGACCA TCACAGGTTG TATGATGACG TTTTACAGGA CTACGCCGCG TGTGCTGTTT    120
TGGCAGTGGA TTAACAGTC CTTCAATGCC GTCGTCAATT ACACCAACAA AAGTGTGAG    180
```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GAATTCGGNC	AAAGAGGCCT	ACCACCTTCT	CTGCCAGAAG	ATACCATTTT	AACTTTAACA	60
CAGCATGATC	GAAACATACA	ACCAAACCTT	TCCCCGATCT	GCGGCCACTG	GACTGCCCAT	120
CAGCATGAAA	ATTTTATGT	ATTTACTTAC	TGTTTTTCTT	ATCACCAGAG	TGATTGGGTC	180
AGCACTTTT	GGTGTGTATC	TTCATAGAAG	GTTGGNCAAG	ATAGAAGATG	AAAGGRAWYY	240
TYMATKRARR	WTTTCKKWTY	MWKRAACSR	WVMCARRRRW	KSMAMMMMRG	RRRRRRRWCC	300
YYWYCYTWC	YTKRWSYTKK	KRRGRRRWTW	AAARCCMRKT	TKGWRGGSYT	TKKKRWRGRW	360
TTWTWKKTW	AAMMAMRRRG	RRRMSRCGR	RARRAAAMMR	CYTTTGNAAT	NCNCCNAGGT	420
GATCAGAATC	CTCACATTGC	GGCACATGTC	ATAAGTGAGG	CCANCAGTAA	AACAACATCT	480
GTGTTACAGT	GGGCTGANAA	AGGATACTAC	ACCATGAGCA	ACAACTTGGT	AACCCTGGAA	540
AATGGGAAAC	AGCTGNCCGT	TAAAAGACAA	GGACTCTATT	ATATCTATGC	CCAAGTCGAG	600

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

NCCTGTTTCA	TTAATTAAAT	TTCCCGAAAG	AACCTGAGTC	ATTTTCCNAC	ATGAGAATAC	60
TAGAAGAATG	ACCAAGACTT	GCGAGACGCG	ATTTCGCGG	TGGTGCGAAC	AATAGANCGA	120
CCATGACCTT	GAAGGTGAGA	CGCGCATAAC	CGCTAGAGTA	CTTTGAAGAG	GAACANCAA	180
TAGGTGCTA	CCAGTATAAA	TAGACAGGTA	CATACAACAC	TGGAAATGGT	TGTCGTGTTG	240
AGTACGCTTT	CAATTCATTT	GGGTGTGCAC	TTTATTATGT	TACAAATATG	AAGGGAACCT	300
TACACTTCTC	CTATGCACAT	ATATTAATTA	AAGTCCAATG	CTAGTAGAGA	AG	352

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GAATTCGGCC	AAAGAGGCCT	AAAGAAGACA	AAGATGATAG	GCGGCACAGA	GATGACAAAA	60
GAGATTCCAA	GAAAGAGAAA	AAACACAGTA	GAAGCAGAAG	CAGAGAAAGG	AAACACAGAA	120
GTAGGAGTCG	AAGTAGAAAT	GCAGGGAAAC	GAAGTAGAAG	TAGAAGCAAA	GAGAAATCAA	180
GTAACATAAA	AAATGAAAGT	AAAGAAAAAT	CAAATAAACG	AAGTCGAAGT	GGCAGTCAAG	240
GAAGAACTGA	CAGTGTGAA	AAATCAAAAA	AACGGGAACA	TAGTCCAGC	AAAGAAAAAT	300
CTAGAAAGCG	TAGTAGAAGC	AAAGAACGTT	CCCACAAACG	AGATCACAGT	GATAGTAAGG	360
ACCAGTCAGA	CAAACATGAC	CGTCGAG				387

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```
GAATTCGGCC AAAGAGGCCT AAGGAAGTTG GATGTTTGA TTTTACTGTT TATAGATGTT      60
AGATTGTACA GATTTGTCTG TATTTCTCAC CATATCTAAT GATACTTTTT TCATTAGATT      120
GGTCTTCAAG AACAGTATTA GTTATAATTA TTTTGTTAT TCAGTATATA GTTAGCTCTT      180
ACAGTTTAGC TTTATTCACC ATATTTATAC TGTGGATTCA CAGCGAGAGG TAGAGGTTAT      240
TCCAGGAGAG TTGATGACCT TCATTTAAAG TCCAACATAA ATCAGTAGTA GAAACATAAG      300
AAAACATCTT TGCAATATTT ACTTTTGTTT CTGTTTGCCG TAAATAGTAA CATTGTTTTT      360
TTTTATTTTG TGTGTGTAT AAAACAGTTG CATTACAAT ATTATTGGCC TGAGATATTG      420
ATGATATTGT GATGGTATGA AAATGTGTAC ATTCCTGTG CAACATCAGA TTTGCAGGAA      480
AAATGAAGCA CTTACTGAAA TCGCTGGTAC TCGTCGAG      518
```

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```
GAATTCGGCC AAAGAGGCCT AGGACAAAAC AAAACATTTT CCTTGGGTT TTTTCTTCT      60
TTCTTTTTTC TCCCCTTTAC TCTTTGGGTG GTGTGCTTT TCCTTTCCTT TTCCCTTTGA      120
GATTTTTTTG TTGTGTTTC CTTTGTGTAT TTTACTGATA TCACCAGGAT AGTTTACTCT      180
CCTTCTAGCT TTCTGCTTAC CGCACACTGG ATAACACACA CATACACACC CACAAAAATG      240
CTCATGAACC CAATCCGGAG AAGGTTCCAG CAGGTCCCCC ACCCTCCCCT CCTCCTCCTA      300
CTTCTCCTCT TGACAGCGAG GACAGGAGGG GGACAAGGGG ACACCTGGGC AGACCCGCCG      360
GCTCTCCCCC CACCCACCC CGGCACCTC GAG      393
```

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

```
GAATTCGGCC AAAGAGGCCT ACGAAGTTAC AGAACTGAGA TTCTGGGTC CCAGACACGC      60
ACCTATGTAC CTCCCACTGG TGTCCCTGCA AAGCCTGGCG CTTTGACAT CAATAATAAA      120
AGTGGCAGGG CTGAGCAACA CCTCAGGAGT TACTCTGGAA GGATGGAGGA GTTATGTAAC      180
ACACGAGAGT CAGGAGCCCT GTGGAAGTGC TTTTATTAGC AGTAAGGCTG ATCGTACAAA      240
AAATTCTCAG AGCTTCATAG GACAAGGTAG TACAAGTATG GATGATACAG GACTGAGGAA      300
CGGGGGACGG CTCAAAAGAA ATCAACATCG TCTGGGGCAT CCAGGTCCCC ATATTCCACA      360
ATGGCCCTTG GGTCTCCACG AACCATCCTG TGAGGTGAGA GGTACAGGAT CAGACCTCGA      420
G      421
```

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

TAGGAGATCT GGATGGCATC TACTTCGTAT GACTATTGCA GAGTGCCCAT GGAAGACGGG	60
GATAAGCGCT GTAAGCTTCT GCTGGGGATA GGAATTCTGG TGCTCCTGAT CATCGTGATT	120
CTGGGGGTGC CCTTGATTAT CTTCAACATC AAGGCCAACA GCGAGGCTTG CCGGGACGGC	180
CTTCGGGGAG TGATGGAGTG TCGCAATGTC ACCCATCTCC TGCAACAAGA GCTGACCGAG	240
GCCCAGAAGG GCTTTCAGGA TGTGGAGGCC CAGGCCGCCA CCTGCAACCA CACTGTGATG	300
GCCCTAATGG CTTCCCCTGG ATGCAGAGAA GGCCCAAGGA CAAAGAAAG TGGAAGNATC	360
TCGAG	365

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GAATTCGGCC AAAGAGGCCT AACACAGGAA ACATTACAAT TGAACAATGC CTCAGCTATA	60
CATTTACATC AGATTATTGG GAGCCTATTT GTTCATCATT TCTCGTGTTT AAGGACAGAA	120
TCTGGATAGT ATGCTTCATG GCACTGGGAT GAAATCAGAC TCCGACCAGA AAAAGTCAGA	180
AAATGGAGTA ACCTTAGCAC CAGAGGATAC CTTGCCTTTT TAAAGTGCT ATTGCTCAGG	240
GCACTGTCCA GATGATGCTA TTAATAACAC ATGCATAACT AATGGACATT GCTTTGCCAT	300
CATAGAAGAA GATGACCAGG GAGAAACCAC ATTAGCTTCA GGGTGTATGA AATATGAAGG	360
ATCTGATTTT CAGTGCAAAG ATTCTCCAAA AGCCGAGCTA CGCCGGACAA TAGAATGTTG	420
TCGGACCAAT TTATGTAACC AGTATTGCA ACCCAGCTC GAG	463

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 353 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GAATTCGGCC AAAGAGGCCT ACTTAGCTTC AAATCCCTAC TCCTTCACTT ACTAATTTTG	60
TGATTGGAA ATATCCGCGC AAGATGTTGA CGTTGCAGAC TTGGCTAGTG CAAGCCTTGT	120
TTATTTTCCT CACCACTGAA TCTACAGGTG AACTTCTAGA TCCATGTGGT TATATCAGTC	180
CTGAATCTCC AGTTGTACAA CTTCACTTCTA ATTCACTGC AGTTGTGTG CTAAAGGAAA	240
AATGTATGGA TTATTTTCAT GTAAATGCTA ATTACATTGT CTGGAAACA AACCATTTTA	300
CTATTCCTAA GGAGCAATAT ACTATCATAA ACAGAACAGC ATCCACGCTC GAG	353

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 419 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GAATTCGGCC	AAAGAGGCCT	ACACTCGTCT	CTTTTTTTCC	CCATCTCATT	GCTCCAAGAA	60
TTTTTTTCTT	CTTACTCGCC	AAAGTCAGGG	TTCCCTCTGC	CCGTCCCGTA	TTAATATTTT	120
CACTTTTGGG	ACTACTGGCC	TTTTCTTTT	AAAGGAATTC	AAGCAGGATA	CGTTTTTCTG	180
TTGGGCATTG	ACTAGATTGT	TTGCAAAAGT	TTGCGATCAA	AAACAACAAC	AACAAAAAAC	240
CAAACAACTC	TCCTTGATCT	ATACTTTGAG	AATTGTTGAT	TTCTTTTTTT	TATTCTGACT	300
TTTAAAAACA	ACTTTTTTTT	CCACTTTTTT	AAAAAATGCA	CTACTGTGTG	CTGAGCGCTT	360
TTCTGATCCT	GCATCTGGTC	ACGGTCGCGC	TCAGCCTGTC	TACCTGCAAC	ACACTCGAG	419

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GAATTCGGCC	AAAGAGGCCT	ACCCAGAAAC	ATCCAATTCT	CAAACGAAG	CTCGCACTCT	60
CGCCTCCAGC	ATGAAAGTCT	CTGCCGCCCT	TCTGTGCCTG	CTGCTCATAG	CAGCCACCTT	120
CATTCCCAAA	GGGCTCGCTC	AGCCAGATGC	AATCAATGCC	CCAGTCACCT	GCTGCTATAA	180
CTTCACCAAT	AGGAAGATCT	CAGTGCAGAG	GCTCGCGAGC	TATAGAAGAA	TCACCAGCAG	240
CAAGTGTCCC	AAAGAAGCTG	TGATCTTCAA	GACCATTGTG	GCCAAGGAGA	TCTGTGCTGA	300
CCCCAAGCAG	AAGTGGGTTC	AGGATTCCAT	GGACCACCTG	GACAAGCAAC	CCAAACTCGA	360
G						361

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

TAGGACAAAA	CAAACATTT	TCCCTTGGGG	TTTTTTTTTT	CTTCTTTTTT	TCTCCCTTTT	60
ACTCTTTGGG	TGGTGTGCT	TTTCTTTTCC	TTTTCCCTTT	GAGATTTTTT	TGTTGTGTGT	120
TCCTTTTGTG	ATTTTACTGA	TATCACCAGG	ATAGTTTACT	CTCCTTCTAG	CTTTCGTGCT	180
ACCGCACACT	GGATAACACA	CACATACACA	CCCACAAAAA	TGCTCATGAA	CCCAATCCGG	240
AGAAGGTTCC	AGCAGGTCCC	CCACCCTCCC	CTCCTCCTCC	TACTTCTCCT	CTTGACAGCG	300
AGGACAGGAG	GGGACAAGG	GGACACCTGG	GCAGACCCGC	CGGCTCTCCC	CCCACCCAC	360
CCCGGCAC						368

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```
GAATTCGGCC AAAGAGGCCT AGACTAACCC AGAAACATCC AATTCTCAAA CTGAAGCTCG      60
CACTCTCGCC TCCAGCATGA AAGTCTCTGC CGCCCTTCTG TGCCTGCTGC TCATAGCAGC      120
CACCTTCATT CCCCAAGGGC TCGCTCAGCC AGATGCAATC AATGCCCCAG TCACCTGCTG      180
CTATAACTTC ACCAATAGGA AGATCTCAGT GCAGAGGCTC GCGAGCTATA GAAGAATCAC      240
CAGCAGCAAG TGTCCCAAAG AAGCTGTGAT CTTCAAGACC ATTGTGGCCA AGGAGATCTG      300
TGCTGACCCC AAGCAGAAGT GGGTTCAGGA TTCCATGGAC CACCTGGACA AGCAAACCCA      360
AACTCCGAAG ACTTCACACG AG                                     382
```

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 496 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```
GAATTCGGCC AAAGAGGCCT AGTATAATAC TAAGTTGAGA TGATATCATT TACGGGGGAA      60
GGCGCTTTGT GAAGTAGGCC TTATTTCTCT TGTCCTTTCC TACAGGGAGG AATTTGAAGT      120
AGATAGAAAC CGACCTGGAT TACTCCGGTC TGAAGTCAGA TCACGTAGGA CTTTAATCGT      180
TGAACAAACG AACCTTTAAT AGCGGCTGCA CCATCGGGAT GTCCTGATCC AACATCGAGG      240
TCGTAAACCC TATTGTTGAT ATGGACTCTA GAATAGGATT GCGCTGTTAT CCCTAGGGTA      300
ACTTGTTCCG TTGGTCAAGT TATTGGATCA ATTGAGTATA GTAGTTCGCT TTGACTGGTG      360
AAGTCTTAGC ATGTACTGCT CGGAGGTTGG GTTCTGCTCC GAGGTGCCCC CAACCGAAAT      420
TTTAAATGCA GGTTGGTAG TTTAGGACCT GTGGGTTTGT TAGGTACTGT TTGCATTAAT      480
AAATTAAAGC CTCGAG                                     496
```

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```
TTNGGCCAAA GGGGCTTAGG ACAAACAAA ACATTTTCCT TTGGGTTTNA NTTCTNTCT      60
TTNTTCTCCC ATTANTNNT GGGGTGGTGT TGCTTTTCCT TTCCTTTTCC CTGGGAGATT      120
TTNTNGTTGT NGTTTCCTTT TTGTATTNTA NTGATATCAC CAGGATAGTT TACTCTCNTT      180
NTAGCTNTGT GCTTACCGCA CANTGGATAA CACACACATA CACACCCACA AAAATGNTCA      240
TGAACCCAAT CCGGAGAAGG TTCCAGCAGG TCCCCCACC TCCTCTCTC CTCNTACTTC      300
TCCTCTNGAC AGCGAGGACA GGAGGGGAC AAGGGGACAC CTGGGCAGAC CCGCCGGCTN      360
TTCCCCCAC CCCACCCCG CACCCTCGAG                                     390
```


(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GAATTCGGCC	AAAGAGCAAT	TCTCAAATG	AAGCTCGCAC	TCTCGCCTCC	AGCATGAAAG	60
TCTCTGCCGC	CCTTCTGTGC	CTGCTGCTCA	TAGCAGCCAC	CTTCATTCCC	CAAGGGCTCG	120
CTCAGCCAGA	TGCAATCAAT	GCCCCAGTCA	CCTGCTGCTA	TAACTTCACC	AATAGGAAGA	180
TCTCAGTGCA	GAGGCTCGCG	AGCTATAGAA	GAATCACCAG	CAGCAAGTGT	CCCAAAGAAG	240
CTGTGATCTT	CAAGACCATT	GTGGCCAAGG	AGATCTGTGC	TGACCCCAAG	CAGAAAGTGGG	300
TTCAGGATTC	CATGGACCAC	CTGGACAAGC	AAACCCAAAC	TCCGAAGACT	CTCGAG	356

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAATTCGGCC	AAAGAGGCCT	ACCGAGACTG	ACACACTGAA	CTCCACTTCC	TCCTCTTAAA	60
TTTATTTCTA	CTTAATAGCC	ACTCGTCTCT	TTTTTTCCCC	ATCTCATTGC	TCCAAGAATT	120
TTTTTCTTCT	TACTCGCCAA	AGTCAGGGTT	CCCTCTGCCC	GTCCCGTATT	AATATTTCCA	180
CTTTTGGAAC	TACTGGCCTT	TTCTTTTAA	AGGAATTCAA	GCAGGATACG	TTTTTCTGTT	240
GGGCATTGAC	TAGATTGTTT	GCAAAAGTTT	CGCATCAAAA	ACAACAACAA	CAAAAAACCA	300
AACAACTCTC	CTTGATCTAT	ACTTTGAGAA	TTGTTGATTT	CTTTTTTTTA	TTCTGACTTT	360
TAAAAACAAC	TTTTTTTCC	ACTTTTTTAA	AAAATGCACT	ACTGTGTGCT	GAGCGCTTTT	420
CTGATCCTGC	ATCTGGTCAC	GGTCGCGCTC	AGCCTGTCTA	CCTGCAGCAC	CACTCTCGAG	480

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GAATTCGGCC	AAAGAGCCTA	ACACAGGAAA	CATTACAATT	GAACAATGCC	TCAGCTATAC	60
ATTTACATCA	GATTATTGGG	AGCCTATTTG	TTTCATCATT	CTCGTGTTCA	AGGACAGAAT	120
CTGGATAGTA	TGCTTCATGG	CACTGGGATG	AAATCAGACT	CCGACCAGAA	AAAGTCAGAA	180
AATGGAGTAA	CCTTAGCACC	AGAGGATACC	TTGCCTTTT	TAAAGTGCTA	TTGCTCAGGG	240
CACTGTCCAG	ATGATGCTAT	TAATAACACA	TGCATACTA	ATGGACATTG	CTTGCCATC	300
ATAGAAGAAG	ATGACCAGGG	AGAAACCACA	TTAGCTTCAG	GGTGTATGAA	ATATGAAGGA	360
TCTGATTTTC	AGTGCAAGA	TTCTCCAAAA	GCCAGCTAC	GCCGGACAAT	AGAATGTTGT	420

CGGACCAATT TATGTAACCA GTATTGCAA CCCACGCTCG AG

462

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GAATTCGGCC AAAGAGGCCT AACACAGGAA ACATTACAAT TGAACAATGC CTCAGCTATA	60
CATTTACATC AGATTATTGG GAGCCTATTT GTTCATCATT TCTCGTGTTC AAGGACAGAA	120
TCTGGATAGT ATGCTTCATG GCACTGGGAT GAAATCAGAC TCCGACCAGA AAAAGTCAGA	180
AAATGGAGTA ACCTTAGCAC CAGAGGATAC CTTGCCTTTT TTAAGTGCT ATTGCTCAGG	240
GCACTGTCCA GATGATGCTA TTAATAACAC ATGCATAACT AATGGACATT GCTTTGCCAT	300
CATAGAAGAA GATGACCAGG GAGAAACCAC ATTAGCTTCA GGGTGTATGA AATATGAAGG	360
ATCTGATTTT CAGTGCAAAG ATTCTCCAAA AGCCGAGCTA CGCCGGACAA TAGAATGTTG	420
TCGGACCAAT TTATGTAACC AGTATTTGCA ACCCAGCTC GAG	463

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TACGAGAAGT CCTGTAAGAC GTAAATATTT TTAATAATCA CTGAATTTTT GTCTTTCTCG	60
GTACCATAGA ACACCACAGC CAAGAGATCT CGATCACTGC TTATGATCTT ACTGATGTAC	120
ACACTTTGGA TACTGCGAT GCTCATGTCA AAAGGTGTCA ACTCATCTTC ATCTCCATCC	180
TCTTCCTCAC CATCACCTTC TTCTCCTCC TCCTCTTCTT CCCCACCTTC TTCCTCTTCT	240
TCGTCTACCT CATGTGACG CTCTGCTCC CCATTTTCTT CATTAGCATT CCGTTAGCA	300
GGGGCGTCTC TTCCATTTTC TGCCTCTTCC ACAACTTCTT TCTTCTCTT TAAGTCCTTG	360
GTGGTGAGT	369

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GAATTCGGCC NAAGANGCCT ATGATCNTCT TCTTTGAAGA AACATGAAGT TACACTATGT	60
TGCTGTGCTT ACTCTANCCA TCCTGATGTT CCTGACATGG CTCCACAAT CACTGAGCTG	120
TNACAAAGCA CTCTGTGCTA NTGATGTGAG CAAATGCCTC ATTCAGGAGC TCTGCCNGTG	180
CCGGCCGGGA GAAGCAATTG CTCTGCTGT NAGGAGTGCA TGCTGTGTCT TGGGGCCCTT	240

TGGGACGANT GCTGTGACTG TGTTGGTATG TGTAATCCTC GAAATTATAG TGACACACCG 300
CACCTCNAG 309

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAATTCGGCC AAAGAGGCCT AATTCTGGTT TAAGATTCTA TCCATTTCTC ACTCTCAGAT 60
CTGTTTGTTT CACCCTCTCC CCCTAAATAT TTGGATTTTA TATAGACCAG TAGGCTAAGG 120
TAGGGAAGAC CACTGACAAG TATAAATTTA AGAGTTTACA AAACCAAGGA GGCCATCCAG 180
CCCCTAGTTC TAAGCCATGT TCAGCACAGT GCCAACTTTG CCTTCCCTGG CTGTCCTTGC 240
TTGCTTTCTG GTTGCTGTAA TTCTGAGGGG CAACCAGGCT TGCTGTAGAG AGGAGAGCCA 300
GATGATGTGG AAGCCTAAGG CCACACCCCT CGAG 334

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

TAACCAGCCT TGAAAAGCCC TTCCTCTGGC TTGCTAGGAA GTCATTGGA GACCCTAACT 60
TGGAATTTGT TGCCATGCCT GCTCTGCCC CACCAGAAGT TGTCATGGAC CCAGCTTTGG 120
CAGCACAGTA TGAGCAGGAC TTAGAGGTTG CTCAGACAAC TGCTCTCCCG GATGAGGATG 180
ATGACCTGTG AGAATGAAGC TGGAGCCCAG CGTCAGAAGT CTAGTTTAT AGGCAGCTGT 240
CCTGTGATGT CAGCGGTGCA GCGTGTGTGC CACCTCATTA TTATCTAGCT AAGCGGAACA 300
TGTGCTTCAT CTGTGGGATG CTGAAGGAGA TGAGTGGGCT TCGGAGTGAA TGTGGCAGTT 360
TAAAAAATAA CTTCAATTGT TGGACCTGCA TATTTAGCTG TTTTGGACG CAGTTGATTC 420
CTTGAGTTTC ATATATAAGA CTGCTGCAGT CACATCACAA TATTCAGTGG TGAATCTTGT 480
TTGTTACTGT CATTCCCATC CTTTTGCTT TAGAATCAGA AT 522

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTCGGCC AAAGAGGCCT AGGACAAAAC AAAACATTTT CCTTTGGGTT TTTTITTTCT 60
TTCTTTTTTC TCCCCTTTAC TCTTTGGGTG GTGTTGCTTT TCCTTTCTTT TCCCCTTTGA 120
GATTTTTTTG TTGTTGTTTC CTTTTGTAT TTTACTGATA TCACCAGGAT AGTTTACTCT 180

CCTTCTAGCT TTCTGCTTAC CGCACACTGG ATAACACACA CATAACACACC CACAAAAATG	240
CTCATGAACC CAATCCGGAG AAGGTTCCAG CAGGTCCCCC ACCCTCCCCT CCTCCTCCTA	300
CTTCTCCTCT TGACAGCGAG GACAGGAGGG GGACAAGGGG ACACCTGGGC AGACCCGCCG	360
GCTCTCCCCC CACCCACCC CGGCACCTC GAG	393

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAATTCGGCC AAAGAGGCCT ATTCTAGGAC AAGAGCCAGG AAGAAACCAC CGGAAGGAAC	60
CATCTCACTG TGTGTAAACA TGACTTCCAA GCTGGCCGTG GCTCTCTTGG CAGCCTTCCT	120
GATTTCGCA GCTCTGTGTG AAGGTGCAGT TTTGCCAAGG AGTGCTAAAG AACTTAGATG	180
TCAGTGCATA AAGACATACT CCAAACCTTT CCACCCAAA TTTATCAAAG AACTGAGAGT	240
GATTGAGAGT GGACCACACT GCGCCAACAC AGAAATTATT GTAAAGCTTT CTGATGGAAG	300
AGAGCTCTGT CTGGACCCCA AGGAAAAC TG GGTGCAGAGG GAGCTCGAG	349

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GAATTCGGCC AAAGAGGCCT ACAAGAAAGC AAGCTCATCA TACTGGCTAG TGGTGGACCC	60
CAAGCTTTAG TAAATATAAT GAGGACCTAT ACTTACGAAA AACTACTGTG GACCACAAGC	120
AGAGTGCTGA AGGTGCTATC TGTCTGCTCT AGTAATAAGC CGGCTATTGT AGAAGCTGGT	180
GGAATGCAAG CTTTAGGACT TCACCTGACA GATCCAAGTC AACGTCTTGT TCAGAACTGT	240
CTTTGGACTC TCAGGAATCT TTCAGATGCT GCAACTAAAC AGGAAGGGAT GGAAGGTCTC	300
CTTGGGACTC TTGTTAGCT TCTGGGTTCA GATGATATAA ATGTGGTCAC CTGTGCAGAT	360
CTCGAG	366

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TACAGCCACA TCTGGATACA CACACACACT CTTACATTCA TACCCAGAGA CTGGTGCACA	60
GACACACACA CATCCCCCGT CTTGCCAATC AGTCCCAGGA ACACACAGGT CTCTATCAAC	120
ACCCAGAAAT TCTGACACCA CAAGCACAGG CCAACCTACA GCTAGAGGAT TAATGTCCAG	180

```

ACCCACAGGC TGGTGTGCGC ATGTCCTTCC ACGTGAATGT CACATGGGAG GACAGACTGC      240
ATGGATTTTT TTAATGACAC TATTTTATTT ATTTTTTGAG ACAGAGTCTC ACTCTGTCCG      300
CCAGGATGGA GTGCAGTGGC GTGATCTCGG CTCACTACAA CCTCCGCCTC CTGGGTTCAA      360
CCGATTCTCG TGCCTCAGCA TCCAAGTAC CTGGGATTAC AGGCGCATGC CACCAGTCC      420
A                                                                                   421

```

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

```

GAATTCGGCC AAAGAGGCCT AGGGAGATCT GGATGGCATC TACTTCGTAT GACTATTGCA      60
GAGTGCCCAT GGAAGACGGG GATAAGCGCT GTAAGCTTCT GCTGGGGATA GGAATTCTGG      120
TGCTCCTGAT CATCGTGATT CTGGGGGTGC CCTTGATTAT CTTCAACATC AAGGCCAACA      180
GCGAGGCCTG CCGGACGGC CTTCGGGCAG TGATGGAGTG TCGCAATGTC ACCCATCTCC      240
TGCAACAAGA GCTGACCGAG GCCCAGAAGG GCTTTCAGGA TGTGGAGGCC CAGGCCGCCA      300
CCTGCAACCA CACTGTGATG GCCCTAATGG CTTCCCTGGA TGCAGAGAAG GCCCAAGGAC      360
AAAAGAAAAA GGAGGAGCTC GAG                                                                                   383

```

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

```

GAATTCGGCC AAAGAGGCCT ACCCCAGTCC AGATCCAGGA CTGAGATCCC AGAACCATGA      60
ACCTGGCCAT CAGCATCGCT CTCCTGCTAA CAGTCTTGCA GGTCTCCCGA GGGCAGAAGG      120
TGACCAGCCT AACGGCCTGC CTAGTGGACC AGAGCCTTCG TCTGGACTGC CGCCATGAGA      180
ATACCAGCAG TTCACCCATC CAGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCAGC      240
TGCTCTTTGG CACTGTGGGG GTGCCTGAGC ACACATACCG CTCCCGAACC AACTTCACCA      300
GCAATACAA CATGAAGGTC CTCTACTTAT CCGCCTTCAC TAGCAAGGAC GAGGGCACCT      360
ACACGTGTGC ACTCCACCAC TCTGGCCATT CCCACCCAT CTCCTCCGAG AACGTCACCA      420
GTCTCGAG                                                                                   428

```

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAATTCGGCC AAAGAGGCCT AAAGAGCTCT CACTTCAGTC TTACTTACCC CACTGCTATT	60
CCCTGTGGAG AAAGCCGGCT AATTGTTTTG ATAAGGCTAT CTGCCATTGT AGAATACCTT	120
TCTCTAGTAG CTGAATGACA ATCAACTATA CGTTCCATAC TAAACATGCC AGAGATAGGA	180
CTTTTAGGCC TTGCTTTACA AACTGGTTT TTAACAGCTG ACATGAATAT TTCCCGTTTC	240
TATTTCTTT TTTTTTTTT TTTTTTTTT TGAGACGGAG TCTCGCTCTA TCCCCACGC	300
TCGAG	305

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 0 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAATTCGGCC AAAGAGGCCT AANAGAAGAT GCCCCTGCTG ATCACTCTAA CCTGCTCCTC	60
TTCTGGCTCT CAGGCTACTC CATTGCCACT CAAATCACCG GTCCAACAAC AGTGAATGGC	120
TTGGAGCGGG GCTCCTTGAC CGTGCACTGT GTTTACAGAT CAGGCTGGGA GACCTACTTG	180
AAGTGGTGGT GTOGAGGAGC TATTTGGCGT GACTGCAAGA TCCTTGTTAA AACCAGTGGG	240
TCAGAGCAGG AGGTGAAGAG GGACCGGGTG TCCATCAAGG ACAATCAGAA AAACCGCACG	300
TTCATGTGA CCATGGAGGA TCTCATGAAA ACTGATGCTG ACACTTACTG GTGTGGAATT	360
GAGAAAACCTG GAAATGACCT TGGGGTCACA GTTCAAGTGA CCATTGACCC AGCACCAGTC	420
ACCCRAAGAAG AACTAGCAG CTCCCCAAGT CTGACCGGCC ACCACTTGGA CAACAGGCAC	480
AAGCTCCTGA AGCTCAGTGT CCTCCACCC CTCGAG	516

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GAATTCGGCC AAAGAGGCCT AGCGCCCTGA AGACAGAATG TTCCATATCA GAGCTGTGAT	60
CTTGAGAGCC CTCTCCTTGG CTTTCCTGCT GAGTCTCCGA GGAGCTGGGG CCATCAAGGC	120
GGACCATGTG TCAACTTATG CCGCGTTTGT ACAGACGCAT AGACCAACAG GGGAGTTTAT	180
GTTTGAATTT GATGAAGATG AGATGTTCTA TGTGGATCTG GACAAGAAGG AGACCGTCTG	240
GCATCTGGAG GAGTTTGGCC AAGCCTTTTC CTTTGAGGCT CAGGGCGGGC TGGCTAACAT	300

TGCTATATTG AACAACT TGAATACCTT GATCCAGCGT TCCAACCACA CTCAGGCCAC	360
CAACGATCCC CCGAGGTGA CCGTGTTCC CAAGGAGCCT GTGGAGCTGG GCCAGCCCAA	420
CACCCTCATC TGCCACATTG ACAAGTCTT CCTACCAGTG CTCGAG	466

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TAGGCAGAAT GGGACTCCAA GCCTGCCTCC TAGGGCTCTT TGCCCTCATC CTCTCTGGCA	60
AATGCAGTTA CAGCCCGGAG CCCGACCAGC GGAGGACGCT GCGCCAGGC TGGGTGTCCC	120
TGGGCCGTGC GGACCCTGAG GAAGAGCTGA GTCTCACCTT TGCCCTGAGA CAGCAGAATG	180
TGGATCGACG T	191

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT	60
TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG	120
GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCTCAC CTGCACTGTC TCTGGTGGCT	180
CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCGCCAGGG AAGGGGCTGG	240
AGTGGATTGG GAGTATCTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTCAAGAGTC	300
GAGTCACCAT ATCCGTAGAC ACGTCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTGTGA	360
CCGCCGAGA CACGGCTGTG TATTACTGTG CGAGACATTC TGGGCGCAGC AGCTGGTTCA	420
CGTCTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AGGGAGTGCA TCCGCCCCAA	480
CCCTTTTCCC CCTCGTCTCN TGTGAGAATT CCGCGTCGGA TACGAGCAGC GTGGCCGTTG	540
GCTGCCTCGC ACAGGACTTC CTTCCGACT CCATCACTTT CTCCTGAAA TACAAGAACA	600
ACTCTGAACT CGAG	614

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 0 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 427 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GAATTCGGCC AAAGAGGCCT ANACTGCAGC TCTTTTCATT TTGCCATCCT TTTCCAGCTC	60
CATGATGGTT CTGCAGGTTT CTGCGGCCCC CCGGACAGTG GCTCTGACGG CGTTACTGAT	120
GGTGCTGCTC ACATCTGTGG TCCAGGGCAG GGCCACTCCA GAGAATTACC TTTCCAGGG	180
ACGGCAGGAA TGCTACGCGT TTAATGGGAC ACAGCGCTTC CTGGAGAGAT ACATCTACAA	240
CCGGGAGGAG TTGCGCGGCT TCGACAGCGA CGTGGGGGAG TTCCGGGCGG TGA C GGAGCT	300
GGGGCGGCCT GCTGCGGAGT ACTGGAACAG CCAGAAGGAC ATCCTGGAGG AGAAGCGGGC	360
AGTGCCGGAC AGGATG T GCA GACACAATA CGAGCTGGGC GGGCCCATGA CCCTCACAGA	420
ACTCGAG	427

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

TAGGGATGTC AACATGATCT TTTCATATAT GCTGGCTATA GAAATTGGTC TCGGTGAAGT	60
AATGGTCTGT CTGTCAAGCA TGACATCCTT GCCTGTGTTA AGTTTTGTGT GCTCTTCTGG	120
GATGTTGATC GTGACGTCTT GTCCGGGATT GAGAAGCTTC TGTTGCTCTT CTGGGATGTC	180
ATTGATGATC TCTTCATATA TGCTGGCTAT AGAAATTGGG CTCTGTGAAG AAATAGTGTG	240
TCCCCAACCT TGGTACAGNC CCCCTGGGGA GGGTACCTTT GAAGAACCAG AAGTTAGANC	300
TTGTGAAGAA GAAGAAAGTA GG	322

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GAATTCGGCC AAAGAGGCCT ATGGAGTGTG AGAACAGCAA AAAATAATAA TTCAACCACT	60
TGGTTATTAT GAACATCATT TTCATATTTT TAAAAATATG CTATATCATG GAATTCAATG	120
TAAACCTCA AGAGATGCCA TCCTTGAGA GGGCTGCACC AGCCTGTGCC CCAAGTTACC	180
CAGGATCACC CCCTACTTCT CCTGACGGCC CCCCAGAGAA GGCCTGCATT CTGGGCGACG	240
TGGCCTTCAG GGGCTCAACC CTTGGCCTCG AG	272

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```
GAATTCGGCC AAAGAGGCCT AGCCAATTTG GTTTTCTAAG TATTTTCACG CCTTCTCCTC   60
GTGTCCGCGT CACTGCTCTG ATTCAGGCCC TTGTCAATTC TCATCTTTGC CATTTTAGTA   120
GTTTTTGGAT TGGGCTCCCG GCTGCTAATT TTGTCCCCTT TTCCACTATC TTCCACATTG   180
TCACCGCAGT CATGTTTCTA AGGCAGAATC TCACTGTGCC CCACATCGTG TTGCTGGGCC   240
CTTGCAATGCC GTACCCCTGGC CTTTGTGAAA TGCCCTTCAT CTGTGCTCTT CCCTCCACCT   300
GGAATGTCCG TCTCTCTTTT TCTGCCAACC CACNCGACCC CTCCTCCTN CAAGCCCGTG   360
AGTGTCCCN CCCTCATGT CCTGTGGTGA CAGAGCTCGA G                               401
```

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```
GAATTCGGCC AAAGAGGCCT ACGATATTTG CTGCGACCCG CAGGCGCTAT CCGTGCCCGG   60
GTTCTGGCGC GCCCTTTCAG TTCTGCTTGC TGTCGCGACC GNTGCGTTAC CCGGAACCGC   120
CGGGCCGAAC AGCATGACGT CCGCTTTGGA GAACTACATC AACCGAACTG TTGCCGTTAT   180
TACATCAGAT GGGAGAATGA TTGTGGGAAC ACTGAAAGGT TTTGACCAGA CCATTAATTT   240
GATTTTGGAT GAAAGCCATG AACGAGTATT CAGTCTTCA CAGGGGGTAG AACAAAGTGGT   300
ACTAGGATTA TACATTGTAA GAGGTGACAA CGTTGCAGTC ATTGGAGAAA TCGATGAAGA   360
AACAGATTCT GCGCTTGATT AGGGGAACAC TCGAG                               395
```

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```
GAATTCGGCC ANAGAGGCCT AAGAGCCAGT AAAAAAATTG TTAGAAAGCA GATACCATCA   60
AATTGGTTCT GGGAAAGTGTG AAATCAAAGT TGCACAACCC AAAGAGGTAT ATAGGCAGCA   120
ACAGCAACAA CAAAAAGGTG GAAGAGGTGC TGCAGCTGGT GGACGAGGTG GTACGAGGGG   180
TCGTGGCCGA GGTCAGGGCC AAAACTGGAA CCAAGGATT TATAACTATT ATGATCAAGG   240
ATATGGAAAT TACAATAGTG CCTATGGTGG TGATCAAAAC TATAGTGGCT ATGGCGGATA   300
TGATTATACT GGTATAACT ATGGGAACTA TGGATATGGA CAGGGATATG CAGACTACAG   360
TGGCCAACAG AGCACTTATG GCAAGGCATC TCGAG                               395
```

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GAATTCGGCC AAAGAGGCCT AGTTTGGTCG TTCGTTGGGC GGTGCTGGTT TTTCGCTCGT	60
CGACTGCGGC TCTTCCTCGG GCAGCGGAAG CGGCGCGGCG GTCGGAGAAG TGGCCTAAAA	120
CTTCGGCGTT GGGTGAAAGA AAATGGCCCG AACCAAGCAG ACTGCTCGTA AGTCCACCGG	180
TGGGAAAGCC CCCC GCCAAA CAGTTGNCCA CGGAAANCCG CCAGGAAAAG CGCTCCNTCT	240
ACCGGCGGGG TGAAGAAGCC TCATCGCTAC AGGCCCGGGA CCGTGGCGCT TCGAGAGATT	300
CGTCGTTATC AGAAGTCGAC CGAGCTGCTC ATCCGGAAGC TGCCCTTCCA GAGGTGGTG	360
AGGGAGATCG CGCAGGATTT CAAAACCGAC CTGAGGTTTC AGAGCGCAGC CATCGGTGCG	420
CTGCAGGAGG CTAGCGAAGC GTACCTGGTG GGTCTGTTTC AAGATACCAA CCTGTGTGCC	480
ATCCACGCTA AGAGAGTCAC CATCATGCCC AAAGACATCC AGTTGGCTCG CCGGATACGG	540
GGAGAGAGAG CTTTCTCGAG	560

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GAATTCGGCC AAAGAGGCCT ACTAGTTTAC TTTATCCCAT CCATTATAT ATACATATAT	60
ATACACATAT ATGTGTGTTG TTTTGTGTTT GTTTGTGTTT GTTTTGTGA GATGGAGTCT	120
CGCTCTGTCG CCCAGGCTGG AGTGCACTGG TGTGATCTTG GCTCACTGCA ACCTCTGCCT	180
CCTGGGTTC AAGCAATTCTC CTGCCTCAGC TTCCCGAGT AGCTGGGACT ACAGGTGTGC	240
GCCACCACGC CCGGCAAATT TTTTGTGTTT TTTTGTGTTT TTGATATTT TAGCAGAGAT	300
GAGGTTTCCC CACGTTGGCC AGGCTGGTCT CGAACTCTTG ACCTCAGGTT ATCTGCCTGC	360
CTTGGCCTCC CAAAGTGTG GGATTACAGG CGTGAGCCAC CGAACCTCGA G	411

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 0 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

```
GAATTCGGCC AAAGAGGCCT ACGTGGTGCG CGAGAGCGTA TCCCCAACTG GGA CTTCGGA      60
GGCAACTTGA ACTCAGAACA CTACAGCGGA GAGCCACCC GGTGCTTGAG GCGGGACCGA      120
GGCGCAGAGA GACCGAGGCG CATAGAGACC GAGGCACAGC CCAGCTGGGG CTAGGCCCGG      180
TGGGAAAGGA GAGCGTCGTT AATTTATTTT TTATTGCTCC TAATTAATAT TTATATGTAT      240
TTATGTACGT CCTCCTAGGT GATGGAGATG TGTACGTAAT ATTTATTTTA ACTTATGCAA      300
GGGTGTGAGA TGTTCCTCT GCTGTAAATG CAGGTCTCTT GGTATTTATT GAGCTTTGTG      360
GGA CTGGTG AAGCAGGACA CCTGGAACTG CGCCAAAGTA GCGGACTCGA G      411
```

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

```
GAATGCTGAT TGACCAGCTA AAAATCAAAT TACAAGATAG CCAAATAAC TTACAGATTA      60
ATGTATCTGA ACTTCAGACA TTGCAGTCTG AACATGNTAC ACTGCTAGAA AGGCACAACA      120
AGATGCTGCA GGAAACTGTG TCTCAGCTCG AG      152
```

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

```
GAATTCGGCC AAAGAGGCCT ACACNTCTGC ACCTCAACCA CAGACTACAC TTGCTGAACT      60
GGCTCCTGGG GCCATGAGGC TGCTACTGCC ACTGCTGCTG CTGCTGCTGG GAGCCTGGGC      120
CATCCCAGGG GGCTCGGGG ACAGGGCGCC ACTCACAGCC ACAGCCCCAC AACTGGATGA      180
TGAGGAGATG TACTCAGCCC ACATGCCCGC TCACCTGCGC TGTGATGCCT GCAGAGCTGT      240
GGCTTACCAG GTGAGTCCTT CACCACTGTC ACCCTGCCCT GCTCACACCC CTTCTCAAGC      300
CAGACCCCTC CACCCACCTC ACATTCCACC ACCGGCCTTT GATCCCCGCC TCGAG      355
```

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

```

GAATTCGGCC AAAGAGGCCT AATTATAAGC ACTCAATAAT ACATTATCAA CTATTATTAC      60
TCAATTAAAA CTGGTTAACT TTAATTGAAT TTGAACTGCC ACCTAGAATA GACAAGAAAA      120
TGAAACACAA TTCTGTATGG ATGTCAGAAA CATGAAATAT AAAATGTAAT AAATAAAAAAT      180
ATTAAAAACC CCTTAGCAAA TGTTAAGGAG CGTGTCAAAT GATTCTGTG TTGAACCTTA      240
AGCATTTAGG TGGCTGGAGC CTTGAAAGTT ACCATCCCCC AATTTTCTGC TGTGTCACTA      300
GGTTTTTTTC TATTGAGCAA TTCTTTCAGG TCGCCTCCAC TCTGCTCTGC CTAAAGGACA      360
ACTTCATATA GTGCATTCGT GTCTTAGACT CCACGATCTC GAG                          403

```

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

```

GAATTCGGCC AAAGAGGCCT AAGCGCTAAG CCTGGAGTGT GGGCACTGCA GTTTCAGAGG      60
CACCGATTAT GAGAATGTGC AGCTCCACAT GGGCTCCATT CATCCTGAGT TCTGTGATGA      120
TATGGATGCC GGGGGCCTGG GCAAGCTCAT CTTTACCAG AAGAGTGCAA AGCTCTTCCA      180
TTGCCATAAG TGCTTCTTCA CAGCAAGCT GTACGCCAAT GTGTACTATC ACATCAGGGC      240
CAGACACGCA GCCTCGGACA AGTGGAGTGA GCAGCCGAAA GAGCAGCCCA GCAAAGACAC      300
CCGTTCGAG                                     308

```

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

```

GAATTCGGCC AAAGAGGCCT ACTGTGGTAA TTCTAGAGCT AATACATGCC GACGGGCGCT      60
GACCCCTTC GCGGGGGGGA TCGTGCATT TATCAGATCA AAACCAACCC GGTCAGCCCC      120
TCTCCGGCCC CGGCCGGGGG GCGGCGCCG GCGGCTTTGG TGA CTCTAGA TAACCTCGGG      180
CCGATCGCAC GCCCCCCGTG GCGGCGACGA CCCATTGAA CGTCTGCCCT ATCAACTTTC      240
GATGGTAGTC GCCGTGCCTA CCATGGTGAC CACGGGTGAC GGGGAATCAG GGTTTCGATTC      300
CGGAGAGGGA GCCTGAGAAA CCGTTACCAC ATCCAAGGAA GGCAGCAGGC GCGCACCTCG      360
AG                                     362

```

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GAATTCGGCC	AAAGAGGCCT	ATTCTTTTTT	AACTAATCA	CCATATTGTA	AATTCAGGG	60
TTTTTTTTTT	GGTTAAGCT	GACTCTNGC	TCTAATTTT	GAAAAAAGA	AATGTGAAG	120
GTCAACTCCA	ACGTATGTG	TTATCTGTG	AAGTTGCACA	GCGTGGCTTT	TCCTAAACTG	180
GTGTTTTTCC	CCCGCATTG	GTGGATTTT	TATTATTAT	CAAAACATA	ACTGAGTTTT	240
TTAAAGAGG	AGAAAATTTA	TATCTGGGT	AAGTGTAT	CATATATATG	GGTACTTTGT	300
AATATCTAAA	AACCTAGAAA	CGGAAATGA	ATCCTGCTCA	CAAAATCACT	TTAAGATCTT	360
TTCGAAGCTG	TTAATTTTTC	CTAGTGTGT	GGACACTGCA	GACTTGTC	GTGCTCCAC	420
GGCCTGTACG	GACACGACTC	TCGAG				445

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GAATTCGGCC	AAAGAGGCCT	ACTTCACTCT	CTCATTCTTA	GCTTGAATTT	GGAAATGACT	60
TTTGATGACC	TAAAGATCCA	GACTGTGAAG	GACCAGCCTG	ATGAGAAGTC	AAATGGAAAA	120
AAAGCTAAAG	GTCTTCAGTT	TCTTACTCT	CCATGGTGGT	GCCTGGCTGC	TGCGACTCTA	180
GGGGTCCTTT	GCCTGGGATT	AGTAGTGACC	ATTATGGTGC	TGGGCATGCA	ATTATCCAG	240
GTGCTGACC	TCCTAACACA	AGAGCAAGCA	AACCTAACTC	ACCAGAAAAA	GAAACTGGAG	300
GGACAGATCT	CAGCCCGCA	ACAAGCAGNA	GAAGCTGTTT	TCGAG		345

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 511 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GAATTCGGCC	AAAGAGGCCT	ACTGGGGAGT	CTGCTATATT	GTGTGAAGG	TCTCTTTGTT	60
AGTGGTGGTA	GAAATTGGAG	TATTCCTCT	CATTGTGGT	TGGTGGCTGG	ATATCTGTTT	120
CTTGAAATG	TTTGATGCTA	CTCTGAAAGA	TCGAGAACTG	AGCTTTCAGT	CGGCTCCAGG	180
TACTACCATG	TTTCTGCATT	GGCTAGTGGG	AATGGTATAT	GTCTTCTACT	TGCTCCTT	240
CATTCTATTA	CTGAGAGAGG	TACTTCGACC	TGGTGTCTG	TGGTTTCTAA	GGAATTTGAA	300
TGATCCAGAT	TTCAATCCAG	TACAGGAAAT	GATCCATTG	CCAATATATA	GGCATCTCCG	360
AAGATTTATT	TTGTCAGTGA	TTGTCTTTGG	CTCCATTGTC	CTCCTGATGC	TTTGGCTTCC	420
TATACGTATA	ATTAAGAGTG	TGCTGCCTAA	TTTTCTTCCA	TACAATGTCA	TGCTCTACAG	480
TGATGCTCCA	GTGAGTGAAC	TGTCCCTCGA	G			511

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GAATTCGGCC	AAAGAGGCCT	AGTTTATACC	CACAGAATTT	TTCATAAAA	TTAACCAAAC	60
CCTTTTCACT	TTGCTTAAGA	CTTCAGTTTT	GTCCCATTAC	TCTTTAAGGT	TAAGACCATC	120
TATAAAATCC	TCTGAACCTG	ACAAAATTAC	ATTCTCTTTA	NCAAAATCCA	TATTCCTATG	180
CCTTCTTATA	ATCTTTTACC	AAAAACACCT	TCCCTATACA	CCTTGACGT	AAAACGTGTT	240
CTCCAGTGGT	CTCAACTACA	TATTATACTG	TTAACTCTTA	CTCCTTTTAG	CATAGCTAGT	300
AGGCATGGCT	CTCCATATGT	TCCCAGGCAT	CTCGAG			336

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GAATTCGGCC	AAAGAGGCCT	AGTGGGTAGA	TACAGACCCT	AACTTTGAGC	TCTAAGATGA	60
AATTTGTTTA	TAAATCCCTA	GTTTCCATTG	AGTTTITTTCA	ATATTATCA	AACACCTACT	120
GTGCCAGGCA	TTGTTTAGGC	ACAGGGGATA	CAGCAGAAAA	ACTCGAG		167

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GAATTCGGCC	AAAGAGGCCT	ACACAGCCT	TTGGCACAAT	GAAGTGGGTA	ACCTTTATTT	60
CCCTTCTTTT	TCTCTTAGC	TGGGCTTATT	CCAGGGGTGT	GTTTCGTGGA	GATGCACACA	120
AGAGTGAGGT	TGCTCATCGG	TTTAAAGATT	TGGGAGAAGA	AAATTTCAA	GCCTTGGTGT	180
TGATTGCCTT	TGCTCAGTAT	CTTCAGCAGT	GTCCATTGTA	AGATCATGTA	AAATTAGTGA	240
ATGAAGTAAC	TGAATTTGCA	AAAACATGTG	TTGCTGATGA	GTCAGCTGAA	AATGTGACA	300
AATCACTTCA	TACCTTTTTT	GGAGACAAAT	TATGCACAGT	TGCAACTCTT	CGTGAAACCT	360
ATGGTGAAAC	CCTCGAG					377

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

```

CTTGGGGGTG GGTTCNNNT ANAAAAATT ANAGNCGTTG GGGGTTGGGG GGCNGAGAAG      60
GAANANAGAA CCCNCGNAA AATTTGAAAA CNGGGTNATT TATCCNGTNT TTTNAANGAG      120
AATCCCANNC CCGGAAAAAA AAAAAAANG AGGAANANAN AGATTGTAAG TTAACACAAA      180
AATCTATCTG TATAAGTCTT TACTGTACA AGTCTGTACA AGTCAGTNAG GTTGGTCTC      240
TGCAGAGCCA GAACTTCAGA GAAGGTGATT TAATTGTAGG CNTCTTGGT AGGCCTCTTT      300
GGCCGAATTC                                     313

```

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

```

GAATTCGCCC AAGAGGCCTA AAGAGGCCTA GAAGCCAAA AACCTTTCCC GAAAGGAGTC      60
TTCACCAAAG AGCTCCCATC TGGCAAGAAA TACCTCCGCT ACACACCCCA GCCTTAAGTC      120
TCTTGGAGAA GCTGGTGTCTG TGAGCCAGAG GATGTCAGCT GCCAATTGTG TTTTCCTGCA      180
GCAATTCCAT AAACACATCC TGGTGTCTC ACAGCCAAGG TTTTAGGTT GCTATACCAA      240
TGGCTTATTA AATGAAAATG GCACTAAAAG TTTCTTGAGA TTCTTTATAC TCTCTGCCTT      300
CAGCAATCTC GAG                                     313

```

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

```

GAATTCGGCC AAAGAGGCCT AGGAACCACT GGCTTGGTGG ATTTTGCTAG ATTTTCTGA      60
TTTTTAACT CCTGAAAAT ATCCAGATA ACTGTCATGG AGCTGGTAAC TATCTTCTG      120
CTGGTGACCA TCAGCCTTTG TAGTTACTCT GCTACTGCCT TCCTCATCAA CAAAGTGCCC      180
CTTCCTGTTG ACAAGTTGGC ACCTTTACCT CTGGACAACA TTCTTCCCTT TATGGATCCA      240
TTAAAGCTTC TTCTGAAAAC TCTGGGCATT TNTGTTGGG ACCTTGTTGA GGGGCTAAGG      300
AAGTGTGTAA ATGAGCTGGG ACCAGAGGCT TCTGAAGCTG TGGAGCAACC GCTCGAG      357

```

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

```

GAATTCGGCC AAAGAGGCCT ATTAATGTG TCATTGGAAG CCATCCCTTT TTTTACATT      60
CATACAACAG AAACCAGAAA AGCAATACTG TTTCCATTTT AAGGATATGA TTAATATTAT      120

```

TAATATAATA ATGATGATGA TGATGATGAA AACTAAGGAT TTTTCAAGAG ATCTTTCTTT 180
 CCAAAACATT TCTGGACAGT ACCTCGAG 208

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TNAAACCAAT AGTTTTTTAA AAGACAAGCT TGGGTGGGTG CANGNTGGGG ACAGTGCTGG 60
 TCTTTCACNG CAGCCAGGC ACCCNTGAG AGTCCAGNG NGNGTNATGC CCCGAGCCAG 120
 TNAAGATGAA GGGAGAGCGG GTGCGGGGGC CATCNTCGGN GTCCAGCCC GGCCCATGGG 180
 ANTGAGTNGC GGCCTCTGCT TGTCGACNTG GGNCTGGCT GTCCNATTTT ACTACTATTG 240
 ACCCTGAAGG CCATCGAGGA GGGCAGCATG GAGGAGATCG AAGAGGAGGT CCGGCAGAAG 300
 AAATCATCAC GGAAGCGCAA GCGAGACTAG GCNTCTNTGG CCGAATTC 348

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GAATTCGGCC AAAGAGGCCT ACTTCTCTG CAGATCATGG GGCCTTGAT TGTGCTTG 60
 GGATTGTGTT TCTTCGTGGT TGCCCATGTT AAGAAGAGAA ACACGCTGAA TGCTGGCCAG 120
 GATGCCTCTG AGAGAGAAGA GGGACAGATC CAGATTATGG AGCCTGTCCA GGTCACCTGA 180
 GGTGACTCGG TAATAATATT TCCACCCCTT CCACCACCTT ACTTTCCTGA ATCTTCAGCT 240
 TCTGCGGTG CTGAGAGTCC TGGAACTAAC AGTCTGCTTC CGAATGAAAA CCCCCCTTCA 300
 TATTACAGTA TTTTCAACTA TGGCAGGACC CCAACTTCAG AGGGTGCAGC CTCTGAAAGA 360
 GATTGTGAAT CTATATATAC CATTCTGGG ACGAATTCAT CTTCTGAGGC CTCACACACT 420
 CCACATCTTC CATCTGAATT GCCTCCTAGA TATGAAGAAA AAGAAAATGC TGCAGCACTC 480
 GAG 483

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 500 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GAATTCGGCC AAAGAGGCCT ACGATTACAA TCATGATTTC CAGAATGGAG AAGATGACGA 60
 TGATGATGAA GATATTGATT ATGTTTGCTC TTGGAATGAA CTAAGGTCT TGCTCAGGTT 120
 TCCAGTGTA CGACTACGAT CCATCCTCCT TAAGGGATGC CCTCAGTGCC TCTGTGGTAA 180

AAGTGAATTC CCAGTCACTG AGTCCGTATC TGTTCGGGC ATTCAGAAGC TCATTAATAA	240
GAGTTGAGGT CCTAGATGAG AACAACTTGG TCATGAATTT AGAGTTCAGC ATCCGGGAGA	300
CAACATGCAG GAAGGATTCT GGAGAAGATC CCGCTACATG TGCCTTCCAG AGGGACTACT	360
ATGTGTCCAC AGCTGTTTGC AGAAGCACCG TGAAGGTATC TGCCCAGCAG GTGCAGGGCG	420
TGCATGCTCG CTGCAGCTGG TCCTCCTCCA CGTCTGAGTC TTACAGCAGC GAAGAGATGA	480
TTTTTGGGGA CACTCTCGAG	500

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 497 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GAATTCGGCC AAAGAGGCCT AGGAGAAAGA AGATATTGAC ACCATCTACG GGCACCATGG	60
AAC TGCTTCA AGTGACCATT CTTTTCTTC TGCCCACTAT TTGCAGCATT AACAGCACAG	120
GTGTTTITAGA GGCAGCTAAT AATTCATTG TTGTTACTAC AACAAAACCA TCTATAACAA	180
CACCAACAC AGAATCATT CAGAAAATG TTGTCACACC AACAACTGGA ACAACTCCTA	240
AAGGAACAT CACCAATGAA TTA CT TAAAA TGTCTCTGAT GTCAACAGCT ACTTTTTTAA	300
CAAGTAAAGA TGAAGGATTG AAAGCCACAA CCACTGATGT CAGGAAGAAT GACTCCATCA	360
TTTCAAACGT AACAGTAACA AGTGTTACAC TTCCAAATGC TGTTTCAACA TTACAAAGTT	420
CCAAACCCAA GACTGAACT CAGAGTTCAA TTAACAAC AGAAATACCA GGTAGTGTTT	480
TACAACCAGA NCTGAG	497

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 154 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GAATTCGGCC AAAGAGGCCT ACTTTTTTAA TATAAATTT GTTGATATGG AATTAGGTAA	60
GTTTAAGTGT CTATGTGCAT ATGTTTTTTA TATAAGTTT TTCTATTCAG TTTCACNGAT	120
CCAAGTGGCA GTGGGTAAAT ATGGCGAGCT CGAG	154

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GAATTCGGCC AAAGAGGCCT AGGAATGGTT TTNATTGGT CCTTATTTTT AACCTGCCCC	60
TGAGACTTAT ATGCTTGTTT ATACCATGTA CGTAGTGTGT GATTGTATGT GTTTGTATTT	120

```

GTCCACATGT CCCAAACAT GGGCTGTTAC TCCCTTTTCT ATCTTGGTTT CCTTATTCCC      180
ACCCCTTCTCT TTCCACCCAG GTATCTGGAC AGGAAGACTT CTACCATCAG CTTTACCAGA      240
GGAAGCTGCA GGCCCCACTG TGGCCCAGCT CCTGGGCAT CACTGATTGC TATCAGTATG      300
TCACCTCCTG TCACCCAAG AGATCAGAGA GACGCAAGTA TGGCCGAGAC TTCCTGCTAC      360
GTTTCCGCTT CTGCAGCATC GCTCGAG                                         387

```

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

GAATTCGGCC AAAGAGGCCT ACCTTCATTT GTTAGATTAT ATCAGTACCC CAACTTGGCT      60
GGACCTCATG CAGCTTTAGC TAATAAAAGT TTCTTTAAGG CAGATAAAGT TACAATGCTG      120
TGAATAAAA AAGGTATGTT AAGTATATTT TATCCCTCCC TTTGTTTATC AGTTGTAAAT      180
TTAGGCTATA TTCCTATGTG TATAACAGAA GAATCAATGC CCATTGTGT TTTAAATCTA      240
ATTAAAGTTT TTAAGTTAT AGCTACTGCT GTGTTGGTAA TAGCTAGCAC AGATGTTGAC      300
AAGACAGGAG CTTCTACTA TGGAGAACGA CTCGAG                                         336

```

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

GAATTCGGCC AAAGAGGCCT AGGGACATTG GTTGAATTGG CATGACTAGA ATAGTTGGGA      60
ATGTTTGGGA ATGGGGAGAG ATTGCTAATG GGATGTCTGC CAGGGGCAAT ACTGAAATCT      120
GCTGGTTGGT AAAGGTAGTG CCTGAGCCCA GTGCTAACCA TAGTAGTTGG AAAATTGTGT      180
ACGTTGGCTG TGGAAATCCTT ATGCGAATAT TTGTCCAATC CATCTAAATT TCTCTCTGCA      240
GCATTTTAA AAAGACATAT AGCTGAAATT TTGTCACTCC TAAAAATATT TTGATTTTCT      300
CTGCCCAGAT TTGCATTGG GTAGATCGTG CTGTAGAAGA TATATCTTGC TTTAAGATAG      360
CTGCCACTGA TTAGTTTATT TTAGTCTATT TTAATCAACT TATTGCCTTG TAATCTTTCC      420
TTTTTCATTC TCTAAATTC TGAAATTCTA TCTTTCATGT TCCCCAGGAA ACACTCGAG      479

```

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

GAATTCGGCC TTCATGGCCT ACATGATGTC AACCAACCGT GCTCACAAGA TGAAAGAGCA      60

```

CATTCCTTTT TTTGAAGATA TGTGTAAAGG CATTAAAGCT GGTGACACCT GTGAGAAGCT	120
GGTGGGATAT TCTNCCGTGT ATAGAGTCTG TTTTGGAATG GCTTGTTTCT TCTTTATCTT	180
CTGTCTACTG ACCTTGAAAA TCAACAACAG CAAAAGTTGT AGAGCTCATA TTCACAATGG	240
CTTTTGTTT CTTTAACTT CTGCTGTTGG GGGCCATGTG CTCAGGAGCT TTCTTCATTC	300
CAGATCAGGA CACCTTCTG AACGCCGGGC AGCTCGAG	338

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GAATTCGGCT TCATGGCCTA CCCGAAACCA CTCAGGGTCC TGTGGACAGC TCACCTAGTG	60
GCAATGGCTC CAGGCTCCCG GACGTCCCTG CTCCTGGCTT TTGCCCTGCT CTGCCTGCC	120
TGGCTTCAAG AGGCTGGTGC CGTCCAAACC GTTCCGTTAT CCAGGCTTTT TGACCACGCT	180
ATGCTCCAAG CCCATCGCGC GCACCAGCTG GCCATTGACA CCTACCAGGA GTTGAAGAA	240
ACCTATATCC CAAAGGACCA GAAGTATTCA TTCTGCATG ACTCCAGAC CTCCTTCTGC	300
TTCTCAGACT CTATTCGAC ACCCTCCAAC ATGAGGAAA CGCAACAGAA ATCCAATCTC	360
GAG	363

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 374 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GAATTCGACC TTCATGACCT AGCGTAAGAG GAGAGAGACA CATTGAGCAG CCAAAGGACT	60
CGGTGGAAG AGCAGAACAC CATAGACAAT ATGTCGCTCT TGGGACCCAA GGTGCTGCTG	120
TTTCTTGCTG AATTCATCAT CACCTCTGAC TGGATACCCC TGGGGGTCAA TAGTCAATCG	180
AGGAGACGAT GTGACTCAAG CGACTCCAGA AACATTGACA GAAGATCCTA ATCTGGTGAA	240
TGATCCCGCT ACAGATGAAA CAGTTTGGC TGTTTTGGCT GATATTGCAC CTTCACAGA	300
TGACTTGGAG TGCTGGGATG AGAAATTAC CTGCAGCAAG GCTCTACTCT GTGCATCGGC	360
CGGTAAACT CGAG	374

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GAATTCGGCC TTCTGGCCTA GGGTGGGATA AGTGATTNGT ATTTGTTNG GTTTAAAAAC	60
------------------------------------------------------------------	----

ATACTTTGAT AGAAATTAGT CCCTTTCTTT TCCTTCTCTT CTACAATGTC AATTGCCCAT	120
TTCATTGTG TGTTTCTAAC ATTTTCTTTT GTTAAGAAAT GTTGGGGCTA TAATTTTTTT	180
GAAATCACTG AAGGAGGGG AAAAATAATT TTAACAACCT GTGTTGAAAC CTTCCATAGC	240
TTAATTGACT GGAATAATCC TGCCATCATT AATAAGATGT ACAAGGTGTA CCTTGGAGAT	300
ATACCACTGA AGACAAAGA GGAGCTCGAG	330

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

TTACACCCTG GAAACCAAGC ATAAGCACAC TTTAGCAGA TGAAGTAGAA ATTAAGTTGT	60
TTGAATCNAG TGAACACACT GAAGACTCCA ACAACCCACA ACTCGAG	107

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GAATTCGGCC TTCATGGCCT ACCCGTCGTT AGTGAAGGGG AAATGGGTTG TATCCTAAGG	60
GATTGGGAAA TGGGAAGTGA ATTTCAAGGAG ATTGTGGAGT ACAAGGTATG TGTTTACGTT	120
AGGTGATGAG CAGTGTCAAG ATAGTGAAGT GTGGACAGTG TCAAATGCTT TTCTGTAGGG	180
AAGATGAAGT TAGCATCATC TTATCACTTT TGACATGCTT TTGTGGTTTA TTTTGTGTTG	240
TATTTGTTTT TTACTAGAAA TGAAAGGCTT TGCCAAAGCC TCTGTACTAT GCTTCAGAGT	300
AGGACACACA ATTCTGAGAT TGCTGTAGAG GGCTCGAG	338

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GAATTCGACC TTCATGGCCT AGTCAGAGCC AAAGGAAAGC TTGAAAAATG AAGACATTAG	60
CAGGACTTGT TCTGGGACTT GTCATCTTTG ATGCTGCTGT GACTNCCCCA ACTCTAGAGT	120
CCATCAACTA TGAAGCAGAA ACCTATGATG CCACCTTAGA AGACCTGGAT AATTGTGACA	180
ACTATGAAAA CATACCTGTT GATAAAGTTG AGATTGAAAT AGCCACAGTG ATGCCTTCAG	240
GGACACAGAG GCTCCTCACT CCACCCACAC AGCCTGAGAA GGCCACAGAA GAGGAAGAGG	300
AGGAGGAATC TACTCCCAGG CTGATTGATG GCTCTTCTCC CCAGGAGCCT GAATTCACAG	360
GGGTTCTGGG GCCACACACA AATGAAGACT TTCCAACCTG TCTTTTGTGT ACTTGATATA	420

GTACCACCGT GTACTGTGAT GCCCATGAAC TCGAG

455

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GAATTCGGCC AAAGAGGCCT AGGGGGGTGA TGGTGTGTGC TTTGGACTGT GTGCCTACAG	60
GGTTTTTTTG TTTTGTTTTG TTTTACTGTA ATGGAAATGG GTTTAGGATA AGCATACTCA	120
AAGCTCCACA GTGTATCCTT GAGCTTTCCA TGACTGCCAG TTACACACTG GAGAGGGTTA	180
AATGAATCTT AAAGTGTTCa TGATTACTAT TAAATATCAT TATAAAACAA ATTCTTTCGG	240
GGGGGCACAA ATGCTAATAT GTACAAGAAA ATCTTAGACT TGAAAATATC TTTAAAATGA	300
AAATAACTTT TTTTTTCAGC TGACTGTATT CACAACCTTG ATGGATGTTA CCAAAGGTCA	360
ATTTGAAAGT CACCTTCGAG ATTGCCAGA CCCTTGATA GGCTGGTGAG CACACGTTGG	420
CCAGCCTCGA G	431

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GAATTCGGCC TTCATGGCCT ACTACAATCC GTGGCTGCTC NTTCTTGCTT ACTTTACTCT	60
CCCACTGAAG CAGGTTANCG TTGAAGGTGG TATGGAAAAG CCTGCATGCC TGTTCAATTC	120
TTTGTGTTCT TCTCCTTCCC CTTCCCTTCT CTTCTTCCC CTACCTCCTT CGCTCGAG	178

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GAATTCGGCC TTCATGGCCT ACATCAACAG CATCAAGTCC AGACTAAGCA AAAGTGGGCA	60
CATACAAACT CTGCTTAGAG CATTTGAAGC TCGTGATCGA AACATACAAG AAAGCAACTT	120
TGATAGAGTC AATTTCTGGT CTATGGTTAA TTTAGTGGTC ATGGTGGTGG TGTCAGCCAT	180
TCAAGTTTAT ATGCTGAAGA GTCTGTTGA AGATAAGAGG AAAAGTCTCG AG	232

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

```
GAATTCGGCC TTCATGGCCT ACAAACCTA ACTTGCAGC AAAACAAGAT GAGATTGGCA    60
TGGCTTTATT TGTTTTTTT GTTTTGT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 120
GATTTAAAAA CTGGAACGGT GAAGTGACA GCAGTCGGT GGAGCGAGCA TCCCCAAAG    180
TTCAC TGGGC TCGAG                                         195
```

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

```
GAATTCGGCC TTCATGGCCT ACATATCCT AAATGGTAGT CATCTGGGA CTAAGCAACA    60
GGTGTTC A GGAATAATT CTCTGGGTTT GAAAGTTCA CAGTCTGTC AGTCTATTG    120
TCCTCCATAT AACCGAGCAG TGTCTCTGGA TAGCCCTGTT TCTGTTGGCT CAAGTCCTCC    180
AGTAAAAAAT ATCAGTGCTT TCCCATGTT ACCAAAGCAA CCCATGTTGG GTGGGAATCC    240
AAGAATGATG GATAGTCAGG AAAATTATGG CTCAAGTATG GGAGACTGGG GCTTACCAA    300
CTCAAGGCC GGCAGCGGAC TCGAG                                         325
```

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

```
GAATTCGGCC TTCATGGCCT AGGAGGCTAT TTTAGGATTT CAATGAGAAG CAAATCATA    60
TCCAATCAA AGTAAAGGTC ATCGGTGGCC AATGAAGAGC GGAGAAAACG GAGGCGGGAG    120
AACAGACGCG ACCTCAAGAC AGAAGAATGG AAGACGCAAC TTTCAAGAAA AGAGGAACTG    180
AAACGAAAAG AGAGGCACAG TCCAATGAG GAAGAGAACA AGGAGCCTTC AGTCTCCTGG    240
GGGCCAGGGA GCCTCGCCAC GCGGTCACAG GTACACGGGG ACATTTAGAG GCCATCTCCT    300
TTAAAGCCAG ACATTCTTCT TACTGGAATC TAGGCCATGA AG                                         342
```

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

```
GAATTCGGCC TTCATGGCCT AGGCGGGTGA CATTAGCCG GCGGTTCGGG GGGACGGANT    60
CTCCATTCCA GAACCATGGC CCAATTGTGTC CGTAACCTTG TGGAGAAGAC CCCGGCGCTG    120
GTGAACGCTG CTGTGACTTA CTCGAAGCCT CGATTGGCCA CATTTTGGTA CTACGCCAAG    180
GTTGAGCTGG TTCCTCCAC CCCTGCTGAG ATCCCTAGAG CTATTAGAG CCTGAAAAAA    240
ATAGTCAATA GTGCTCAGAC TGGTAGCTTC AAACAGCTCA CAGTTAAGGA AGCTGTGCTG    300
AATGGTTTGG TGGCCACTGA GGTGTTGATG TGGTTTATG TCGGAGAGAT TATAGGCAGG    360
CGGGTCACTC GAG                                     373
```

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 514 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

```
GAATTCGGCC TTCATGGCCT AAACAGGACC TGCTTCACAC CACCAAGCAT CAGGATGTGT    60
TGCTCAGTGA GCAGACCGA CTCCAGAAGG ACATCAGTGA ATGGGCAAAT AGGTTTGAAG    120
ACTGTCAGAA AGNAGAAGAG ACAAACAAC AACAACTTCA AGTGCTTCAG AATGAGATTG    180
AAGAAAACAA GCTCAACTA GTCCAACAAG GAAATGATGT TTCAGAGACT CCAGAAAGAG    240
AGAGAAAGTG AAGAAAGCAA ATTAGAAACC AGTAAAGTGA CACTGAAGGA GCAACAGCAC    300
CAGCTGGAAA AGGAATTAAC AGACCAGAAA AGCAAACTGG ACCAAGTGCT CTNCAAAAGT    360
GCTGGCAGCT GAAGAGCGTG TTAGGACTCT GCAGGAAGAG GAGAGGTGGT GTGAGAGCCT    420
GGAGAAGACA CTCTCCCAA CTAAACGGCA GCTTTCAGAA AGGGAGCAGC AATTGGTGGA    480
GAAATCAGGT GAGCTGTTGG CCCTCACGCT CGAG                                     514
```

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

```
GAATTCGGCC TTCTGGCCTA GGACTCTATA GAACCCACTG CCTCCTGATG AAGTCCCTAC    60
TGTTCAACCCT TGCACTTTTT ATGCTCCTGG CCCAATTGGT CTCAGGTAAT TGGTATGTGA    120
AAAAGTGTCT AAACGACGTT GGAATTTGCA AGAAGAAGTG CAAACCTGAA GAGATGCATG    180
TAAAGAATGG TTGGGCAATG TCGGGCAAAC AAAGGGACTG CTGTGTTCCA GCTGACAGAC    240
GTGCTAATTA TCCTGTTTTT TGTGTCCAGA CAAAGACTAC AAGAATTCA ACAGTAACAG    300
CAACAACAGC AACAACACT TTGATGATGA CTACTGCTTC GATGTCTTCG ATGGCTCCTA    360
CCCGTTTCTC CACTGGTTG AACATTCCAG CCTCTGTCTC CTGCTCTAGG ATCCCCACGC    420
TCGAG                                     425
```

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GAATTCGGCC TTCATGGCCT ACAAAGGAA AGAAGAAAAA GGGCCAAAAG CAAAAATGAA	60
ACTGATGGTA CTTGTTTTCA CCATTGGGCT AACTTTGCTG CTAGGAGTTC AAGCCATGCC	120
TGCAATCGC CTCTCTTGCT ACAGAAAGAT ACTAAAAGAT CACAACCTGC ACAACCTTCC	180
GGAAGGAGTA GCTGACCTGA CACAGATTGA TGTCAATGTC CAGGATCATT TCTGGGATGG	240
GAAGGGATGT GAGATGATCT GTTACTGCAA CTTCAGCGAA TTGCTCTGCT GCCCAAAGA	300
CGTTTTCTTT GGACCAAAGA TCTCTTCGT GATTCTTGC AACAACTCG AG	352

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GAATTCGGCC TTCATGGCCT ACACAATGGT GTTCGCATT TGGAAGGTCT TTCTGATCCT	60
AAGCTGCCTT GCAGGTCAGG TTAGTGTGGT GCAAGTGACC ATCCCAGACG GTTTCGTGAA	120
CGTGACTGTT GGATCTAATG TCACTCTCAT CTGCATCTAC ACCACCACTG TGGCCTCCCG	180
AGAACAGCTT TCCATCCAGT GGTCTTTCTT CCATAAGAAG GAGATGGAGC CAATTTCTAT	240
TTACTTTTCT CAAGGTGGAC AAGCTGTAGC CATCGGGCAA TTTAAAGATC GAATTACAGG	300
GTCCAACGAT CCAGGTAATG CATCTATCAC TATCTCGCAT ATGCAGCCAG CAGACAGTGG	360
AATTTACATC TCGATGTTA ACAACCCCCC AAGACTCGAG	400

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

GAATTCGGCC AAAGAGGCCT AAGAGATTCA GGACCTGCAG AGTCGCCAGA AGCATGAAAT	60
TGAATCTTTG TATACTAAAC TGGGCAAGGT TCCCCTGCT GTCAATTATC CCCCAGCTGC	120
TCCTCTGTG GGGAGAAGAA GGAGACCCAC TAAAGCAA GGCAGCAAGT CTAGTCGCAG	180
CAGCTCATTG GGCAATAAAA GCCACAGCT TTCAGGCAAC CTGTCTGGTC AGAGTGGAAC	240
TTCACTCTTA CACCCCAAC AGACCCTCCA CAGTCGAG	278

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GAATTCGGCC TTCATGGCCT AGTTTATATA CTTTCTCTGA AGGATCCTAA TGATAGTTAA	60
CCATTCTCA TTTTATTTT GCTGGATTGT TTTCTGTTT TTGCTTCAGC ATTCTTGCTT	120
TTGCTGTGCT TACTTTTGGA GTTTTGATTG CCTGTGTAC TGTTTTCTTT CGCATCCACC	180
ACTCGAG	187

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GAATTCGGCC TTCATGGCCT ACTTCTCTGG AAAGGTCCT GATTGTTTGT TTTTTCGAGA	60
CAGGGTCTCG CTCTTCACCC AGACTGCAAT GCAGTGGCAC AATCATAGCT TATTGCAACC	120
TCAAACCTCGT GGGCTCAAGC AATGCTCGCT CCTCCCAAGT AGCTAGGACC ACAGGCATGC	180
ACCACGATGC CCACCTAGTT TTTGTATT TCTATAGAGA NGGGGTCTC ACTGTGTTTC	240
TCAAGCTGGT CACATACTCT TGGCCTCAGG CAGTTCTCCC ACATCAGANT CTCAAAGCAC	300
TGGGCTTACA GCTGNGAGCC NGNCCTTTT AAAAAAAAAA AAAAAATCAA AACAAACAA	360
AACAAGATTA TGTCTTCC ACGCATCTCG AG	392

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GAATTCGGCC TTCATGGCCT ACTTGGGAAT TAACATCTTC GATAAATCCC AGAAGTCTTT	60
AAGTGACAGT AGAGAGCCTA CAGAGAAGCC TGGGAAAGCA GAAAAATCTA AGAGCCCAGA	120
AAAAGTGTCA TCGTTCTCAA ACTCCTCCTC CAACAAGGAA TCAAAAGTAA ACAATGAGAA	180
GTTTCGTACT AAGAGCCCCA AGCCTGCCGA AAGCCCCCAG TCAGCCACTA AGCAGTTGGA	240
TCAGCCCACT GCTGCTTATG AGTATTATGA TGCTGGCAAT CACTGGTGCA AAGACTGCAA	300
CACCATCTGT GGGACTCGAG	320

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

GAATTCGGCC TTCATGGCCT AATCAGAAGC TTTTCAAAAT TCCGTCTTCA AGAAGAAACA	60
CCCGTGGAGG AAGAAGACAT TATACAAAAC AAATTTAGAA ACTGGGATCA TGAGTGGAAA	120
AACAAAGGCA AGAAGGGCTG CCATGTTTTT TAGACGTTGC TCTGAAGACG CCAGCGGTAG	180
CGCCAGTGGC AATGCTTTGT TATCAGAGGA CGAAAATCCT GATGCGAATG GGGTAACTCG	240
ATCATGGAAG ATTATTCTAA GTACAATGCT TACACTGACT TTTCTTCTTG TAGGACTCCT	300
AAATCATCAG TGGCTTAAAG AAACAGATGT TCCTCAGAAA TCCAGACAAT TATATGCCAT	360
GCTCGAG	367

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GAATTCGGCC TTCATGGCCT AAAGTAGTTC TGTTATAAAA AGCCAGGAAT CCTAAAACCA	60
AAATATTAGA ACGAAAACAG AAACATGGCT CACTATATTA CATTTCTCTG CATGGTTTGT	120
GTGCTGCTTC TTCAGAATTC TGTGTTAGCT GAAGATGGGG AAGTAAGATC AAGTTGTCGT	180
ACTGCTCCGA CAGATTTAGT TTTTCATCTTA GATGGCTCTA ATTGTGTGTG CCCAGAAAAC	240
TTTGAAATAG TGA AAAAGTG GCTTGTCAAT ATCACAAAAA ACTTTGACAT AGGGCGAAG	300
TTTATTCAAG TTGGAGTGGT TCAATATAGT GACTACCCCTG TGCTGGAGAT TCCTCTCGGA	360
AGCTATGATT CAGGAGAACA TTTGACGGCA GCAGTGAAT CCATACTCTA CTTAGGAGGA	420
AACACAAAGA CAGGGAAGAA CCTCGAG	447

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GAATTCGGCC TTCATGGCCT AAATGAAGCA AAATCCATA CATCATTTTG AAAATAGTGT	60
TTCTTTCCCT GATAGGCCTG TTCTGCATCA TTCTTTTAGC TTCCTTCTGC CCTGTTTATC	120
ACTTGGTCCC ACTTTTATAT TTTTCTCTT CGGTCCAGAA TTTCTTATTT AGTTTCTTGT	180
ATTTTGCTTA CTCCCTCCCT TCTCCATGAT TCAGCCTAGT CTTTCCGTCC TCTGTGGACT	240
TGGGTGTGCC TTCTCTGGG CCACCTCGTC TTTTGTCTGT GTTAGCCCTC CGCCTGCGC	300
ACCTGCCACT TCACCTCGC CTGTGGTCCA CTTACGTTCC ACTCAGCCCG GTCAGTCTGT	360
CTTTGTTCTT CTCCACCGCC TAGGTCTCGA G	391

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

```
GAATTTAAGT TCCAGTATGA GATCTTCAAA GCTGTCTTTT TTTTCTCTC TTCCGTTCTC 60
AGATCCTGAG 70
```

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

```
GAATTCCGGCC AAAGAGGCCT AGTCAAATTC TTACCTCGCT CTTTCACTGC TAGTAAGATC 60
AGATTGCGTT TCTTTCAGTT ACTCTTCAAT CGCCAGTTTC TTGATCTGCT TCTAAAAGAA 120
GAAGTAGAGA AGATAAATCC TGCTTCAAT ACCTGGAAGG AAAAACAAAA TAACCTCAAC 180
TCCGTTTTGA AAAAACATT CCAAGAACTT TCATCAGAGA TTTTACTTAG ATGATTTACA 240
CAATGAAGAA AGTACATGCA CTTTGGGCTT CTGTATGCCT GCTGCTTAAT CTGCCCCCTG 300
CCCCTCTTAA TGCTGATTCT GAGGAAGATG AAGAACACAC AATTATCACA GATACACTCG 360
AG 362
```

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```
GAATTCTAGA CTGCCTCGA GTGCGGATCC AGCCGGAGGC GAAGAGAAGC ACTTTGGGGG 60
CAAAAGAAGA GAAAAATGAA GACGGGACAT TTTGAAATAG TCACCATGCT GCTGGCAACC 120
ATGATTCTAG TGGACATTTT CCAGGTGAAG GCTGAAGTGT TAGACATGGC AGATAATGCA 180
TTTGATGATG AATACCTGAA ATGTACGGAC AGGATGGAAA TTAAATACGT TCCCCAATG 240
CTAAGGAGG AAAAAGCAAG CCACCAGCAA TTAGATACTG TGTGGGAAAA TGCAAAAGCC 300
AAATGGGCAG CCCGAAAGAC TCAAATCTTT CTCCTATGA ATTTTAAGGA TAACCATGGA 360
ATAGCCCTGA TGGCATATAT TTCCGAAGCT CAAGAGCAAA CTCCTTTTA CCATCTCTTC 420
AGTGAAGCTG TGAAGATGGC TGGCCAATC GAG 453
```

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```

GAATTCGGCC TTATGGCCTA CTTTAAAAAA AAACCAATAC CAAAGAAGCC TACAATGTTG      60
GCCTTAGCCA AAATTCGTGT GATTCAACG TTGTTTTATT CACTTCTATC GGGGAGCCAT      120
GGAAAAGAAA ATCAAGACAT AAACACAACA CAGAACATNG CAGAAGTTTT TAAAAAATG      180
GAAAATAAAC CTATTCTTTT GGAAAGTGAA GCAAACCTAA ACTCAGATAA AGAAAATATA      240
ACCACCTCAA ATCTCAAGGC GAGTCATTCC CCTCCTTTGA ATCTACCCAA CAACAGCCAC      300
GGAATAACAG ATTTCTCCAG TAACTCATCA GCAGAGCATT CTTTGGGCAG TCTAAAACCC      360
ACATCTACCA TTTCCACAAG CCTCCCTTG ATCCATAGCT TTGTTTCTAA AGTGCCTTGG      420
AATGCACCTA TAGCAGATGA AGATCTTTTG CCCATCTCCC TCGAG                        465

```

(2) INFORMATION FOR SEQ ID NO:261:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

```

GAATTCGGCC TTCATGGCCT AGCGGCGGGG CGAGCGCCTC CACGAGCAA CTCCGGAGTC      60
CCCGCTTGC CCGAGCGCAG TTTCTCCGCT GCTGTTTCCA CCGGCTTTGT AACACTGGGA      120
ATTACATCC TCACCGGCAC CCTCACGCC CGAGGATTTT AAACACCTT TACTCTCGA      180
ACTGAGATT GCGGTAGATG GGATTTTTCG CTTTCCCCCA GATGGTTGAA GGTTAAGATT      240
TTTGAAAACC CCCCCACCTC CTTATTTCTA TTATTATTC TGCNAGAAAA GTATAAAGAG      300
AGTTGTAGTG GAGGTGAGAT TTGTGATCGG GAAAGCCTTC GACTCCCTCC TTCTCCGTCT      360
TCCGCTTCTC TCTCTCTGAT TAGTTCCTAT CCAGCAGCAG ATTGAAGCAG GAGATGATTC      420
TTCTCAAGGT TTGTTAGCA GCTTCACTTC TAGGCGAAGG CTTTCATGAAC CAAGTGACGA      480
ACAACCTCGA G                                     491

```

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

```

GAATTCGGCC TTCATGGCCT ACATTTTCT ATTGATATAA AAATTGTTAG AGAAATATAC      60
AGTTGTATAT TTCCCCCTT TATACAGAAA TTTTACAATA ATTCAGATT TTTCTGAGTT      120
TTTTCAGATT TTGATTCTA TAATATGAGA TTATCTTTC TTCCTCTTAT TTTTTAGGT      180
TATTTATTTT TTCTTTTCTT TTTAATTGTC TCATACAGGT TACTCTCGA G                231

```

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 445 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

```

GAATTCGGCC TTCATGGCCT AGTAAAATTT AAAATACATA CTAACATATA ACCCAATTTG      60
AACATATTAA GTGAATATGT ATTCTTAAAA GATCCACTAC TTTACATTTA GATGCGTTAG      120
GATGTATTAG AAATAAAAAC AGAAGAAAAG ATTTAGAATC TAGTCTGTCT TTGCCACTCA      180
AGCTAGTTAC CCTCTCTGAG TTTTATACCC CCTTCATCTA TTAATATGGG GGGTAACGCC      240
AACCTGACTC CTTTAAAATG AGTTTGAGAG TCAGGCAAAT TAGAAAGATA CATAGATGAA      300
AACTTTTAA AAAGTATATA GTCTTTCATG ATTTGTAGAA CACTTTTATA CTTTTCAGAG      360
TACTTTCACA TTGATCATAT TGTTGTACT TTATGAAAGT CTTCTACAAA TCAGAATTAT      420
GCTTATTATA CAGATGTGGC TCGAG                                           445

```

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

```

GAATTCGGCC AAAGAGGCCT AATTACTTTA TATTTTAAAA GCTCTGTGAC TTCAGTAGTG      60
CATTGAAATA AAATTTTAT TCATTATGAG AGAGTCTGTG AGGAACAGAA TCATGGTTCC      120
TGTGTGTTTG AAGATATGGC GTGGGGTGAT AGTGCTGGCA GCAGCTCTGT TGCTCTGTG      180
CCCATGGCAT ACAGACTGGA TCTGCTGGTC CACGGCTCCT GAGGTTAATG TCCAAGCCCT      240
CTGCAATGCT GACAGTCTTC CTCATCCTCA CACCCTACCT CTCAGTTTCT ACCTGCCACC      300
TCCCCAGTAA TATTAGCCTC TTGAGTCCCC AACAACACTC GAG                                           343

```

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

```

GAATTCGGCC AAAGAGGCCT ATTAAATTC ATTTATCAGT AGGATCATTG TGTCTAGAC      60
AAGTTGGCTA TATTATAAAA CATTAAAGCA GCAGGCACTA AGTTAAATAT TGTAGCAGTT      120
GAAATTTAAT GCTAATCTTA CAGTTTACA CAGTTAACAA TCTAGGCCAA ATCTATTGAT      180
ACCTTTGGAA CTACCCTTTA AATTCCATCC TATGCTTGTC AAAAGGTTGC ATATAATTC      240
TTTTCTTTT TCTCTCTTCT CTTCTCTTTC TTTTTCCTT TTCTTTTCTT ATTTCCCTTT      300
TCTTCTTTT TCTTTCACAG AGTCTTGTA TATCACCCAC ACTCTCGAG                                           349

```

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GAATTCGGCC AAAGAGGCCT AGAATAAAAA TGCTTGTGTC AAAAATTCAA ACATTTGTCT	60
CTTTCCTTTC CATTCCAGTT CTAGGTCTCG TTCCAGATCA TATTCTCCAG CTCATAACAG	120
AGAAAGAAAC CACCCAAGAG TATATCAGAA TCGGGATTTC CGAGGTCACA ACAGAGGCTA	180
TAGAAGGCC TATTATTTC GTGGGCGTAA CAGAGGCTTT TATCCATGGG GCCAATATAA	240
CCGAGGAGGC TATGGAACT ACCGCTCAA TTGGCAGAAT TACCGGCAAG CATAcAGTCC	300
TCGTCGAGGC CGTTCAGAT CCCGGCTCCC TCGAG	335

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GAATTCGGCC AAAGAGGCCT AGTGGAAATT TGTGGCTAGT GTGATTTTG TTTGTTTCCT	60
TTTAAGTACT GTTGATCAGT TGTGACACTT ACTGGTTAAA CTTACGTTGC TAAAGATTTT	120
TCTATAATAA GCCACACATT ATATTAGAC TATATTAAGG GACCTTGTT TTCTTCTAGA	180
TAGCAGCTGT CCCAAAGAAA ATATTCTTC TTTGTCTGTT AAGATTAGC TATTATCTGC	240
CAGTTGTTAA GAGGTTTTGG TTCCAACTC AACCAGCAAT GTTGAGAGCT GAACTTAAGA	300
TAGCTGTTGT ACTTTTGCT TTCCATCTGT TACTGTCCTT CATTCTTGGC TCCCTACTAT	360
CTATAAACAG CAAGCTCGAG	380

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GAATTCGGCC AAAGAGGCCT ATCTAGACCT GCCTCGAGTC AGCAACAACA ATTTTAAAA	60
TTTCTTTCTG GATTCTAGAG TGAGTTTTT TCATAACACA AGAGGATAAG AGTGAGGACA	120
ACAGGAGGTA TTGATGATCT GCTGAGCACC AGGCATTATG CTAAGTGCAT TCACACACAT	180
CTCAGTGCCT ATTGCCTCGT TGTGGACTTC TCTATCCCAG CTCGTCCCCC TGGCAAATTC	240
TTTCTCATCC TTCAACTCTC AGACACCTCC CCCGCGCTC GAG	283

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GAATTCGGCC AAAGAGGCCT AACCAGGCAT TTTTCATTAG GGTCTAGGT CCAGGTGAAT	60
TCITGAGTTG GTTCGTTGTG TCATGTATTG GCCTTAATA ATGCTCTTAT TTTGGCCAC	120

GCCTGTGGTC CCAGCACTTT GGGAGGCTGG TCTCGAG

157

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GAATTCGGCC AAAGAGGCCT AACCAGGCAT TTTTCATTAG GGTTCAGGT CCAGGTGAAT	60
TCTTGAGTTG GTTCGTGTG TCATGTATTG GCCTTAAATA ATGCTCTTAT TTTGGCCAC	120
GCCTGTGGTC CCAGCACTTT GGGAGGCTGG TCTCGAG	157

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GAATTCGGCC AAAGAGGCCT ACCCAAATAA AATCAGAGTC AGAAATGGAA ACAGACAGTG	60
GAGTACCTCA AAACACTGGA ATGAAAAATG AAAAAACAGC CAACAGGGAA GAGTGTGCA	120
CCCAGGAGAA AGTTAATGCA ACAGGACCAC AGTTCGTGAG TGGAGTGATT GTGAAGATCA	180
TTAGCACAGA GCCTCTACCT GGCAGGAAAC AAGTCCGGGA TACTTTGGCA GCAATCTCAG	240
AAGTTCTTTA TGTTGATTG CTAGAAGGGG ATACAGAATG CCATGCTAGA TTTAAACTC	300
CTGAGGATGC TCAAGCAGTA ATAAATGCCT ATACAGAAAT TAACAAGAAA CACTGCTGGA	360
AACTCGAG	368

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GAATTCGGCC AAAGAGGCCT ACAACGAACG GCTTGGGNGC GGACTGGTAT CCGGGGACTG	60
TGACTTGCAG GGTCCGCCAT GGAGCCAGAG CAGATGCTGG AGGGACAAAC GCAGGTTGCA	120
GAAAACTCTC ACTCTGAGTA CCGTCTCACA GACAACTTG AGAGAATAGT AGAAAAATGAG	180
AAGATTAATG CAGAAAAGTC ATCAAAGCAG ANGGTAGATC TCCAGTCTTT GCCAACTCGT	240
GCCTACCTGG ATCAGACACT TGTGCTATC TNATNACAGG GACTTGCTGT GCTTGCCAAG	300
GANAGACCAC CACATCCCAT TGAATTCTA GCATCTTATC TTTTAAAAAA CAAGGCACAG	360
ACTCGAG	367

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GAATTGGGT CCTAGGATAT AAATATTTT CCCTTTATAA GATATTTATA GGATATTGCA	60
AACAATTTCT GTTTTTCAT ATCCTTGCCA GCAGTTAGGG TTATCAAATT CTTGATTTC	120
TTACTGATTT GTAAGTTTTT TTGTTGTTT TTAGGTATTT TCAGGATAGT TACAAATGTT	180
AGGAAACTT ATTTTATTT GGCTTTTGAA GTTCCAGAT TTCTTGAACA GTGACCAATA	240
TGGACTCGAG	250

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

GAATTCGGCC AAAGAGGCCT ATCTTTTTTC CTCTTTTTTT GTTGCAGAAA TGATAACCTA	60
CTATTCACCTA TTCTGTGCCT TGCTTTGTTT GCATACTGAA AATTATCCAT GGAAGGATAC	120
AGCACCCTC GAG	133

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GAATTCGGCC AAAGAGGCCT AATGAAACAT TTCTGTAACC TGCTTTGTAT CTTGATGTTT	60
TGTAATCAGC AAAGTGTATG TGACCCGCCT TCACAAAATA ATGCAGCAAA TATTTCCATG	120
GTTCAAGCTG CTTGAGCAGG ACCCCCATCT CTGAGAAAAG ATTCGACTCC AGTTATAGCC	180
AATGTAGTAT CATTGGCAAG TGCCCTGCT GCTCAGCCTA CAGTGAATTC TAACAGTGTC	240
TTACAAGGTG CAGTTCCAAC AGTAACAGCG AAAATCATCG GTGATGCAAG TACTCAAACA	300
GATGCCCTGA AACTGCCACC TTCCCAACCT CCAAGGCTTT TGAAGAACAA AGCTTTATTA	360
TGCAAAACCA TCACACAGAC TAAAGCCACA CTCGAG	396

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```
GAATTCGGCC AAAGAGGCCT ACCCCTCCCC ATTTCTAGTT TCATGAACTG TGCACAGGGA    60
TATGGGGCTG TTCGAGGTAC TTTTGGGCTG ACCAAGGCTC AGAGGCTACT GACAGCTTTG    120
CTGCAAGTAA CTTCTAGGCC TTGTGGGTCC CAGTGCAGGG AACCCATGTG CGGTGACACT    180
GGAGAAGCCA TCTGATCCAG GTCTCTCACT TGACAGATGG GGAAACTGAG GTCCAAAGAG    240
GTACAGCAGC TTGGTTTAAG AGATAGAGAT GGAACCTGGAA CAAAAATAAT AACCATTTGA    300
TAATATTTTA ACATTATTG ATTTGTTTTT ATATGCCAAG ACCTTTTAAA GCATTATCTC    360
CTTTAAACTC TCATAACCAC TCTTACTCGA G                                391
```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```
GAATTCGGCC AAAGAGGCCT ACTGCTTCCT GATCATTTGT CTTTAAAT AAAAATATGA    60
TATTTGAGAT TCTTTATTTC TCTTTAAATA TTTGAATACA GAGTCTATT GAAGGACCAG    120
TATATTGAAT AGCAGTAATA TTTGAAGGAC TAGTCAGCTG TAGAAGCCTT GACTTCAGAT    180
CTTCACCCAA GAAACTCTGT GTATTGCTT TTCCTGGGCC ACTCAGATAG ACAATTGTGT    240
TTTNGATACA GTAAGAGTTT GCAGCTTAGC TTAAGTAGAA ATAATCCGGA TGCCTCGAG    299
```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```
GAATTCGGCC AAAGAGGCCT ACTAGGATTT GAGGAGGACG CCTCTTTTGC AGGAGGATGC    60
AGTGAACAGC CAAAGTCATC TGACATCCTT TTCCATCTTT TTCCTTCTAG TATCCCAGTT    120
TCAAGGCCCA GGAAAGGCAG GGAATAACAT ATGGAGCAGT TACCCAGAG TTCAAAGGGT    180
TAATCTCTAA GAATTCATTC TCTGACACCA GCCACAGCTC TTGTCCCCAT CTCTGGGACC    240
GTCCCCTCTG AGCCCAGGT TGGCAGCTTC CCTGAATTCC TTCTATGATA TAATTTGTAA    300
TTCGGCAGGG CTCTGGGACC CAGGCTCAGA GACCCAGGCT CTGCTCTCTC CTCAGTTTCC    360
AGGAGTCAGG GCTTGCTCTA AGGGAGGAAG TAAACAGGCC TTTCCCTTGC TCCCTCTCCT    420
TTTCTCTGAG                                430
```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

```
GAATTCGGCC AAAGAGGCCT AGTGGGAGTT AGATGTATTA TATAAAAATG TCCCCAGCAT    60
CAAAATGACT CAGAGTATGA CTGTATTTT AAATTAAATA TCAAGACCTA TCATCTGACA    120
AAACATATGA ATGACAATGA GATATAATAT TTGAAATTAG ATCCGTTCTG GGGAAATCAAA    180
GATATTTTGT AACAGTATAC ACAGTAGGCA TTGGTAAGTA AATGAGAACT CTATGAGCTG    240
TTTTCTGGAA AAGTTTAAAA TGAATTTTGT CAAATATCAA ATGATTGTTA TAAGAAAATC    300
AGTGGAGGCA GTATCCTTGG AAAAATCCAG AACAGTTTT GTNTGTTTGT TGTTTTITAC    360
ATCAAGGCAG ATCAGCAGGT GAACAGCTCG AG                                392
```

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

```
GAATTCGGCC AAAGAGGCCT AGAAGAACT TTTCTTGGG AGCAAGGTAG TTATTTCAAA    60
GCACAGAAAA AGGCGGCGGG GGGCACAGAG AAGCACAGAG AAGCGGGGGC AGTTGCTCAG    120
GTAAACATT CATCTTGGCT TTTCTTTTA AAAGATAAAC TTTGTCCAC GTAAAGAGGA    180
AACTGCATA GATATTCATT GAGATTATCT GATTGTGAC TGTGCCCCAA GAAAAACAA    240
AGGTAAATA CACGAGTTT TGCATTGAGA AGAAAGTATT TCAGGTAAAA ATTAAGTATT    300
AAGCAACTTT TCTCAGCAGA AGAAATGCCC AAATCTTAA GGACAGTACT CGAG                                354
```

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

```
GAATTCGGCC AAAGAGGCCT ACTTTGAGAT TTTTGTGTG TTGTTTCCTT TTTGTATTTT    60
ACTGATATCA CCAGGATAGT TTACTCTCCT TCTAGCTTTC TGCTTACGCG AACTGGATG    120
ACACACACAT ACACACCCGC AAAAATGCTC ATGAACCCAA TCCGGAGAAG GTTCCAGCAG    180
GTCCCCCACC CTCCCCTCCT CGTCCTACTT CTCCTCTTGA CAGCGAGGAC AGGAGGGGGA    240
CAAGGGGACA CCTGGGCAGA CCCGCCGGGT CTCCTCCAC CCCACCCGGC CCTCANATCA    300
TACTCGAG                                308
```

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GAATTCGGCC	AAAGAGGCCT	AGACCTGCCT	TGTGTTTTCC	ACCCTGAAAG	AATGTTGTGG	60
CTGCTCTTTT	TTCTGGTGAC	TGCCATTCAT	GCTGAACTCT	GTCAACCAGG	TGCAGAAAAT	120
GCTTTTAAAG	TGAGACTTAG	TATCAGAACA	GCTCTGGGAG	ATAAAGCATA	TGCCTGGGAT	180
ACCAATGAAG	AATACCTCTT	CAAAGCGATG	GTAGCTTTCT	CCATGAGAAA	AGTTCCCAAC	240
AGAGAAGCAA	CAGAAATTTT	CCATGTCCTA	CTTTGCAATG	TAACCCAGAG	GGTATCATT	300
TGGTTTGTGG	TTACAGACCC	TTCANAAAAT	CACACCCCTT	CTGCTGTTGA	GGTCAATCA	360
GCCATAAGAA	TGAACAAGAA	CCGGATCAAC	AATGCCTTCT	TTGTAAANGA	CCAAACTCTG	420
GAATTTTAN	AAATCCCTTC	CACACTTGCA	CCACATCTCG	AG		462

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GAATTCGGCC	AAAGAGGCCT	AGCAGATTCT	TAATTTCCCT	GTCCATATTT	TCCCCTTTCC	60
TTTCTCCCTG	CCCCTTCCAT	GGCTTATCT	GGCTGCTTTC	TCAATTTATT	CTTGGTTGCT	120
TGTGGATTCC	CTTCTATTAA	TCTTGAAGTC	GTTACTGACA	TGTTTGGCCC	TATACCAGCT	180
AGACCATTGC	CTGAAGACTT	TTTGATGAAC	AATCTGTGTA	AAGAAAAAGG	GAATCTCGAG	240

(2) INFORMATION FOR SEQ ID NO:284:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GAATTCGGCC	AAAGAGGCNT	ACCAGGANTT	TCTATTCAAT	TGAGAAGAAC	CCAGCAAAAT	60
GGGGATCTCC	ACAGTCATCC	TTGAAATGTG	TCTTTTATGG	GGACAAGTTC	TATCTACAGG	120
TGGGTGGATC	CCAAGGACTA	CAGACTACGC	TTCACTGATT	CCCTCGGAGG	TGCCCTTGGA	180
TACAACGTGA	GCAGAAGGTT	CTCCATTTCC	CTCGGAGTTG	ACCCTGGAGT	CAACTGTAGC	240
AGAAGGTTCT	CCGATTTCTT	TGGAGTCAAC	CCTGGAGTCA	ACTGTAGCAG	AAGGTTCTCT	300
GATTCCTCA	GAGTCAACCC	TGGAGTCAAC	TGTAGCAGAA	GGACTCGAG		349

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GAATTCGGCC AAAGAGGCCT AAAAAAATAA GAAATAATCT ATTCCACATT TAATAATTTG	60
AATCTTCCTG CTATAGATAT TTGGTTATCT TGACTTTTAA ANATAACATA TTCTACAGG	120
ATTTTGAGTC TGAGAAGAGA AAGGTAANAT GCAAGACACT TCGATTGTT GCACATTATT	180
ATGGAGCATC ATTAATGGTT TGNACATTTC TTGTCCTTG GGCTTGAATG GACAGTACCA	240
AATTGGGGT AATCAGCAAC TTGATGCACA GCTACGAGGA ATAAATGCTT TTGCTAATGC	300
ACTCGAG	307

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GAATTCGGCC AAAGAGGCCT AAAAGATTAA AAAAAAATTT GTGTGATTG ACTATATATT	60
AAAATCTCTT TCATAATTAG TCAACAATTT AAGCAACAAT TAAATTATTA GTGCTGTGGA	120
AAATATAGAA GAAAGATAAT TTCTTATTCC CTCCTGAGG AAAGCATTG ATACACTGG	180
AAAGGAGCTG CTATGAAGCC AATTTATCTG TTCTTTTAT CAATTCAGCA GCATTAAAGA	240
TCAGATTTT TCTCTAGTGG TCCAGCAGAG GGAGCCCTAG CACATGAATT GTTTTCATT	300
CGTGCTTGCA CCCAGGATCT CGAG	324

(2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

GAATTCGGCC AAAGAGGCCT AAGAGAGATC AGTAAAACCA CTGGNAAAGA AAAGATGGAG	60
AAAATGTTGG AAAACCAGAA CTGTTNGCTG TCAAGNTCAT GTGGAATGTT CAAGAAAGAA	120
TCTGACTCTA TTATCTAATA TCTTACATAC NTCCACCAGA CTGGACTTGC TATTTGAATT	180
TTAAGCAAGT TTCCTTTCCT TTTATACAAA TTGCAAATTT CATATTTTAA TAATCACATC	240
CTAGGAATAG CACAATAATT GGGAAATAGA ACCCTTATCA CTAGNAGAAC CATTTCCTG	300
CCACTCTCGA G	311

(2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

GAATTCGGCC AAAGAGGCCT ATGCCCCATA AAAGGGCTCC TGAAGCTCTT TGTGAAGGGG	60
TCTGAAAAGG GCAGATGAGG GTGTCCTTTG GGGCGGATGT GGGGTTTGGG ACAATTGCAT	120

GTGATTGTCA TTCTTTAGCT GTCTGCATCC CACAGAACT TTTTCTGAG TCTTCCAGCT	180
GGCCCAAGTC CTGGGTCTCT TTTACTGTTT TTGTAGCTGA CTACAGTAGG CAGATGAGGA	240
ACTCTTAGTC AATCTGAAA AACTCGACTG ACTATAACA ATCCTAAATT GAAAGAAAGG	300
TCTCGAG	307

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

GAATTCGGCC AAAGAGGCCT AGCCGGTGTG GGGAGGATTG GCTCAGCCAC CCGCTGGGAA	60
TCGTGCAGGG ATTCTTCGCC CAAAATGGAG TTAATCCTGA CTGGGAGAAG AAAGTAATTG	120
AGTATTTTAA GGAAAAGCTG AAGGAAAATA ATGCTCCTAA GTGGGTACCA TCACCTGAACG	180
AAGTTCCCTC TCATTATTTG AAACCTAATA GTTTTGTGAA ATTTCTGTGC ATGATTCAGG	240
ATATGTTTGA CCCTGAGTTT TACATGGGAG TTTATGAAAC GGTTAACCAA AACACAAAAG	300
CACATGTTCT TCATTTTGA AAATATAGAG ATGTAGCAGA GTGTGGGCCT CAACAAGAAC	360
TTGATTTAAA CTCTCCACGA AATACCACTT TGGAAAGACA GACTTCTAT TGTGTTCCGG	420
TGCCTGGGGA ATCTACGTGG GTAAAAGAAG CCTATGTTAA TGCAAACCAA GCTCGAG	477

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GAATTCGGCC AAAGAGGCCT AAAAAATCT TCTGGAAATA ATTCTTAGCT GTGTAAGAAA	60
TTTGATACTT AAGGAGACAG CAGTGGAGTC ACTTAACTAA TTTGTGTTGG TTTTGGACCT	120
GCATAGTGAC TGCCATTTAC TTTTATGTTT TGGTCAATTA GATACTAAGT AAAAAGATAG	180
TTGGTATTTT GGCTTCAGAT CAGGTCTATT TCTCCAACCT CTATATATCC TTTCTGTGAT	240
TAAAACAAAT AAACAATCCT CAGTATCATC ATTTAACACC TCTAACTGAT AGAAAAAATG	300
AGGTTGTGGG TCCTCGAG	318

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

GAATTCGGCC AAAGAGGCCT AACCTTGGGA TTTTCTATAT ATATGATGGT CTCATTGTG	60
NATAACACA ATTTTATTTT TCCTTTCCA ATCTGGATGC TTTTITTTT TNCCTATTGC	120

ACTGCCTATT GCATTCCTAA AAATCCATT CCAATGTTCA ATAGAAATGG TGAAAGTGGA 180
CATTGGAATG GAGTTTTTAG GAATGCACTC GAG 213

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GAATTCGGCC AAAGAGGCCT AAAAAGAATT AACCAGCTCT TCAGTCAAGC AAATCCTCTA 60
CTCACCATGC TTCCTCCTGC CATTCAATTC TATCTCCTTC CCCTTGCATG CATCCTAATG 120
AAAAGCTGTT TGGCTTTTAA AAATGATGCC ACAGAAATCC TTTATTCACA TGTGGTTAAA 180
CCTGTTCCAG CACACCCAG CAGCAACAGN ACGTTGAATC AAGCCAGAAA TGGTTGCAGG 240
CATTTTCAGTA ACACTGGACT GGATCGGAAC ACTCGGGTTC AAGTGGGTTG CCGGGAANKG 300
CGNTCCACCC AAATACATCT CTGATGGCCA GTGCACCAGC ATCAGCCNTA NGAAGGAGNT 360
GGTGTGTGCT GGCAGGTGAC TTGCCCTGC CAGTGCTCCN TAATTGGNTT GGAGGAGGCT 420
GTGGAACAAAN GTANTGGAGC AGGAGGAGCT CCCAGGNGTG GCGGTGTGTC AATGACAAAA 480
CCNGTACCCA GAGAATCCAG NTGCAGTTCC AAGATGGCNG CACACGCACG TACAAAATCA 540
CAGTAGTCGG TGCCNGCAAG TGCAAGAGGT ACACCGGCA GCACANNGAG TCCAGTCACG 600
ANTTTGAGAG CATNTCACGT GCCAAGCCAG TCCAGCAACT CGAG 644

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GAATTCGGCC AAAGAGGCCT ATTTNTGGAT GGTGCTAGCG AANTAGAGGC TAATCCCCAA 60
CATGAGGTTT TTCTAATTTC ANGTTTGTGA TTTTCCAGTG AAAGAAATNA ANAAGAATTT 120
GCAGATTGCT GGAGACTTGG GAAGGATATN AAGCTGTCTT ACAACCCAG ATTACCCCAA 180
AATTCAGCAA ATCACTGAAT ATTCNNAATA AAAATTGAAG TATTTTCNAA CTTAGTTTTT 240
TATCTCCAGA GGTTNACGTC CNATGTAATC CGAAATCCTC ACGANGACAT AACCTCGAG 299

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GAATTCGGCC AAAGAGGCCT ACAACAACAA CAAAAGAAGA ATACTAATTA GAATTTGAGT 60
TCTAGGGGTT TTTCTAGGT TTTTCATTCT AGACTTAGCT TTTATTCAAA CCTGTTGATC 120

CTGCATAGGG GTAGTCTAGC TTAAAAAAT AAAACAATAA ACATAAATGA GCCTATTGAG	180
TTCAATCAGA GTAGGGAGCA GTTTTATTGA ACAGCACATT TTCAAATTCT TCAGTTGTGT	240
TTGTTTTTC AGCTACGTGT CTCTCTGTGA TAATGAAAAG ACAGGTTGCA AAGCCCGGGA	300
TTCGCTCGAG	310

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GAATTCGGCC AAAGAGGCCT ACATCTATTG AGGAAAACCA CAAAAAATT CAAAACAGCT	60
ACAAACGGGAA AAAGAGAGTT TTGTCCACCA GTCAGCAGGC CACTAGTTTA TTAACCTCCA	120
GTCACTTGA TTTTGTCTAA AATGAAGACT CTGCAGTCTA CACTTCTCCT GTTACTGCTT	180
GTGCCTCTGA TAAAGCCAGC ACCACCAACC CAGCAGGACT CACGCATTAT CTATGATTAT	240
GGAACAGATA ATTTTGAAGA ATCCATATT AGCCAAGATT ATGAGGATAA ATACCTGGAT	300
GGAAAAATA TTAAGGAAAA AGAACTGTG ATAATACCA ATGAGCTCGA G	351

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GAATTCGGCC AAAGAGGCCT AGAGTGAGAC CTTATCTTAA AAAAAAAAAA AAAAAAATTG	60
TCTATGATTT TTTTAAAGC TTTTATTTT GAACATAATT TAGACTTGCT TAAAAGTTGC	120
AAAAATAAGA CACAAGTTT ATATATCACT CAATCTGCTT CCTGTAATAT TAACAACATA	180
AATAGCCACA GGGAAATCTT CAAGACCTGG AAATTAACCT TAGGACAGCA CTATTACCTA	240
AACCACAGCT CTAATTTGAA TTTCATCAGT TTTTCTCCTA ATGCTGATTT TCTGTTCCAG	300
GATCCTATCC AGGAGCCAC ATTGCTCGAG	330

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GAATTCGGCC AAAGAGGCCT AAAAAAATAT AAGTAACAGA GGNAGAAATA ACTGTTATTT	60
GTCAAGTGAC AAGCTTTTAA TGTGAGATG GCTCACCTAA AGCGACTAGT AAAANTACAC	120
ATTAAAAGAC ATTACCATAA AAAGTTCTGG NAGCTTGGTG CAGTAATTTT TTTCTTTATA	180
ATAGTTTGG TTTTAATGCA AAGAGAAGTA AGTGTCAAT ATTCCAAAGA GGAATCAAGG	240

ATGGAAAGGG ACATGAAAA CCAAAACAAG ATGTTGGATT TAATGCTAGA AGCTGTAAAC	300
AATATTAAGG ATGCCATGCC AAAAATGCAA ATAGGAGNCA CCTGTCAGGC AAAACATTGA	360
TGCTGGTGAG AGACCTTGTT TGCAAGGATA TTATACAGCA GCAGAATTGA AGCCTGTCCT	420
TGACCGTCCA CGTCTCGAG	439

(2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 428 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

GAATTCGGCC AAAGAGGCCT AATTATTCT TGTCTCTCCC CAAATGAAAT CTGGGACATT	60
ATGACAAATT ATTTTCTAA GGATGATCTT GGTCTGCCT ATTGAAATGT CCTCACTCAC	120
CTCCAAGAGG AAGGGGATG GCTTCAGAAA ATGCTTTTAA GTGTTTTTAT TTTTCACGAG	180
TTATTTATTG CAACACTAGC TCTTCCCTGC AGGAAGCTAT ATAATTGTGT GCTTAATTGG	240
TAACATAGAA GAATTCCTAG CTACTTCCTA GAGAATATAC TGTGGAATTC CTTGTCACTC	300
AAGTATCTGT TAAAACTCA ACCGTGGGAA ACAATGTCTA TGGATGCCTT TGGGAAAATA	360
CACATTTTAC CTATTATTTC ATCTTTTTTC TCACTTGTGC AAGTAGTAGG TACCCCACTG	420
TACTCGAG	428

(2) INFORMATION FOR SEQ ID NO:299:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GAATTCGGCC AAAGAGGCCT AACATTATCG ATTCCATTTT TTTACTGTTG TAATTCTGCT	60
TCTTATTGCC TGTGTAAATT TCTGCTCTAT ATTAGTTTCC TGATACCCTA TCATTAATTC	120
AGTCTGCCCT TTTTTCATAT CATTCTACTG TTTTGTCTCA TCTTCCTTAT ACTTTATTCA	180
GAGACTGTGT TTTTCATGAAG TTTGTGAAAA ACATTTTAAA AATTGTTTAA AATGTACTCT	240
TTGTCTATTT CTGCTATTT TTTCTTTTGG ATATTCTGGA ATATATCCAC AGCGCTCGAG	300

(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GAATTCGGCC AAAGAGGCCT ATAGATTGTT ACATTTGTTT TGTGCATTCC ATGAAGTTTC	60
TTACCCTTAG AGTTATTTCT GTCTTAGTAA CAGCAACAAG TGGGAATGGA GACTTTGGTG	120
ACTGGAGTGC CTTCAACCAA GCCCATCAG GCCCTGTTGC TTCCAGTGGC GAGTCTTTG	180

GCAGTGCCTC ACAGCCAGCG GTAGAACTTG TTAGTGGCTC ACAATCAGCT CTAGGCCAC 240
 CTCCTGCTGC CTCAAATTCT TCAGACCTGT TTGATCTTAT GGGCTCGTCC CAGGCAACCA 300
 TGACACTCGA G 311

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GAAATCGGCC AAAGAGGCCT AGCGCGGTGT GTCGTGGTGT GGCGCGGTGT GGCATGGCGT 60
 GGTGTCCCAG CTGTCTACAC ATTGTGGT TTAAATGTT TGTGGATAC AGTAACACTT 120
 TGTTAATTTT AATTATATGC AAGATAACTT GATTGCCCTA AACAGCCAT TTGGGTCAAG 180
 ATAAAGCCAT CGCCCTCTGA AGGGGCTGA GCTGGGTGTC TCCTCCATCA GTCGNTGTGA 240
 TAACTCTATG CCAGTTTCTGA TTCCAAAGT CAGAAGTGCA AAGCAGGGCT GGTTATTAAT 300
 CNTGTCAAAT CGTCCAGTTC CTGTGTNGTC GNACTCCATT ANTTATNTAG GTCCATANGA 360
 TGTGTCTTAC NACGNAACAA ACCCCTCTCG AG 392

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GAAATCGGCC TTCATGGCCT AATGGAATTT GAGTCCAAAG GTAAATATAT TAAACATATA 60
 GATAAGAAGA AAAGAAAAAC GTTATTAAAG TATCTGATCA GCTCTGCACC CCAGGGACCT 120
 CCACTTTTGC CCAGGTTTGA GAATTTGATC TATAGAATTA CCTGCATTCT TTCCCGTCA 180
 TCCATCCAAT CAGCCACCTT TCTCCCTTCA AAGAAGTGTC TTCATTTTTT TCCTTCTTTT 240
 GTTATTTTTT TTGACTGCCC ATCACTGTTA TTAAATCCTT CCCTCTTTTT TTGAATGAAG 300
 CAGCAGAGCC TTTTATTTT TTTTCTTGT TTTGTTTTT GTTTTGTGT TTCAGAAATG 360
 ACAGGGCTGT ATCAGAGCAG TCTCGAG 387

(2) INFORMATION FOR SEQ ID NO:303:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GAAATCGGCC TTCATGGCCT AAAAATTAAG CAAGCAATAC CTAGCCAATA GTTCTGCTTA 60
 ACTTTTNGGT TAAGTATTTT GTTGGGATTC CTATAAATAA TTTTTCACAC AAAGTTTTAA 120
 ATTTCTGGTG TACTTTGACT CTCAACTGAG AGTGGATAGA GTTTTCTTT TGAGGATTAC 180

ATCTTAAAT GTCCATCGCC TGGCTGGTTA TAAGCATTG TCACCTTTG AAGGTAAAT	240
ATACTCTGGC CCTTCTTGAC TCAGTTACAG GTCATTTAG GTCCAGTAAT AAGAGTCAGG	300
TGTTTGGTTA TTGCTTTCAG AGTCAGACAA ATCTCGAG	338

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAATTCGGCC TTCATGGCCT ACGAAGAAAA AATATTTTNG AGAGAATTC CAGATTGAA	60
AGAAGATCTG AAAGGGAACA TTGACAAGCT CCGTGCCCTC GCAGACGATA TTGACAAAAC	120
CCACAAGAAA TTCACCAAGG CTAACATGGT GGCCACCTCT ACTGCTGTCA TCTCTGGAGT	180
GATGAGCCTC CTGGGTTTAG CCCTTGCCCC AGCAACAGGA GGAGGAAGCC TGCTGCTCTC	240
CACCGCTGGT CAAGGTTTGG CAACAGCAGC TGGGGTCACC AGCATCGTGA GTGGTACGTT	300
GGAACGCTCC AAAAATAAAG AAGCCCAAGC ACGGGCGGAA GACATACTGC CCACNTACGA	360
CCAAGAGGAC AGGGAGGATG AGGAAGAGAA GGCAGACTAT GTCACAGCTG CTGGAAGAT	420
TATCTATAAT CTTAGAAACA CCTTGAAGTA TGCCAAGAAA AACGTCCTG CTCTCGAG	478

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 568 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GAATTCGGCC TTCATGGCCT AGACGAGCGG AGTAAAATCT CCACAAGCTG GGAACAAACC	60
TAGTCCCAAC TCCACCCAC CGGCGTTTCT CCAGCTCGAT CTGGAGGCTG CTTGCGCAGT	120
GTGGGACGCA GCTGACGCC GCTTATTAGC TCTCGCTGCG TCGCCCCGGC TCAGAAGCTC	180
CGTGGCGGCG GCGACCGTGA CGAGAAGCCC ACGGCCAGCT CAGTTCTCTT CTACTTTGGG	240
AGAGAGAGAA AGTCAGATGC CCCTTTTAAA CTCCCTCTTC AAAACTCATC TCCTGGGTGA	300
CTGAGTTAAT AGAGTGGATA CAACCTTGCT GAAGNTGAAG AATATACAAT ATTGAGGNTA	360
TTTTTTTCTT TTTTTTTTCA AGTCTTGATT TGTGGCTTAC CTCAAGTTAC CATTTTTTCA	420
TCAAGTCTGT TTGTTTGCTT CTTCAGAAAT GTTTTTTACA ATCTCAAGAA AAAATATNTC	480
CCAGAAATTG AGTTTACTGT TGCTTGATT TGGACTCATT TGGGGATTGA TGTTACTGCA	540
CTATACTTTT CAACAACCAA GACTCGAG	568

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GAATTCGGCC TTCATGGCCT AATCAAAAAT ACCTTACCTT GTTCTGCCCT GTGAAAGTAG	60
CCTAAGGCCT GTCAAAAACA CAAAGAGCCC AAACATAATA AAAAAGATTA AAGAAGACAA	120
TATTAAANAA GCATTGTCTC AAAGATCTAC TGCTATATTA TATTTAAGTC AGGAAGTAAA	180
TCATCTTAAA ATAATGGTCA CTTCTTCAAC AGTGAGAGTT AACACCCAAA GTGAACGTAA	240
CACTTCAATC ATCAAGATTA CAATATATGG ACTACTTCTG GTAATAACTT GGTGCTGTT	300
TAGAACTTGT ACCAACTAA CATCATGTGC AGAGAGGAAA GAACTCGAG	349

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GAATTCGGCC TTCATGGCCT AGTGATGGGG ATGTGATGTG GGCATCTGCT AATTCGTCTG	60
CAACTACATG ACCTAAGATG GCCTCATTA TCTAAGGGGC CTCAGCTGGA ACACTTGCCT	120
CTGCTGGATA ACCCAGGTCT AGTGTTATCC TCCAGACTAG ACCTGGCTTC TTCTGTGGCA	180
GTCTCAGGGC AGTGTTCCTA GACGGTGAGA GCAGAAGCCT AGGTTTGGCC ACATATCCCT	240
AACTCATAGG ATGGTGACAT AAACCTTACC TCTTATGGAG AAATAGCAAG TTACTACTGCA	300
TACGGGACGA CTCGAG	316

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GAATTCGGCC TTCATGGCCT AGTGGCAACG ACTTGGACAT CTGAGCTGTC ACTGCCGAAA	60
ACAGGCCGCA AGAGAGATAA TCAATATGCA TTTCCAAGCC TTTTGGCTAT GTTTGGGTCT	120
TCTGTTCATC TCAATTAATG CAGAATTAT GGATGATGAT GTTGAGACGG AAGACTTTGA	180
AGAAAATTCA GAAGAAATTG ATGTTAATGA AAGTGAACCT TCCTCAGAGA TTAAATATAA	240
GACACCTCAA CCTATAGGAG AAGTATATTT TGCAGAACT TTTGATAGTG GAAGGTGGC	300
TGGATGGGTC TTATCAAAAG CAAAGAAAGA TGACATGGAT GAGGAAATTT CAATATACGA	360
TGGAAGATGG GAAATTGAAG AGTTGAAAGA AAACCAGGTA CCTGGTGACA GAGGACTGGT	420
ATTAAATCT AGAACAAAAC TCGAG	445

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

```

GAATTCGGCC TTCATGGCCT AGAAGTTCCT TATGCTACTT TCACTGAGCA TCCTATGAAA      60
TACACCACTG AGAAATTCCT TGAAATTGCG AAGTTGTCTG GGTTCATGTC TAAGCTTGTT      120
CCAGCTATCC AGAATGCCCA CAAGAATTCA ACTGGATCTG GAAGAGGAAA GAAACTGATG      180
GTGTTAACTG AATCCATTTT GATTGAGACC TACACAGGGC TGATGTCATT CATTGGAAAC      240
CGCAACAAAC TTGGCTATTC CTTTGCCCGT GGGAGTATTG GTTTTGTAGA GTCTTTTGG      300
TACCATAAGC ATATCATCCA CAGATATGTC ACTTTGAAAA TTCCAGTTTG ACCCACGCTA      360
TTTTTGGACT NAAACAATTA ATTATTTTAA AATGACGCTT TATGATTAG AAATTTAGTA      420
TTTCCGAAAA TTTAAAAGCT TGATTGGACT GATAGATACA CACTTTAGAC CTCATACAAG      480
AATAATCAAA TTTTCTTAAA ACTAGAAAAT AAATGCTGCT GATACCTCGA G              531

```

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

```

GAATTCGGCC TTCATGGCCT AACTCATGCG TGCCAGTCCC CAAAAGACTT CATTCAATCA      60
ACATATATGT GACCGCCTGC TACGTGCCAG GCGTGGGCCA GGTCTTAGGG ACAAGGAGA      120
GGCCTCCGCA CCCACCCCA TGACCCATAC CTCCTCTTCC CCACCTCCCT GGGCCAGCCT      180
GCCTTCCTTC TCCCTCCTCC TCCTTCCTGG GGAAGGAAG CCCACCTTC TGTGCGCAGT      240
CAGCTCCTAA GCACGCTCCC GCTTCCCTG GCCTCCCAT TAAAAAGGG AGGCAAAGGA      300
TGTCACCACT GTCACACAC TCATGGCTTT GCTCTGGGAA GTCCTGCAA TAAATGAAA      360
GTTCTCCAAC CCGTACTCGA G              381

```

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

```

GAATTCGGCT TCATGGCCTA CTTTGACGCA CCAGGCACAA CCCAGAAAGA CGAGATTGTG      60
GAAATCCATG AGGAGAATGA GGTGCGCATCT GGTACCCAGT CAGGGGGCAC AGAAGCAGAC      120
GCAGTTCCTG CACAGAAAGA GAGGCCTCCA GCACCTTCCA GTTTTGTGTT CCAGGAAGAA      180
ACTAAAGAAC AATCAAAGAT GGAAGACACT CTAGAGCATA CAGATTAAGA GGTGTCAGTG      240
GAAACTGTAT CCATTCTGTC AAAGACTGAG GGGACTCAAG AGGCTGACCA GTATGCTGAT      300
GAGAAAACCA AAGACGTACC ATTTTTCGAG GGGCTCGAG              339

```

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

GCCTGCCTCG	AGTCTTGGAT	ACATCACACT	TGAGTCAAAT	CCTGGATACT	GCCAAAGGAA	60
CCTGAAAATC	CAGGAGACAA	CGCTAGCTAT	TCCTGTGAAC	CTCTAGAGGA	TTTGCGCCTG	120
CTCTTCAAAC	AACAACCAGG	AGGAAAGTAA	CTAAAATCAT	AAATCCCCAT	GGCCCTCCCT	180
TATCATATTT	TTCTCTTTAC	TGTTCTTTTA	CCCTCTTTCA	CTCTCACTGC	ACCCCTCCCA	240
TGCCGCTGTA	TGACCAGTAG	CTCCCCCTTAC	CAAGAGTTTC	TATGGAGAAT	GCAGCGTCCC	300
GGAAATATTG	ATGCCCATC	GTATAGGAGT	CTTCTAAGG	GAACCCCCAC	CTTCACTGCC	360
CACACCCATA	TGCCACACT	CGAG				384

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 547 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GAATTCGGCC	TTTATGGCCT	AGGGGGGTGG	GCTGATGGAG	GGTAAGTAAA	ACCTCCTACT	60
GGAGATGTT	CTCCTAAGAG	TTCACTTCA	TTTTCTATCC	TTTGAGAGG	CGATCGTGAT	120
TGCTGTGTTT	GGAAAGGGAC	AACTGGCCT	GGTGGTGGCA	AATGAGGAGG	ATGATGGGGA	180
GAAAGGTGAG	GAGGATGTAT	AAGAAATGGA	TCAGTAGAAA	TAAGGGGTGG	GAATGCAGCA	240
TATGGTACTG	GTAAGTGCTG	AACTGAACAT	GCCTGAAGCA	TTGGAGGAGG	CACACTACAG	300
ACAGGGAGGT	GCTGTCCACT	GAAAACCACA	GAGCATCCTG	GGACCTGCTG	TGTACTACAA	360
GCAGGGATGT	GCTGGCCTGT	GCAGAGTGA	ATCCCATGTG	GTGCCACTGT	TGTTACTGTG	420
TAAGAAACAG	GGACTGTTCC	TTGATGGAGC	TGATCATGTA	TGTCAACCAT	GACTGCATTC	480
TGCTGGGGTG	GATGAGCAGC	AGGATGTAGC	AGACGGGGAG	ATACATTCGG	AGGGTGGAA	540
GCTCGAG						547

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GAATTCGGCC	TTTATGGCCT	AATTTGTGGC	TTACCTCAAG	TTACCATTTT	TCAGTCAAGT	60
CTGTTTGTTT	GCTTCTTCAG	AAATGTTTTT	TACAATCTCA	AGAAAAAATA	TGTCCCAGAA	120
ATTGAGTTTA	CTGTTGCTTG	TATTTGGACT	CATTTGGGGA	TTGATGTTAC	TGCACTATAC	180
TTTTCAACAA	CCAAGACATC	AAAGCAGTGT	CAAGTTACGT	GTGCAATAC	TAGACTTAAG	240
CAAAAGATAT	GTAAAGCTC	TAGCAGAGGA	AAATAAGAAC	ACAGTGGATG	TCGAGAACGG	300
TGCTTCTATG	GCAGGATATG	CGGATCTGAA	AAGAACAATT	GCTGTCCTTC	TGGATGACAT	360
TTTGCAACGA	TTGGTGAAGC	TGGAGAACAA	AGTTGACTAT	ATTGTTGTGA	ATGGCTCAGC	420
AGCCAACACC	ACCAATGGTA	CTAGTGGGAA	TTTGGTGCCA	GTAACCACAA	ATAAAGAAGC	480
CACACTCGAG						490

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 371 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GAATTCGGCC	AAAGAGGCCT	AGGAAGTAAC	AGTGTATCAT	GTATGCCACT	GATTCCAGGG	60
GACACTCCCC	TGCTTTCCTC	CAACCTCAGA	ATGGAAATAG	TCGTCACCCA	TCTGGCTATG	120
TTCCAGGGAA	GGTTGTCCCA	TTGCGTCCCC	CTCCTCCTCC	AAAGAGTCAA	GCTTCAGCCA	180
AATTTACCTC	CATCAGACGA	GAAGACCGGG	CAACCTTCGC	ATTCTCACCT	GAAGAACAGC	240
AAGCCCCAGAG	AGAAAGTCAA	AAGCAAAAGA	GACACAAAAA	TACTTTCATT	TGTTTTGCTA	300
TTACTAGTTT	CTCATTTTTT	ATAGCACTTG	CAATCATTTT	AGGAATATCC	TCAAAATATG	360
CTCCACTCGA	G					371

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

GAATTCGGCC	TTCATGGCCT	AATTTAAATG	TGGACAGATT	GGAGGGGAAA	GGTTTGCAGC	60
AAAAATCATA	AGTAGAAGGA	AACAGAAATG	TTAAGTACAC	AGTGTAGTAG	CCATTTAGGA	120
AAGTTATAAG	CCATTTAAAT	GCCATGTATA	AAGTGTTTTT	GATAAGAAAA	AATCAAAGTG	180
TAAAGGAGAA	TACAAAATTA	TATGTGTACT	GCGGACACAT	CTGTATTGTT	CTGTGTATGG	240
AAAACAGACT	GGGGAGAAAT	AGCTTTAAGT	CCTAATAGTA	ATTTTCTTTT	TCTCTCTTCT	300
TTTTTCTGCT	TTCTCTTTTC	CCTGTCTCCC	TCAATATTGC	ATATCTTTCC	CATTAAAAAG	360
TATTGTATTA	TATATCTACC	AACAAGACAT	TTGTTTCAGA	TTTTTTGGTT	TTGTCTTCAA	420
GGAACATTCT	TCTGCATACA	AATCGAG				448

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

GAATTCGGCC	TTCATGGCCT	AGAGATGGGG	TTTGCCACG	TGCCCAGGC	TCATCTCCTC	60
GAACTCTTGG	ACTTAAATGA	TCCTCCCGTC	TTGGCCTCCG	AAAGTGCTGG	GATTACAGGC	120
ATGAGCCACA	GTGCCCAGCC	TCTACCCGCT	TTCTGTGGTC	AGAAATAGAC	GCAGGACATT	180
CCATCCATAC	CTTATTTCTT	TCCTGGCTCT	TCCTCCATGT	GTCCTCGTGG	GTCCTGGTCA	240
CCCTCTTAGC	TGCTGTGTAA	TAACCCCTGT	GCAGATGCAG	CAGCCACGAT	GTCTATCAGTC	300
CCCACCCAGT	GATGCATAGG	GGGCTTCTTC	CCCTCCCTGG	GTACAGCACT	ACCAATTCCT	360
GTGTATGGGC	CGTGTACAGC	AGGGGCCACG	TCCTGGCCCC	GCTTCAGTCC	CGGCTCGGGC	420
TCCTCGCCGG	GGTCTCCATG	CACTTCCCT	CTCCCATCTC	CACATCTCGA	G	471

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

GAATTCGCCT	TCATGGCCTA	CAGCATCGTC	GGGACCAGAC	TCGTCTCAGG	CCAGTTGCAG	60
CCTTCTCAGC	CAAACGCCGA	CCAAGGAAAA	CTCACTACCA	TGAGAATTGC	AGTGATTTCG	120
TTTTCCTCC	TAGGCATCAC	CTGTGCCATA	CCAGTTAAAC	AGCTGATTCT	GGAAGTTCTG	180
AGGAAAAGCA	GCTTTACAAC	AAATACCCAG	ATGCTGTGGC	CACATGGCTA	AACCCTGACC	240
CATCTCAGAA	GCAGAATCTC	CTAGCCCCNC	AGAATGCTGT	GTCCTCTGAA	GAAACCAATG	300
ACTTTAAACA	AGAGACCCTT	CCAAGTAAGT	CCAACGAAAG	CCATGACCAC	ATGGATGATA	360
TGGATGATGA	AGATGATGAC	GACCATGTGG	ACAGCCAGGA	CTCCATTGAC	TCGAACGACT	420
CTGATGATGT	AGATGACACT	GATGATTCTC	ACCAGTCTGA	AGAGTCTCAC	CATTCTGATG	480
AATCTGATGA	ACTGGTCTCG	CTCGAG				506

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GAATTCGGCC	TTCATAATTT	TTCTTATCTT	CATTCTTTTCG	GGTGCCCAAA	TAAGCTCATG	60
TTTTCCATGG	TCGGTTTAGT	TTTTACTAGT	CGTTGGCTAG	TTTCCTAATT	GCATGTGAGT	120
TAGCATGTGG	TGATGGCGGA	GTAATGTCAT	GTCTTGAGGA	GAACATTGCT	TGAGTTCCAA	180
ACTTAGCTTT	TCTACTTCTT	GGTGAGACTT	TGGACAAATT	ATTTTGTAGC	TTGTTTCCTC	240
ACTTAAAAAA	ATGGGGTTTG	TACCTTTAGT	TGTTTCAACT	GTTGTGAGGA	CTTGAATAAT	300
AAAGTATATA	GCTATAGATA	AGAAAACCTG	GGGGACTCGA	G		341

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 572 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GAATTCGGCC	TTCATGGCCT	AATTTTTC	AAAACCTTGA	AATGACATGT	TAAAATGCTG	60
CTTTGAACTG	GTTTTTCTTT	AGCCTGTAGA	AAAGAACTTT	GAGTTACTGG	TCAAGTAGTT	120
TTGACCATAC	TGGCTTAGGA	AAACAGCGCA	TCAGCTGTCT	GATTGCTATC	ATGTAAAAAT	180
CTGTGAACGA	CTTTGAGAAG	TCATTGGTGG	ATTATGTTGT	TCAGGAATAG	GAATGGAGCT	240
TTCTTCTAT	CACCTGTATT	TTTTTTTTTT	TTTGGGAAGG	GGGAGGAGGA	GGAATTATTT	300
CCNCCCTAAT	AAANGNGGN	NTTAATCCTG	GGCCCCNNNA	AGGCTGGNNN	GGGTCNGAT	360
KTGGGGGTNC	NNTTTATTGG	GAAGTGACNG	GGNTTTAATT	TTCCGGTTTT	TTTTTTTTTCT	420
TGAATGATCT	TGTGTTGTAG	AGTTGAATAC	AGTTCTAGGG	AAGTATGATC	ACAAAATGAA	480
TGTTGGCAGT	TCCTCCTATG	ATTAATATGT	CAGACATGTC	AAAATTCTCT	CATCATGTGT	540

ATTTCGCGGG TTTATTTCAGT CCAGGACTCG AG

572

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GAATTCGGCC	TTCATGGCCT	AGATAACTTT	GAACAGAATG	GGAGGCAGGT	TTACCCCTAAG	60
CAGTTCCCCA	CTTGAAGTTT	TCCTTTAGTT	TAGTGATTG	AGGGGCCCAA	AATACTTTCA	120
CATTTCCCCC	CTTTCTTTT	TAAAAATCTG	TTGGAGAACG	CATTTTAGAA	GAAAATGAGT	180
CTCTGGCCTC	AGGTTTCGTC	TGATCTCTCA	TGGCTAGGAT	GGTTTATTC	TAGATAGATA	240
GGTCCTGAGT	TATTAGGAAA	GCTCCTTTT	AGAAGGTTGT	GAAGTCTCAT	GTCCTGTGAA	300
GAGAAAATAG	GGGGAGGACA	ACAACAAACA	AAAGAACTCG	AG		342

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 391 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GAATTCGGCC	TTCATGCCTA	CAATATTGTT	TAATAATTAT	TCAGAAATAT	TCAAGTATAA	60
TACTTAATAA	AAATTTCTGC	TATGTGCAAG	GCATGGTGCT	AGGTACTGAG	ACTATAAGGA	120
GGTAAAGAT	AGTTCTCGCC	CTTAAAGACT	TCTATAATTT	AATCAGAAAG	GAGAGTATAT	180
GAAAATCATA	CTGAATAAAA	AGTGGCTCAT	AATAAATGCC	AAGGAATCAA	CACAAAGTCC	240
TTCCCTGGT	AGGGAAAGTT	TTTTTGAGGA	AATGGGACAT	GAATTTGGCT	TTGAAGGATG	300
TGGAGGGTTT	AGATAAGAGG	GAGAACTGT	TGTGTTCTAG	GTTAGAGGAA	CAACATAAAC	360
TCAAAGAGA	CTAAGAAGA	ACGGACTCGA	G			391

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

GAATTCGGCC	TTCATGGCCT	ACCCTGAGCA	GTGCCTGGCC	CATACTGGAT	ACACAGTGTG	60
CATTTTGTGG	GGACTCAAGG	AAGGAAGGTA	ATATTCCAGC	TCAGGGTTCT	CTCTGACCCT	120
GAATAGTGTT	ATGGACTCTT	TGGGAAGGAT	AGAAGCTTTC	TTAGTTTCT	GACAGAGGCC	180
TGTAGCTGC	AAACGTTGTG	TTTGTAGAAA	GAGTTGTAAG	GGTGTCTATG	GCCTTTATTT	240
AAAAGTGCT	TTAATGTATC	TTAGGCATCT	TTTTCTTTTC	ATCTCACACT	ATGGACAGTT	300
TTAAGTGCAA	AAGGGGAAC	CGAG				324

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

```
GAATTCGAGC TCGACTGGAT AGTTTTTCTT TTTAACTTA AAATGCTTTT TAGTTTGGCA    60
CTCCGTAGTA AAGGAGGTTT CAGAAGCCAG TAAGAGAACC TCTGCCAACT ATGAAAGAGA    120
AGATATTTCT ATCTACAAGT TATTCAGGA TCAATTATTC AATTAATATT TTATATAATA    180
GAAAGGTTTT ATTTGTTAGG ACTTTATCTT TAAGTTCCCC AAGAGTAAAA AGGTCTAGTC    240
ATTATTATAC TGTGGGAGAA TGATAGAAGA TTGATTACAT TGAAGTCCA GAACTTCTAT    300
TTATTTAAAA GATTTAAGAT TTGACACACT CTCGAG                                336
```

(2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 409 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```
GAATTCGGCC GGCATGGCCT AANCTAAAAA TAAATNAAC CCAACGCATA NAANACGGGT    60
TTATCTCTCC TAAAAACANT TNAGTTTNGA CTTAAATGAA ACANATCATN NNACAACNTC    120
ATTTTNAAT GAAGATTTTA CCTGGACCCT AGGTGTGCTA TTCTTCCTAC TAGTGGACAC    180
TGGACATTGC AGAGGTGGAC AATTCAAAAT GAAAAAATA AACCAGAGNA GATACNNCG    240
TGCCACAGAT GGTAAAGAGG AAGCAAAGAA ATGTGCATAC ACATTCTGG TACCTGAACA    300
AAGNATAACA GGGCCAATCT GTGTCAACAC CAAGGGGCTA GATGCAAGTA CCATTAAAGA    360
CATGATCACC AGGATGGACC TTGAAAACCN GNAGGAAGTG CATCTCGAG                                409
```

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```
GAATTCGGCC TTCATGGCCT AGGCGGCGGC AGCCGAGGGC GTACTGGCGA CCCGGAGTGA    60
TGAGCCCGCC CGAGACGATG CCGCCGTGGA GACAGCTGAG GAAGCAAAGG AGCCTGCTGA    120
AGCTGACTTC ACTGAGCTCT GCCGGGACAT GTTCTCCAAA ATGGCCACTT ACCTGACTGG    180
GGAAGTACG GCCACCAAGT AAGACTATAA GCTCCTGGAA AATATGAATA AACTCACCAG    240
CTTGAAGTAT CTTGAAATGA AAGATATTGC TATAACATT AGTAGGAAC TAAAGGACTT    300
AAACCAGAAA TATGCTGGAC TGCAACCTTA TTTGGATCAG ATCAATGTCA TTGAAGAGCA    360
GGTAGCAGTT TTTGAGCAGG CAGCTTACAA GTTGGATGCA TATTCAAAA AACTGGAANC    420
CAAGTACAAG AAGCTGGAGA AGCGATGAGA AACTTATTTC TATGGGACAG AGTCTTTTTT    480
```

TTTTAATGTG GAAGGACTCG AG

502

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GAATTCGGCC	TTCATGGCCT	AGAATATTCC	ATATCAGTAC	ATATAGCACT	GCCTCACTTT	60
TTAATGGCTA	TATAAAATAG	TACTATAATT	TTTAACCACT	CACCTGATGG	TGGGCTTAGT	120
AGTTATTCTG	TGGCTGTAAC	CAACATCACT	GCCATGTGCA	CTGGTACACA	TACAGAAGTC	180
CACACAAGTA	GGCCTGTATC	TGTAAGGTAA	ATACTGGTGG	GATTACTGAG	TGAAAGGAGA	240
CGTGAATTTT	TAGATTTTTA	CTATGAAAGA	CAAACCTGCTC	TTTATGGGGA	TTTTATTAAT	300
CTACAACCCC	ATCAACAATG	TATGAGAGCC	CATTTTTCAC	ACACTTGCCA	ACTCAGTAGG	360
TTATTAAACC	TTTTGGTCTC	TGCCACTTGT	ATATCCCAGA	TCAACTTCTA	ATTCTGCTTC	420
ATATTGTTTG	CTATCCTTAA	GAATATTCTT	GTCCCACCTT	GTCTCGAG		468

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GAATTCGGCC	TTCATGGCCT	AGGGAAAGGA	AGTGACATAG	TGGTATAAAA	ATTTGAAATT	60
TGTGATGTGG	CTTAGAAGCT	TGATATATAC	GGGTATGATT	GCAGCTGCTA	CATTTAGCCT	120
TTTTTTCTTT	CTTTTGGAG	AATGAACCGC	ATTAAGAAAT	ACATTTTACA	TCACAATTTA	180
GCAAGTATAT	GTGCTAACAT	ACTTCTGTTT	CTACAAGGGA	TGTATTGTGG	TATTTTCTAT	240
TGCATTTTAC	TCTAATTTAG	TTCAATTTAA	AAAATGCTGA	TTCTAACCCA	TGAACCTGAG	300

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GAATTCGGCC	TTCATGGCCT	ACCACCACAC	CGGGCTAATT	TTTTGTATTT	TTAGTAGAGA	60
CGGGATTTC	CCATGTTAGC	CAGGATGGTC	TTGATCTCCT	GACCTCGTGA	TCCACCCGCC	120
TGGGCCCCCC	AAAGTGCTGG	GATTACAGGC	ATGAGCCACC	GTGCCTAGCC	GACTCTTGAG	180
TTTTGACAAG	AGGTGATATC	TGGGAGATTA	ATAAGTATTT	AGTTTAAGAA	AACATTTAGT	240
AAGCCTGTCC	TGTGTTCCCA	CACAAAGGGT	ATAACAGCAA	TATATTCCAT	AAGAGTAAAG	300
CTCGAG						306

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

GAATTCGGCC TTCATGGCCT ACATTACCAT CAGATTGACA TATTTAATTA TCAGATATCT      60
TTCTTTTGCC AAAAAGTTGT GGTGAGTTG GCCCTGGGAT TTATAAATAC ATGCACACAG      120
CACATTCTCG TCATTGTTCA CTGCAGTCTT TTAACACATC TTCTCAGCAA TATTCTTAAT      180
GTTTCCAGCG GGAAATTTGT AAATTATTTA ACCACTGAAT TAGAGGTGTG TTGTTTTTTA      240
GCTAATCAAT AGCCATTGAA TGCTTAAATG GGCTTTAAAG TAGACAAAAG TAAAAGACAG      300
CAAAGAAAAT TAATCAGTAA GATTGCCCAT ACTCCATAGA CACTTGAGCA GCTACTTTAG      360
TCATTTTGAA ATACAGCTT TATGTTTTCC CTGGGACTGG CATATTCCTG TCATTATATA      420
AAAGAAATATA CATTGTAAA TTTAAGGTGT GGACATTCAT TATTGAAGGT AGAAATAGTT      480
ATAATCATCA GTGTCTAGAT ATATCTGAAG AGAGGTACTC GAG                          523

```

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

GAATTCGGCC TTCATGGCCT AAAGTAGGCA AGGGATAATA ACCAAAGAAG NAAATTTTCAT      60
GAAGACTAGA CATCATAAAG CATAATTTTA ATAGTCACTC AACCAAGTAT TTTTATTTT      120
TTATGGATAC TCTGAATGCG AATTAAATGT GAAACCCAGT TTCTGGGCA AGTCAAATTC      180
TGGAATCACA TCCACCTAAA TTAAATGAC TAGCTCGTAT TTCCCCATC TTCAAGTTTC      240
ACATCCTGGT CATCAAAAGA CTCGACAGCA AGACTTAGAA TGAAAAAGGG TACTTGTTTA      300
TATTAATATT TTTTACTTGA ACACGTGTAG CTTGCAGCAG GTTCTTGATG AATGTGCTTT      360
GTGTCCAAAA TGCCTCCCCA TTGTACACAG GTGTACACCA TGCATGCACC AACACCACTC      420
GAG                          423

```

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

GAATTCGGCC TTCATGGCCT ACAAGCCACA AACTGTGGT GAATGGAAAA GAATGTATAA      60
ACTTCGCCTC ATTTAATTTT CTGGATTGT TGGATAACCC TAGGGTTAAG GCAGCAGCTT      120
TAGCATCTCT AAAGAAGTAT GGCGTGGGGA CTGTGGGACC CAGAGGATTT TATGGACAT      180
TTGATGTTCA TTTGATTG GAAGACCGCC TGGCAAAATT TATGAAGACA GAAGAAGCCA      240

```

TTATATACTC ATATGGATTT GCCACCATAG CCAGTGCTAT TCCTGCTTAC TCTAAAAGAG 300
 GGGACATTGT TTTTGTAGAT AGAGCTGCCT GCTTTGCTAT TCAGAAAGGA TTACAGGCAT 360
 CCCGTAGTGA CATTAACTTA TTAAAGCATA ATGACATGGC TGACCTCGAG 410

(2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GAATTCGGCC TTCATGGNCT ACCTTAGCCT CAGCTCTTTC TTCTGGGTG TTTGTATTTT 60
 CTTTTCTGTC CCAAACAGTT TCCCCACAA AAAGAACTTT ATGTCTTTCT CTGTCTTCCC 120
 TCAGTCCTTC CAGTCAGCAG CCTGTGATTG GGCTTTTCCC CTCAGAAACG AACAATCCAG 180
 AACCCACTGT TTAACAAC TGTATTTTGC CTGGGAAGT CCCATTGCCT TCCCTGAAAA 240
 CATTAAACAT TCCTCCGATC CCCAGCCTGA GTCTCTCTGT CTCTGGGCCC CATCCTGCTC 300
 CACAGCAGGG CTGGTGTGTC CAGCACAGAG TGACCCTCCG ATGCCCTTTC CCACCCGCCG 360
 CCNTGCCTCC CTCGAG 376

(2) INFORMATION FOR SEQ ID NO:334:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GAATTCGGCC TTCATGGCCT ACGGGTTGTT ACATATTAT TCTTTTTTGA AGCCCATCAC 60
 TACATCGCCA TTACGTTTTA CACTGTGTAT GTAACAAATG TTACCACTTT GTTCTTTATT 120
 CCTTTTGGGA TCATCTTCTAG TGGGGGTAAA ACAGTATCAA GCTCTAGAGC TCCCTCTGGT 180
 GGTTTTTGTG ACATATTTGA AGATGGCAGC TTGCTTTTGT AGAATTTCTG GCTCTGCTCT 240
 CCTGTTTT ATCTGTACTT TTTTCTCA TTGTGCCTCT TGCACACACA CACCCCCCCC 300
 ACTCGAG 307

(2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GAATTCGGCC TTCATGGCCT ACATTACTCA GCTTTCCTGA ACAACCAGGC ACGACCTCT 60
 GCCTGCAGGC CAGGCACGTG CTGCTGCCCC TGGAGGCGGG TGGGGGTGCC TCCGCGCTGG 120
 AGGACACGGG GTGCACTGAG GCTTCCATT GGTGATGGGG GAATGTGGTG ATGAGGGGAT 180
 GCGGTGCCCC CGGACCGCAC ACATGCCATG TGTGGACACT CAACAGGAAG CTTGCGTCAG 240

CATTTCAGCT GGAAATGCAG AGCCAGGGCC CTGGAAAGTC CCTCAGCAGC TGTGCACAGG	300
CCTGCTCACC GTGCGTGTGC GGGCAGAGCC TCCCTGGGGA GGCAGAGGCC CCGCGTTCTG	360
CACTCGAG	368

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCC TTCCTGCTCT TCTAGGTAGT	60
CACACTTCAC TAAAGTGTCA TCCACCAAGTG TGTGAATCC GAAGAATGAC AATTTTCTAC	120
CACTGGTGTG AAAAACAAC ATTGAAGAC CCTTGTGCAT TGTGTGTAC AAAGCTAAAT	180
ACATGGAAAT CGTTAATATC GCTGATATTA AGTAATTTCC CCACTCTGAG TGAATACTTT	240
GATGATTGCC AACAGTGGCT AATAAAATGA CGGCTACCAC ACTCATGGGT CACTGGGGCT	300
GCGCAGGGCT CTTTGAGGTG GGTGGCTTCT TTGGAAAGT ACTATGAACG TCTCGAAGCA	360
GTATTCTAGT GATAAGAATT CTTAACATAG CCAAGCGCCC CACGTTTGT CCCCACGTTT	420
GTTCCCTTA TCTCGAG	437

(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GAATTCGGCC TTCATGGCCT ACCAAACCCA ATTTATTAA AAANATACTT CTATATCATT	60
ATATGTATTA CCAATTGTTT TAGCCTTATA CAGGATGCGG TGTNCTGTGC TCCTTNGTGA	120
ATGTCNGTTG CTGGTAGCTG GTTATGCTCA TGATGATGAC TGGGTTGACC CCACAGACAT	180
GCTTAACTAT GATGCGGCTT CAGGAACAAT GAGAAAATCT CAGGCAAAAT ATGGTATTTC	240
AGGGGAAAAG GATGTCAGTC CTGACTTGTC ATGTGCTGAT GAAATATCAG AATGTTATCA	300
CAAACTTGAT TCTTAACTT ATAAGATTGA TGAGTGTGAA AAGAAAAAGA GGGAAGACTA	360
TGAAAGTCAA AGCAATCCTG TTTTAGGAG ATACTTAAAT AAGATTTTAA TTGAAGCTGG	420
AAAGCTCGAG	430

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GAATTCGGCC TTCATGGCCT AGAAATAGAT TTTCTCAG ACTCTCATCT CACATTCCCT	60
-----------------------------------------------------------------	----

TTTAAGATT	CCTNGTCCTA	TCCCCACCCC	AGACGTTTCC	ATTTTGCTTT	TATTTTCTAT	120
AATAATTCCT	GGGGGCCTCT	ATTAAAGGCC	TTTTTCTTTG	ACTACTTACA	TCCATTATAC	180
CAGTATCTTT	GTCAAGTAAA	TTTTATATAT	CTTTTATTCT	GTCAATCAGG	TAAGAAACAA	240
TAATTGTATT	TTTAAAGGAA	AATATTTTAC	GATGCTACTA	AGCAGTTACT	TTGTCCACTT	300
ATGCAGGATA	CTCGAG					316

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GAATTCGGCC	TCATGGCCT	AGCTGGCTGG	CACCTGGAGA	ATCCCTGAGC	TGAAAAAGCA	60
GCTTGGTCTG	CAGAACTGAG	TCACAAGACT	GAGGCACTGG	GGAGCCTCAG	CCCCATCTGG	120
TTGTTGNTCC	CTCTGTGACC	TTGAGCTTGT	CTTCCACTTG	GTGCCGTAGG	CCCTCATTTG	180
TCCATTGAAG	TTAGCACCTG	TCCCTCCCGT	CCTCCAGAGA	GGTCAGGAGG	ATAAGCATT	240
GAAGACTCAC	TGTGGTTTAT	TGAGTGCTTA	CTGTGCAGGT	ACTGCTGTAG	TTTTGTGCAA	300
CTCGAG						306

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

CAAACCTTTG	AGTNNNACAG	TTAAGATATT	ATGTGAAGCT	CAGAATCATG	TTTCAGACCA	60
TTGAAATTAC	TGGTTAAAT	ACAAATAGCT	GAAGACATGA	TGTAAAAGAT	TAAGTACTTG	120
GTTTTGTAAC	ATATTTACCA	ATTAAAGTCA	CAAAATATTT	CTCATTATTT	ATTCATGCAG	180
GTAACCTGAG	AAAAGATAGT	GCAGAAATCA	ACTTTAAATA	AAAAATTATT	CCTCCCCTTC	240
CTCCCACTCC	CCTATACTCT	ACAAAATGTT	TTCCCTGGGA	CTAGGCCTTG	AAAAGGCCAC	300
TACATATTAG	TGTGACATGC	ATTACTGTCT	GCAATTAAAA	AAGCTAACCT	TGTGGTGATT	360
GTAATTACAT	TATAAAAATG	TCCACATGCA	TAAATCTAAA	AAAGGTTGAA	AACCTACAGT	420
AAATCTACAA	TATAGTGTTT	ACATTTGACC	ACTGGTTTGT	GTTATGTAGA	AGTCATAGAT	480
TTGGTAAAGC	ATTGTAAACAA	TTAGGAAGG	CATCTAAATC	TTTAAGTTCT	GGACAAATTT	540
TATGTTTTAA	TCTACAAAAT	TGCATGAAGG	CTAACTCGAG			580

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GAATTCAGAN TTNTGCTATG GTAGCACCAG ATGTCCAAAT TGAAGATGGG AAAGGAACCC	60
TCCTAATATC TTCCGAAGAG GGAGAGACGG AAGCTACTAA NTCACAAGAA GTTNTTCAGA	120
ATTTGGAATT AGAANTGGCA NCCGGCTTCA AGCAGATGAC TTCNTCCAGG ACTATACTTT	180
ATTGATCAAC ATCCTTCATA GTGAAGACCT AGGAAAGGAC GTTGAATTTG AAGTTGTTGG	240
TGATGCCCCG GAAAAAGTGG GGCCCAAACA AGCTGAAGAT GCTGCCAAAA GCATAACCAA	300
TGGCAGTGAT GATGGAGCTC AGCCCTCCAC CTCCACAGCT CAAGAGCAAG ATGACGTTCT	360
CATAGTTGAT TCGGATGAAG AAGATTCTTC AAATAATGCC GACGTCAGTG AAGAAGAGGG	420
AAGCCAGCTC GAG	433

(2) INFORMATION FOR SEQ ID NO:342:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GAATTCGGCC TTCATGGCCT AAAACTCTAA TAGTCTCTCT TCAGCGGAGC CACTGAAGGA	60
AGATAAGCCT GTCAGTGGCT CTAGGAACAA GACTGAAAAT GGACTGACTC CAAAGAAAAA	120
AATTCAGGTG AATTCAAAAC CTTCAATTCA GCCCAAGCCT TTATTGCTTC CAGCAGCACC	180
CAAGACTCAA ACAAACTCCA GTGTTCAGC AAAAACCATC ATTATTGAGA CAGTACCAAC	240
GCTTATGCCA TTGGCAAAGC AGCAACCAAT TATCAGTTTA CAACCTGCAC CCAAACCTCGA	300
G	301

(2) INFORMATION FOR SEQ ID NO:343:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GATTCAGATG GAGATGCCAA GCAGGCCCTT AGGTGAAGGA GTCTGGAGTC TGAAAGCATT	60
TGGGATGGGG ATATAGACTT GAGAGCCATC AGCTTATAAA TAGGACTTGG TCAAGAAATGG	120
GTGGCCTCCA TCCTAGATGG ATATAAATAA GAAATAAATA TCAATTTTTC TTCTTATAAC	180
ATTCCTAGGT TTTCATTTT ATGACTTTAA GAAAAATATG AATGACAAAA ATAAACATA	240
AAATCAAATA TATCGTATT GCCCTTTGGG GGACACCATC TCTTGCTCAC TTTACACAGT	300
AAGTGCCATT TCCTTCACCT CCATGGAAAA CATTTCGTAA ATTACTAAGT TGAATAACTT	360
AAAATATAGG ACGGGACATC TCGAG	385

(2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GCAGAAACCT TCAGGGAAAC CCCATGCTAG CGGCAACTGC ACCACACTTT GAGGAGAGCT	60
GGGGGCAGAG ATGTCGTCGA CTCAGGAAAA ATACAGGGAA TCAAAAAGCT CTAGACAGTG	120
ATGCTGAGAG TTCCAAAAGT CAAGCAGAAG AAAAAATCCT AGGTCAGACT TATGCAGTTC	180
CCTATGAAGA CGATCATTAT GCAAAAGACC CAGACATTGA AGCACCCAGC AACCAGAAAT	240
CAAGTGAAAC GAATGAAAAG CCAACGACAG CTCTTGCCAA CACCTGTGGA GAGCTCGAG	299

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

GCATTGGTT CTTTTATAT CTCTATTTC TCTCACTATA TTCTGTTTT TCTTTTAATG	60
CTGTACATC ATTAACTCG CTGTTATCCT TGTCTGTGAG TCATCTGGTC ATTTCTGTGT	120
GTTTTATTA ACTGATTATT CTCCTTGTC TGGCCACATT TCTGTGCTTT TNGGCGTTTC	180
AGTAACCTCT GATTGGATGT TGGGTATTAT AAAGATTATA TTATTGAGTG TCTGGATTTG	240
GGGTGGTAGT TACTTGTGGA TCAGTATGAT CCCTTTGAGG CCTATTTTGA AGCTTCAGCT	300
CGAG	304

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GAATTCGGCC TTCATGGCCT AGATTACAAC ACGTGTGCCA CCACACCTGG CTAATTTTTC	60
TATTTTTAGT AGAGACGAGG TTTCACCATG TTGACCAGGT TGGTGGTCTT GAATTCCTGG	120
CCTCCAGCCT GGTGACAGAG CGAGACTCCA TTTCAAAAAA AAAAAACAAA CTTCATGCTG	180
AGAAGTCTGA AGAAAAAAA GATTTTAAAG AGGAAATGT GTAAGAAAAA TACTTCAGCT	240
TCTGTTACAA AATCAAAATA GAAAAAACA CAAAATTGGT GTTTCCTCGA G	291

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GTAACCTTAG CTGTACCTTG CAAACCAGAA CATATGGTCA CCCTACCTC CGGTCACTTT	60
TTCTTCTTTG TTTCATTCT TTTAATTTT TTCCCTTTA AACACACAGC ATTATCTTTC	120
CCTGAGCACC ATTGTCTTG CAAATGCTCT TGCAATCGGG ATATTTTGA CCTGGCAACA	180
TGCATATTCA GTCTGAACAG TCTCTCTGAA CCTACCCCAA AACCTGGTTT TAGCTTCCAG	240

GCAGAAGACT CTGTTCCCTG GCTTGCAACC CCCAAACTCG AG

282

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

GAATTCGGCC	TTCATGGCCT	ATATCAATGC	AATTTTAAAT	TTTGTGTAAT	ATCAACAGCA	60
AAAGCCTAGT	GCATTGGGAG	ATGTGCAACC	TCCCTGAAAA	TCCTTTCTGT	TTCTGGAGTA	120
CTTCAGGGGT	GGCCTCTGGC	CCCAGAGCCT	TTGCCACAGT	GCTCCCACCA	GCCCCACCT	180
CATCCGCTG	TTTGCAGAGC	CTCATCTACA	GGTCCCCACG	CTGCCTTCTT	TACTCACTCT	240
GCGCTTGGCC	GTTTGTAT	TTGGCTTAGT	CTACATTGGG	CGGAAGTCTG	TGTGCACAGA	300
GTGGGTGTTT	CTTCGAGCCC	CTTCCACTCA	GAGGGCCACA	CG		342

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GAATTCGGCC	TCATGGCCTA	CAAAGAGCTG	GGATTACTGG	TGTGAGCCAC	CGTGCCCGGC	60
CTGGACATCT	GGTTTAACT	AGATGGAAGG	GAAGAACATT	ATGAATCTTT	AAAATACGGC	120
TGTTGCCATT	TTTCTCTCTT	CTTAACATGC	AGCATAGGTG	ACAAGCTTTT	CTGTCATCAT	180
CATGGAGCAT	TCTGAATCAT	GACATTTTGT	TTTGAGAGTT	CATTCTTGAA	TTTTCAGTTC	240
AAAATATTGT	TTGAACTATT	ATTCCACATT	CAAAGATTAT	ATAAGGTCCT	GTGCTTTTGA	300
ATCTTTTTC	AAAAATTAT	TTCTGCCTGC	TTAAAAAA	TACTTTTATT	TCCCCACAGA	360
GAGTTCAGGA	CTTCAGATTA	GTTTGTGTTT	AGCTCACTTA	ACTGGATAGA	CAATTTTGCG	420
TTTTGCAACA	CCATAGCTCG	AG				442

(2) INFORMATION FOR SEQ ID NO:350:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

GAATTCGGCC	AAAGAGGCCT	AAAAAATGA	AATTCCTTAT	CTTCGCATTT	TTCGGTGGTG	60
TTACACCTTT	ATCCCTGTGC	TCTGGGAAAG	CTATATGCAA	GAATGGCATC	TCTAAGAGGA	120
CTTTTGAAGA	AATAAAGAA	GAAATAGCCA	GCTGTGGAGA	TGTTGCTAAA	GCAATCATCA	180
ACCTAGCTGT	TTATGGTAAA	GCCCAGAAAC	GATCCTATGA	GCGATTGGCA	CTTCTGGTTG	240
ATACTGTTGG	ACCCAGACTG	AGTGGCTCCA	AGAACCTAGA	AAAAGCCATC	CAAATTATGT	300

ACCAAAACCT CGAG

314

(2) INFORMATION FOR SEQ ID NO:351:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

GAATTCGGCC AAAGAGGCCT AGCTACCAGA GTGTGAGAGA CCATTGTCTC GTTGGCTGGC	60
GCTCACGGAC ATGCAGTCAC GGTAGCGGGA GCAATCACAA AACTGTAATT TACTTACCAA	120
ATCTCTTCCT TTCCTAGCC TCGCCTGCCT GACTTAGAGA AAGAAAAGCA ATAATTTTAC	180
AGGCATTTTG AGGTGTCTCT TTGGGTCTT TCTGTTTGAA AGGATATTTG TCGAAAAAAA	240
GAGCAAAACC GTTTTAAATA AACTCCCCCT GGAAAAAAC CCAAACACT TGCATCTCGA	300
G	301

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GAATTCGGCC AAAGAGGCCT AGCAAATACA CATTAAATAAG AATGCCTAGA AGAGGACTGA	60
TTCTTCACAC CCGGACCCAC TGGTGTCTGT TGGGCCTTGC TTTGCTCTGC AGTTTGGTAT	120
TATTTATGTA CCTCCTGGAA TGTGCCCCC AGACTGATGG AAATGCATCT CTTCTGGTG	180
TTGTTGGGGA AAATTATGGT AAAGAGTATT ATCAAGCCCT CCTACAGGAA CAAGAAGAAC	240
ATTATCAGAC CAGGGCAACC AGTCTGAAAC GCCAAATTGC CCACTAAAA CAAGAATTAC	300
AAGAAATGAG TGAGAAGATG CGGTCACTGC AAGAAAGAAG GAATGTAGGG GCTAATGGCA	360
TAGGCTATCA GAGCAACAAA GAGCAAGCAC CTAGTGATCT TTTAGAGTTT CTTCAATCCC	420
AAATTGACAA AGCTGAGCTC GAG	443

(2) INFORMATION FOR SEQ ID NO:353:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

GAATTCGGCC AAAGAGGCCT ATAGGCTCTT TTGGCCGGCC AAAGAGGCCT AAAAAATCT	60
CAGCTATGGT TCATTATTAC TAGCTCAGCT TTTAATCTT TAAATTGGTT GAATTATTCT	120
CTATGTCAGT TATTTTATT GACCAGTTT GGAATATTT TGTTCATTTA TCAGGGAGTA	180
TGCGGTAAAT GAAGTTGTGG CAGGGATAAA AGAATACTTC AACGTAATGT TGGGTACCCA	240
GCTACTCTAT AAATTTGAGA GACCACAGTA TGCTGAAATT CTTGCAGATC ATCCCGATGC	300

ACCCATGTCC CAGGTGTATG GAGCGCCAAC TCGAG

335

(2) INFORMATION FOR SEQ ID NO:354:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

GAATTCGGCC AAAGAGGCCT ACAGAGATTA TATTGGGGTT NCCATTTTGT GAAGCCANAG	60
ACATNTGGTC ATTGGGATGT GNGATTGCAG AATTATTTCT TGGANGCCCG NTNTACCCAG	120
GAGCCTNGGA GTATGCTCAG ATTCGANACA TTTCTCAGAN TCAAGNTTN CCAGGAGNAC	180
AGTTGTTANA TTTGGGTACT AAATCCACAA GATTTTTTTG ACANAGAAAC AGATATGTCT	240
CNTTCTGGTT GGAGATTAAA GACACGGAA GAGCATGNGG CAGAGACTGG AATGNAGTNT	300
TAAGAAGCCG GACTCGAG	318

(2) INFORMATION FOR SEQ ID NO:355:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

GAATTCGGCC AAAGAGGCCT AGTGGGAATT TTAAATACAA GATCCTGTTG AAAATATTGA	60
TATTCAAAGA AACAAACAGC TTTGGATCCA TAGCCACAAT TTAGGTTTTT CTAGATTAAA	120
ATCAGAAAGTG ATTTTATTGT TGAAGATAC ATTAATTCTT TGAAGTCAGA ATAAGAGGCT	180
TGACAATTTA ATTTCTAATT AAGTGACTGA ATAGACAAAG GATCAAATAC AAACAGTAGT	240
GCAGGAAGAA AATAAATTGG AAGAAATAAT TGTTCAACCA GTAGTAATAA TTAAGACCAC	300
CATTTTAAAA TTTTCTATAC ACAAGAATG AGAAAATATT GTTATTATTA TTATACTTCT	360
TTCTTCTTCA GTATTAGTGG ACCCACATTA TCTCCTGTCA ATTCATTGTG TTTATNATGT	420
GAACCATCTC TCGAG	435

(2) INFORMATION FOR SEQ ID NO:356:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 158 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GAATTCGGCC AAAGAGGCCT ACAGGCTCAC ATTGACTACA CACGTTTATA CCAGGCGCCA	60
TGTTCTTTGC CGAAACTCCC GTCAGAGCC TGGATGATCT GCCCTCACC TCTGCCCTCG	120
TTCCCATCCA CTCTCCCTC CTGCTCTGT TCCTCGAG	158

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```

GAATTCGGCC TTCAAGGCCT ACTCTTCTTG GCATATTATT TTCCTGAATT GCTGCCTCTG      60
TTGTTCAAAC CATCCCGGAT TAATGACAAA ACACATATCTT ATTCAAACCA AGAATTATCT      120
ACAACCCTCC TTCTCAACTA GTTTNNGCAA GATCATTTCA GTTTTCTTT TTGTGCTACA      180
TCCTGGATTA ATTCTTCAGT TTNGTCTTCT CTGGAATCAC TACCTAAGGC TTATTCATG      240
TTTCAAGTTT TTTGTTTTTT GTTTTTTTTT ACTTTGATGA GTATGTTTAC CAACGCTCTC      300
GAG                                     303

```

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```

GAATTCGGCC TTCATGGCCT ACAAAGTGTT GGAATTACAG GCGTGAAC TA CCGTGCCCGAG      60
CCTTTTTTTT CATAGCAGTT TTATTAAGTT GTATTTGCCA TACCACCCAA TGTATCCATT      120
TAAGCACCTG ATTCAGTGGT TTTTCATGTA CTCATGGAGT TATGCAGCCA CAATCTTAGC      180
GCATTTTCAT TACCCAGAA AGAACTGTA CCCATTATGC ACCCCGTTCC CNTCNTCCGG      240
TCNTGGCAAC CACGAGTGTA CTGCTGTCT TCATGGATT GCCTATTCTC GACGTTTCAT      300
TGGGATGAAA TCACACAGTG TATGGCTTCC ACACTTTACT GTGCTGTTGT CAAGGTTTAT      360
CTATGTGTTG GGTGCAGCCA CCCCTTGGTA TCCACAGGGA TTGGACCCAG GAGCCTGCAC      420
CGATCCCCTG CAGGGATGCC TGTGTCCCAC AGTGCCCCCT GCAAACTCA CTGATATGAA      480
GAGTCGGCTC GAG                                     493

```

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```

GAATTCGGCC TTCATGGCCT AGTTAACATG ACACAAAATC TTTACCTGCA GTTCTAATAT      60
TTTGCAAGGC TGAAGTCCAT ATTTACAAC TCTTAGATC ATCTCAATCT GATTATTTAA      120
CTATTCTCTC TAACTGCTAG TCCAGCCCCT AAAACTGCAT TTCTCTGCTC CTCCAAAGCT      180
TAGTGGCTTA TTGAAGTCCA TATTTGCAAT GTGACAGAGC CAACTCCCAA GAATGGATTG      240
CCACTCAGTG TAATGCAATA GGAGCACTTT AATTTATCT CCATTTTCTG GACCCAGTGC      300
ATCATTCTAG CCCTTTTTC TTGGAATGAA GTCTGGCTGA GAATGATGAT CCATTAGTAA      360
GAATTACTTA ATAAATCAAC TCTTGGTTAT GAGTGGCAGA AAATAAAGC CAGGCTCGAG      420

```

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

```

GAATTCGGCC TTCATGGCCT AATGTCACCA CTGTGGAAAA CCATATAGGT CGAAGGCTGG      60
ACTTGCCATAT CACCTGAGGT CAGAGCATGG GCCTATATCC TTCCTTCCAG AGTCAGGACA      120
GCCAGAGTGC TTAAAGGAGA TGAACCTAGA GTCAAAGAGT GGGGGCCGAG TTCAGATACG      180
TTCTGCCAAG ATAGCTGTAT ACCACCTACA GGAGCTGGCC TCTGCTGAAC TGGCCAAGGA      240
ATGGCCCAAG AGGAAGGTGC TTCAGGACCT GGTACCTGAT GATCGAAAGT TAAAATATAC      300
TCGTCCAGGG CTCCTACCT TCAGCCAGGA AGTACTACAT AAATGGAAGA CTCGAG      356

```

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

GAATTCGGCC TTCATGGCCT ACATGATGAA ATGTTGGCTA AAAGAGTCAC CCTAATATTA      60
ATAAAATGTT TTATTCTTCA TGTGACTAAA TCAGTGTGCA TGCAAGAAAA AGAAAGAAAA      120
AATGCTTAGA TTCCTTTTTT AAATTATCTC CAGAAATTTCT AATTTTTATA AATTAAGGAC      180
CAACAAATCC CATTTTGTTC TCACGTTTGA CATTTGTTCC TTTGACTTAA ATAACTTCTC      240
CACTCTTTAT TTTCTATTT GTGGTGATTT GAATAATTTT TCAGAAAATA TGTACTTTCT      300
GATAAATTGT AGTGTGTCAG TAATGAAAAC TGCTCTATGG TGCTCCCCTC GAG      353

```

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```

GAATTCGGCC TTCATGGCCT ACGAACTACT CTAAGTAATG GGCCAAGTCA TGAGCTGCAC      60
AAAGGCCCCC AAGACCCAGA CGGGTTTAAT GTTAAGCAAA ATGCCGCCTG GTCTCAGGTA      120
GACACTCAGC CACCGCTAGC CCCAGTCAAC TGTCCCATGG GAAGGCAGAA GGCCCGGTGT      180
TGCCAGGTCT TAAGTTTTC AAGAGGAAATC CTAAACGAT GGTGTTTCAC TATAATGGAT      240
TCATTTTAT GTTTTATAAA TCTCTATGTT CATGTACTGG TATTAGTACT TTTATGTGAT      300
AAAACTTTT TTTTAAACAT TGGTAATTCA AAAACACAAC ACCCACATAC AGTGAGGACC      360
AAACAAAACC CGTCTGCAAG CAGGCTCTCT CCGAG      395

```

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

```

GAATTCGGCC AAAGAGGCCT ACAAAGGACA GCCCTGTCTG CACTGTAGT TACTGTGGAT    60
TTTAAAGAAA CTTCGCTAAA GAATTAGGC ATTCTGATT CAGTTAAAGG ATTGCCAATT    120
CATCAGTCCC TGAACTAGA GCAATCTCAA CAGGACAAGA AAAGAAAATG GGCTTTTAA    180
GTCCAATATA TGTCCTTTTC TTCTGTTTGG GAGTTAGAGT ATACTGCCAA TATGAAGCTT    240
ACCGATGGGA TGACGATTAT GACCAAGAGC AAAATGTCTGA G          - - -    281

```

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

```

GAATTCGGCC TTCATGGCCT AGTGCCACTG CACTCCAGCC TGGTGACAGA GTGAGNCTCC    60
GTCTCAAAAA AAAAAAAAAA AACTCAGCTT CTTAGAGAG ATAAATTTGG GGGAGGAGCC    120
CAGGGCCACA TACCAAGCTT TGGGACATGG TGCCTCATGC TCTCTGGGAT TGCAGACCAT    180
CCAGGTCTGT CTTCGCCCCCT GTTAGTGAC ATATATCCAC TCACATGTCT TCCCTCAGGC    240
TATCGGGCAG GGGGACTTCA CCAGGGGGTT TATGGATAGG CTTCAAGAGG GTCTGTGAGC    300
CCCCAGAAAT TGTGTGTGAG ACTGAGTATG TGTTCTTTT TCCAGGAAAT TCTCGAG    357

```

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

```

GAATTCGGCC TTCATGGCCT ATTACAATAT GCTTAAAGCT CAAAATGATC GAGAAACACA    60
AAGTTTGGAT GTCATATTTA CTGAAGACA AGCGAAAGAA AAACAAATCA GAAGTGTCTGA    120
AGAAGAAATT GAACAGGAAA AACAAGCAAC AGATGACATT ATCAAAAATA TGTCTTTTGA    180
AAACCAAGTC AAGTACCTAG AGATGAAAAC CACAAATGAG AAAGTGTAC AGGAATTAGA    240
TACACTTCAA CAACAATTGG ATTCACAGAA CATGAAAAAA GAGAGCCTGG AAGCAGAAAT    300
AGCTCACTCC CAGGTGAAAC TCGAG          - - -    325

```

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GAATTCGGCC TTCATGGCCT AGTGAATTGA GTTTGTAAA CCTCCTTAGC ATATCACACA	60
ACACTAATTT TCCACTCTCA ATATGTGGCT GTAGAGTGTT TAATGTTTAC TTTCATATCG	120
CTTTTCCATA GTAGTGCAAG ACCTCAGTTT AGCTTGTTTA CATTATTTGC AGATTTACTT	180
ACAGTGTAAT ATTTATTTCT GTTTTAAATA GTGTTTGCAA TAGGAGAAAA TCATATGATC	240
TTAAGCATAT ACACCAAAGG TAAGAAAGGA AGCCACTATT GTATCTTTT GATGAATTCC	300
AGATGAGCTG GGATCAAATT GAACTGCTTA GGCAGAAATT TAAGAGACAA GTAGAAGTGG	360
TGCAGAAAGA CATTGTGACT GCAATGTCCT ATTTACAGCT ACTGCCCAGA GGAGAACACT	420
CCCAACATGA CAAAGAGTTC ATCAGCTTGA ATGTTAACTT TTGAAAACAA TTAATTGAGC	480
CACGACCCG GGCCAATCTA GTGAATTGAG TTTTGTAAAC CTCCTTAGCA TATCACACAA	540
CTACTCGAG	549

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GAATTCGGCC TTCATGGCCT AGGAGGCGGA GTTTGCACTG AGCCGAGATC ACGCCATTGC	60
ACTCCAGCCT GGGCGACAAC AGCAAGACTC CATCTCAAAA AAAAAAAGTG AGATCCTGCC	120
GATGGGCGCT TCCTGTCCAC CTGTGAGGAA AACCTGCAAA AGGTTCTTGT CGCACCATTA	180
GAGCCAGTTT TTCCCAAATG ACACCCATAC CTGATTTTCC TTGTTCTTCT AAGACAGTTT	240
TAATTAGGAT AATCTCATAA GTGCTACATT TTCAGTGAAT TTTTCAATAT AGTGGCCCAT	300
GTCTTTTCTT TTTTTTTAAA GTCTTTTTC TCTGGTAGCA CATGTGATTT AATGCTTGCT	360
TTCTGAATT GTAGAAATAA AAGGAAATCA CAAGTATTTT CCAACAAAGT GGAAGTGGG	420
CCGAAGGTG CAGAAAAAAA CTATAGAAAT TAGTTAAAAA TTAGGAAGGG GCAGTCTCGA	480
G	481

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GAATTCGGCC TTCATGGCCT ACCAACTCAG AAGGGAATGG AATGTGGAAA AAAAGAAAGA	60
AAACCTGAGT AACTTTTCCT AAAAAAGTCT AGCTGTTCTC AGTTTGTGGC ACCAAATGGG	120
GAGCAGGGAA TGTTCCAGTC GCAACTGACT AATTAGCCA ACCCTNATTT ATTGATAATA	180
ATAATGATAA ATAATAATGC TAGCTAACAC TTAGTGAGCA AATACTAGGT ATTATGTGAA	240
ATCATTTTCT TGTATTAACT CACTTAATCT ACACAGCAAC TCGAG	285

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```
GAATTGGCCT TCATGGCCTA NGTGTGGATA GTGGAGGCAT TGGTAGCCAG AACATGTCAC    60
TTTATGACAG CATATGGACA GCAATATGGA AGCCCAGCAT GGTTGGTAAA AAATGGGGCA    120
GCCTAAGGTC AATGACTTTT GGCTGAGTCT GTGAAGATCT CAAAGCTTGG TGGTTTTTAG    180
CATAGCCTTT ATACCATACT TAACTCCGGG TAAGGACCAG GACCACTGTA GCGACCAATT    240
GATTGACAGA GTAAAGTATG TGGGTTTTTT TTTTCCCCCA ACTGGGCTGA TTCTCTTAGA    300
ATAAAAATTG TATACCATTA TATTATGTTA ACTTGATCAC AAAGAACAAA ATGTTATTTA    360
TTAATAATAT AGCATTGTCA TCTGTTTGAT GAATTTTCTT GATTTAATGC TTGTTTAGAT    420
TCAGTAAGCC ATTTCAGGA ACTATAATAA ATGCTTCTTC CAACTTCTCG AG            472
```

(2) INFORMATION FOR SEQ ID NO:370:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```
GAATTGGGCC TTCATGGCCT ACGAGTGCTT GCTGGAATCG TTTACCCTNG TTAATTTTTA    60
TCATNTCCTC TTTATGAGCA TGATATGGCT TCAGCTGTTC CACTTTGATC CAGGCATGAT    120
CTTCTGTTCC AAAAAATTTC ACAAAGAAGC ATTTCTTTCC GCGAGGTTTC TTCAAGTCCT    180
TTGGTGGATT AACAATCTTT CCTGGCCAAG GAGGATATCG GCCGAGTTTC CCCACACCA    240
AGTCGCCGAG CCGCAGACTC ACAGCCGCCA TCTTACCACC CAACCACCGC CGACGCACGG    300
GCCGCCG            307
```

(2) INFORMATION FOR SEQ ID NO:371:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

```
GAATTGGGCC TTCATGGCCT ACAACGATCT TGTCTTCTTC TATCAGGTTT GCGAAGGTGT    60
TGCGAAGGCC AGCCATGCCT CCCACACAGC TGCCCAGGCT GGGCTTCCTG ACAAGCTTGT    120
GGCTCGTGGC AAGGAGGTCT CAGACTTGAT CCGCAGTGGA AAACCCATCA AGCCTGTCAA    180
GGATTGTGTA AAGAAGAACC AAATGGAAAA TTGCCAGACA TTAGTGGATA AGTTTATGAA    240
ACTGGATTG GAAGATCCTA ACCTGGACTT GAACGTTTTC ATGAGCCAGG AAGTGCTGCC    300
TGCTGCCACC AGCATCCTCT GAGAGTCCTT CCAGTGTCTT CCCCAGCCTC CTGAGACTCC    360
GGTGGGCTGC CATGCCCTCT TTGTTTCCTT ATCTCCCTCA GACGCAAACCT CGAG            414
```

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GAATTCGGCC	AAAGAGGCCT	ACTGGATGGC	ATCTACTTCG	TATGACTATT	GCAGAGTGCC	60
CATGGAAGAC	GGGGATAAGC	GCTGTAAGCT	TCTGCTGGGG	ATAGGAATTC	TGGTGCTCCT	120
GANCATCGTG	ATTCTGGGGG	TGCCCTTGAT	TATTTTCACC	ATCAAGGCCA	ACANCGAGGC	180
CTGCCGGGAC	GGCCTTCGGG	CANTGATGGA	GTGTCGCAAT	GTCACCCATT	TCCTGCAACA	240
AGAGCTGACC	GAGGCCCAGA	AGGGTTTCA	GGATGTGGAG	GCCCAGGCCG	CCACCTGCAA	300
CCCACTGTG	ATGCCCNAA	TGGCTTCCN	GGATGCAGAG	GAGGCCCAAG	GACAAAAGNA	360
AGTGAGGNAG	CTCGAG					376

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GAATTCGGCC	AAAGAGGTCC	TGTAAGTATG	ACTATTTAAT	TTATTTCTTT	TCACAAATATA	60
AAAAGCACAT	GCGATATTTT	GAAAGACTAT	TAAAGGTGGG	GACAAGAGGT	TATTTAAATC	120
TATGTTTGA	TGCAACTTTT	ATGGCTTAAA	CTACAAAGAA	TTATCCTTTT	TATATATTAA	180
ATGATTGTAT	AGTTCCTTTA	ATACTGTTTT	TGATACAAG	TGTGAAATNC	TTAAAGAAAA	240
TGGCAACAT	CACTAACAA	CATTACAATT	CTAATAGCTA	ACTTTTCTGA	GCCATTACTT	300
GGAACCATGC	ACTGTTTAAA	ATGCCTCACT	TGGCCAATGC	TCGAG		345

(2) INFORMATION FOR SEQ ID NO:374:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GAATTCGGCC	AAAGAGGCCT	AAAATGCCGA	GTTATAATCC	AGAAGGGGAG	TCTTCAGGGA	60
GATACCGAGA	AGTAAGGAT	GAAGATGACG	ATTGGTCCTC	TGATGAATTC	TGAAGATAAT	120
CTCCTAAATC	ACTGACGTTG	AGATGTCATC	ATCTTACATC	AGACTTTCTA	ACTAGTATCA	180
AGATCAGTGT	CAGATATTGT	TGAGGGAAGT	AATTTTATAA	AGTTACACAA	AGGTAGTTAT	240
AAAAAAGCC	CAGTTTGCT	TTCAGAAAGT	GACTTTCATG	TGCTTGAAAA	GTTTAAATATT	300
TGAATATTGT	GTTTAACCAC	ATGGTATTAA	AATTTTGCAA	TATATTGTGT	ATTGGTCTGA	360
TATTTTAGTA	TATAGTAGAA	CATACTTTT	TTTCTTTAA	GCCAAATGAA	AAGAGGTAAC	420
TTTGCTTTT	TCCTTTTCT	TACCTATCAA	ATAGCATTTA	TTACATGTCT	TTCAGTGAAA	480
TACTTAGTTG	TTCCAGGCAC	GCTCGAG				507

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

```

GGAACGAATA GAAGTGTGTTG TATCTGTGGG TTNGACACAC TACTGAATCA CAAAGTCTTT      60
GGAATAATTC TCAAAAGCCA TCACTTTTAG CCCACTTTCT CATTCAATTAA TGCTCTATTC      120
TTTTTCTAGC ATGTCTAGCA GAATTCTCTT GAATTCTTGC AGTGAATTGG TGCTCCTTAA      180
ATACCTGCTA TTTTGGAATA GTTTTGACTT AAATACATTT TCCTTTTCTC CCAAGTGTCAA      240
AATGTCAGGG CTGACAACTG AAAGGGCTTC TGAAGATTGT CAGTGTCTCT ATATTCAGAT      300
AGGTAGCAAA GAATCTGACA CATTTGGTAT AATAAACCCA CTCGAG                        346

```

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

```

GAATTCGGCC TTCATGGCCT AGGATGAATG ACCTTAAAGA TCGAACATGA ATAAGAGACA      60
TCATTTACCC TCAAAGAAAC TAGAGTCTGA TTGGGCAGGG AGGAAAAGGT ATTAAAATTA      120
TGCTTTTCTG CATTGTGTGG ATTTGAAGTT TGTTTTTGTG TGTTAAGAGT CTTATTATTA      180
GGATAATGAC ACTGTTTTTT CTTTATTAAG TTACTTGTGT GGCAGTTAAG ATGATTCTGG      240
TGGCTCTTAA CATTTTTTTT TTCTCCAGTC GGGAAATGCG CCTGTGTGCC GCCGTCATTT      300
CCCACCTGCG GTTATTGAAG CATCTGCAGC TCCTTCCTCT GAGCCTGATC CTGATGCCCC      360
ACGGTCTCGA G                                     371

```

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

```

GAATTCGGCC AAAGAGGCCT AGGAACTGTT CTGTTGAAAA TACCCATCCA ACAGTTTCTT      60
ACTATTGCTCA TCCCCAAGTG GCATCCTACA ATACCTACTA CCATAGCCCT CCTCACCTGC      120
CACCATATTC TGCTTATGAC TTTCAGCATT CCGGTGTCTT TCCATCCTCC CCTCCCTCTG      180
GACTTTCTGA TGAGCCCCAG TCTGCCTCTC CCTCAGCCAG CTACATGTGG TCCTCAAGTG      240
CACCGCCCAA AACTCGAG                                258

```

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 436 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

GAATTCGGCC	AAAGNCGCCT	AATATAACTT	AGCTGCTATT	TACAACACTA	GAAATTTAGT	60
ACTTTAAGTA	ATTTACATC	TATGATAACA	TTTGTTACTT	TATTTTAAAT	GATTTTTTTA	120
CAGTAGTTAT	GACAGTAGGA	TGGTTATGGA	ATTGGAATTT	AAACTCCCAA	CTAATGAGCT	180
TAAGCTGCTT	GGAATATTAA	TTATGTAGTT	TTTACATTCC	ATTTTAAAAAC	AAAAACTTAG	240
NAAAGGTGCT	GGCATTCTGA	GGCCTGCAAT	TAGGCCACAT	AGCAGAAGCT	TGCTCCTTCC	300
TTATCTGGGT	GAAATATTTT	ATTTTGCAC	TTTGAGTCAT	ATTCCACCC	CTGTATAAGC	360
TACATAGGAG	CCTGAATGAA	TTGGGTAGGA	AAGGAAATTA	TGCAACAAG	TCTCAGCTAG	420
TGCTGAATGA	CTCGAG					436

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 535 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

GAATTCGGCC	AAAGNNGCCT	AGCACATGCG	TCCCCGCAGT	TGTCTCTTTC	TCCTTTCCAA	60
GTTCGTGNCT	CTAAGGAGAT	GGAAGTATTC	TAAATTTTCC	TACTTCTAAT	TTTTACTATG	120
CAACCAGCAA	AGGCGGGAAG	GTTGCAGGGA	AAATGTCCG	GTCTTTCACA	ACTAAGNNGG	180
AAATTACTTC	TCCTATGTTT	TTATTCAAGA	GTTGTCTTTA	AAACTGCCTG	CCGGCTTTCC	240
CTTTTAACTT	TTAGGATTAT	AGTTAAGGTT	ATGGAAAGTA	GTCATTCAAT	AGTTCAGTAC	300
GTTCATATAA	GTTCTCTAAC	ATAGAAGAAA	ACTCAGTCAC	CAGACAGTGA	AGTCATTTAG	360
CAGTGGTTAT	TGGAAGATAA	TCCACAGTGA	TGGTAATGGA	ATACTGGAAA	CNCATCCTAA	420
ATAATCTGTA	ATTATTATTA	TTATTATTTT	GGGACAGNGC	GAGGCTCCGT	CTCCAAAAAT	480
AAATAAATAA	AATAAATAAA	TAAATAAATA	AATAAAGGAT	GGTGACGTC	TCGAG	535

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

GAATTCTAGN	CCTGCCTCGN	GTOGCACCCA	TGTTCAATCG	TTCTTCCTT	CCTTCCTACA	60
TTCTTTTTTT	TTNCCTTCTT	CTTCAGGGTC	TCACTCTGTC	ACCCTGGCTC	GAG	113

(2) INFORMATION FOR SEQ ID NO:381:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

```

GAATTCGGCC AAAGAGGCCT ACACACATCG TTCATGTACA TGATCGCCGG ACTCTGCATG      60
CTGAAGCTCT ACCACAAGCG GCACCCGGAC ATCNACGCCA GCGCCTACAG TGCCTACGCC      120
TGCCTGGCCA TTGTCATCTT CTTCTCTGTG CTGGGCGTGG TCTTTGGCAA AGGGAACACG      180
GCGTTCTGGA TCGTCTTCTC CATCATTCAC ATCATCGCCA CCCTGCTCCT CAGCACGCAG      240
CTCTATTACA TGGGCGGTG GAAACTGGAC TCGGGGATCT TCCGCCGCAT CCTCCACGTG      300
CTCTACACAG ACTGCATCCG GCAGTGCAGC GGGCCGCTCT ACGTGGGACC GATGGTGCTG      360
CTGGTCATGG GCAACGTCA" CAACTGGTCG CTGGCTGCCT ATGGGCTTAT CATSCGEEC      420
AATGATTTCC CTTCTACTT GTTGGCCATT GGCACTGCA ACCTGCTCCT TTACTTCGCC      480
TTCTACATCA TCATGAAGCT CCGGAGTGGG GAGAGGATCA AGCTCATCCC CTGCTCTGCG      540
ATCGTTTGCA CCTCCGTGGT CTGGGGCTTC GCGCTCTTCT TCTTCTTCCA GGGACTCAGC      600
ACCTGGCAGA AAACCCTGC AGAGTCGAGG GAGCACAACC GGGACTGCAT ACCCCTCGAG      660

```

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

```

GAATTCGGCC AAAGAGGCCT AGTGTGGGA GCTGTGGGCT GTGCCCTTCC AGTCCCCCAC      60
AGCAGTGTCT TTGCCAAGA ATCTCCTAGC GAGAGACCAG GGGCTACTGC CAGGTGACAG      120
AAAAGGGAAC ATCAGTTCCG CTATACCCAC AGCTCACCTG GCGGCCTGGG GCCTGCACAG      180
GGCCTGGTTG AGGCAGTGA CCCCATTITT GGGCCGTCTG TGGAGTTGAT GTTCCTGCCA      240
GCTGGTCCCT CTCTGTCTT CCTGGAACTT CACCTGCAGT TTGATGCCTG AGTTAAAT      300
GTTCTTCTAA ATAATCACT GTAGACTTTC TGTTTTTCAG TATGTGAAAA CTTCTGAGAA      360
ACTTGGAGAG TCTCGAG      377

```

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```

GAATTCGGCC TTCATGGCCT ACTGGGCGGT CTTTGCAGCA ATAACAATAT CTGCTCCATC      60
CTTTGCTGCT TTCAATGCAA TAGCTTTGCC AATGCCACGG CTGACACCTG TGATAAAAAC      120
TGTACATCCT GCCAGCCTCC CGGTGTTGGG TAACATGACT TTCGTAGATC AGAGGAGGCG      180
GCGGGCGAAG CGCACGTGCA GCGGGGGAGC GCGGCTGCCT GTGGAGATCC GCGGAGGCCG      240
ACAGGATTCT TGGGCTGCC TCCCCGCTGC TGTGCATTGG GTTAAAAACG ACAACCAACT      300
CGAG      304

```

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```

GAATTCGGCC AAAGAGGCCT ACTTATTTTA CACAGCTTGA TTAAGGTCTA TGTCGGTATA      60
ATTTTTTTTA TGAGTCTNAC ACGTGGGATT TGTTGAGCTT CTTGAATTTG TATGTTTATA      120
CAAATTTAGG AATTTTTTTC ATCCATTATT TATTTGAATA TATTCTCTGT CTTCACTGTC      180
CTTTGAGGAC TCCAATTACG CATATACCTA ATTGCCTGGA GTTGTCCCAT AGCTTACTGA      240
TGCTTTGTTT ATTTTTTTCT TTCTTTTTTT CTCACCATGC TTTAGTTAGG ATAGTTTTTA      300
TTACTGTTTT TTTAAGTTTG CTAATCTTTT CTTCNCAGCAT GCCAGCTCGA G              351

```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

```

GAATTCGGCC AAAGAGGCCT AGCGTCTTGG ACATGCCAGG AATAAAAAGG ATACTCACTG      60
TTACCATTCT GGCTCTCTGT CTTCCAAGCC CTGGGAATGC ACAGGCACAG TGCACGAATG      120
GCTTTGACCT GGATCGCCAG TCAGGACAGT GTTTAGATAT TGATGAATGC CGAACCATCC      180
CCGAGGCCTG CCGAGGAGAC ATGATGTGTG TTAACCAAAA TGGCGGGTAT TTATGCATTC      240
CCCGGACAAA CCCTGTGTAT CGAGGGCCCT ACTCGAACC CTACTCGACC CCCTACTCAG      300
GTCCGTACCC AGCAGCTGCC CCACCACTCT CAGCTCCAAA CTATCCCACA TATCTCGAG      359

```

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

```

GAATTCGGCC AAAGAGGCCT ACTACATGTA AAACACTTTT ATTCATTAAA AAGAAAACTG      60
ACTGGCTTGG ACCTACAAAT TAGTTTCATT ATTTGTTAAT GTTTGAAAGC CATTAAAAGA      120
TGAATATTAA GGTTCCTTTA TACTCAATAC TTGTAGTTTT GTTTGGGGGA ATGAGAGGAT      180
GCCCTTGGA CTTTGTGAG GCCTCTCCAC TGAGGGTCAA TCATGACTTC TGTTTTAAAC      240
CAGCCCATCC CATCTTCTCC AGCTGCTCTC CTTATGTCTT GCTTCTCTCC CCTCCAACCT      300
TCTCAGCACC AGGACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

```
GAATTCGGCC TTCATGGCCT AGTGGGAGCT ATTTTCTTTT TTGTGCATAT AGATATTTCT    60
TAAATGAAGC TGCTTTCTTG TCTTTTATTT CTAAAAGCCC CCTTATACCC CACTTTGTGC    120
AGCAAAGATC CCGTGCAGG TCACAGCCTG ATTTGTGGCC AGGCTGGACA AATTCCTGAG    180
GCACAACTTG GCTTCAGTTC AGATTCAAG CTGTGTTGGT GTTGGGACCA GCAGAAGGCA    240
AACGTCCAGC CAACACACAG GACTGCAAGA GGTCTCGAG - -- 279
```

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

```
GGTAGAAGCA GGAGGTTTTC AACCTAGTCA CAGAGCAGCA CCTACCCCTT CCTCCTTTCC    60
ACACCTGCAA ACTCTTTTAC TTGGGCTGAA TATTAGTGT AATTACATCT CAGCTTTGAG    120
GGCTCCTGTG GCAAATTCCT GGATTAAGG GTTCCCTGGT TGTNAAAATA CATGAGATAA    180
ATCATGAAGG CCACTATCAT CCTCCTTCTG CTTCACAAG TTTCTGGGC TGGACCGTTT    240
CAACAGAGGC TCGAG - -- 255
```

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

```
GAATTCGGCC TTCATGGCCT AGGCCACAT AGAAGAAATG AATGAAAAGA CTTTAGAAAA    60
GCTTGATGTG AAGCAAACAG AACTAGAATC ATTATCTTCT GAACTGTCAG AAGTATTAAA    120
AGCCCGTCAC AACTAGAAG AGGAACTTTC GTTCTGAAA GATCAAACAG ATAAAATGAA    180
GCAGGAATTA GAGGCCAAGA TGGATGAACA GAAAATCAT CACCAGCAGC AAGTTGACAG    240
TATCATTTAA GAACACGAGG TATCTATCAA GAGGAACTCG AG - -- 282
```

(2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GAATTCGGCC	TTCATGGCCT	AGATAGAGCT	CAAAAACATG	GCATGGATGA	ATTTATCTCT	60
TCCAACCCCT	GTAACCTTGA	CCACGCTTCC	CTCTTTGAGA	TGGTACAACG	CCTTACTTTG	120
GATCACAGAC	TTAATGATTC	CTATTCTTGC	CTGGGCTGGT	TCAGTCCTGG	CCAGGTGTTT	180
GTACTAGACG	AGTATTGCGC	CCGAAATGGA	GTCCGGGGGT	GTCACCGACA	TCTCTGCTAC	240
CTCAGAGACT	TGCTTGAACG	GGCAGAAAAT	GGCGCCATGA	TCGACCCAC	CCTTCTTCAC	300
TACAGCTTTG	CCTTCTGTGC	ATCCCATGTC	CATGGGAACA	GTCAACAAAT	GCATGTGTAC	360
CTTAGTGGGC	TGCCACCAAA	TACAGACCAC	GGTTCTTCCC	TATAGTGAGT	CGTATTAAT	420
TCAGAGGAGT	ATTTAGAAGA	GAAGCTGAAG	CTGTCGAG			458

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GAATGGGACT	CCAAGCETGC	CTCCTAGGGC	TCTTTGCCCT	CATCCTCTCT	GGCAAATGCA	60
GTTACAGCCC	GGAGCCAGAG	GAGCGGAGGA	CGCTGCCCCC	AGGCTGGGTG	TCCCTGGGCC	120
GTGCGGACCC	TGAGGAAGAG	CTGAGTCTCA	CCTTTGCCCT	GAGACAGCAG	AATGTGGAAA	180
GACTCTGGGA	GCTGGTGCG	GCTGTGTCGG	ATCCCAGCTC	TCCTCAATAC	GGAAATATCC	240
TGACCCTAGA	GAATGTGGCT	GATCTGGTGA	GGCCATCCCC	ACTGACCCTC	CACCTCGAGG	300
TTCTCCCTAT	AGTGAGTCGT	ATTAATTTTC	AGAGGAGTAT	TTAGAAGAGA	AGCTGAAGCT	360
GTCGAG						366

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GGGGGGTGGG	GGTTAATTAT	CTGAAACCTA	CTAAAACGGA	CTACAGTTAT	CTCTAGGCAA	60
TGCTGTGGGA	GTGTTTCCTG	CAAAATGCATT	TCACCTATTT	TTTTGTGATT	ATTTTATAAG	120
TATACTGGGG	CAAAAATTTT	ACATTCTAAA	TTGTTCTTAT	TTATTATTTT	TATTATAGAT	180
ATATGAGGAT	ATTACTTACT	CTATTACACA	TATAATTTAT	CTTTTAAATT	TTCAAGTGAG	240
TTCTACAATT	AACCTTATCA	TCTAAATTCT	CATTACAGAT	AGCATTTTAA	TGTCCAGAAA	300
GAAAAAAAGG	TTTTTTATTG	TTATATGTGA	AACCATAAAA	ATATTACCAG	CTTGTGGCCG	360
GGCGTGGTGG	CTCAGGCCTA	TAATCCCAGC	ACTTTGGGAG	GCCGAATCAC	CTGAGGTCAG	420
GAGTTCAAGA	CCAGCCTGGC	CAACATGCGG	AAACCCCGTC	TCTACAAAAA	TGGAAAAATT	480
AGCCCGGCAT	GATGGCAGGT	GCCTGTAATC	CCAGCTACTC	GAG		523

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GAATTCGGCC	TTCATGGCCT	ACCCAGATGA	AACTTTTGGG	GGGAGAGTGC	CCAGACCAGC	60
CTTTGTCCAC	TATGACAAGG	AGGAGGCATC	TGATGTGGAG	ATCTCCTTGG	AAAGTGACTC	120
TGATGACAGC	GTGGTGATCG	TGCCCCGAGG	GCTTCCCCCC	CTGCCACCCC	CACCACCCTC	180
AGGTGCCACA	CCACCCCTTA	TAGCCCCCAC	TGGGCCACCA	ACAGCCTCCC	CTCCTGTGCC	240
AGCGAAGGAG	GAGCCTGAAG	AACTTCTGTC	AGCCCCAGGG	CCTCTCCCGC	CACCCCACC	300
TCCGCCGCCG	CCTGTTCTCTG	GTCCTGTGAC	GCTCCCTCCA	CCCCAGTTGG	TCCCTGAAGG	360
GACTCCTGGT	GGGGGAGGAC	CCCCAGCCCT	GGAAGAGGAT	TTGACAGTTA	TTAATATCAA	420
CAGCAGTGAT	GAAGAGGAGG	AGGAAGAGGA	AGAAGAGGAA	GAAGAAGAAG	AGGAAGAAGA	480
GGAAGAGGAG	GAAGACTTTG	AGGAAGAGGA	AGAGGATGAA	GAGGAATATT	TTGAAGGGGT	540
TACTCGAG						548

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 577 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GAATTCGGCC	TTCATGGCCT	ACTTACTAGG	AATTAAAAGA	CGGATTTCGA	AGGAGATTCA	60
GAGGCAGCAA	GCACTACAGA	AGTCAGAACT	CCAGCACCAT	CTGCTCCGTT	TCTTGAAGTT	120
TGCTGAACGA	GGACTCACAG	CTGCAACGTG	GGGTGATTGT	ATTGATCAAA	ACCCACTGGG	180
AAGGACAAAG	AGTTTGCCGC	CTTTCGGGGA	TCCAAGGGAC	TGTGGCGACC	GTGCCTCTGT	240
GCCAGCGTCC	CAGGAAGGAA	GCCAACCCTG	AGCGAGCCTG	TCCTCTGTGG	CAGGTCCACA	300
CGGTGTGGGT	GGGCAGGGCT	TGGACCCCG	TCTCCATGGC	AGGTCCATAC	AGCATGGGTG	360
GCAGGGTTTG	GACCCGCCCA	GCAGCACCAC	GGACCCAGC	CACCTCTCGG	GGCAGACGTC	420
AGAATCCGTT	CCTGAGCAGC	TCCCGTGCCC	TGGGGGCAGT	CACAGAGCCC	CCCAACACCC	480
CCGTGCTCTG	CACCAGCCTC	TCCCTCCACA	CCCGAAGCAG	GCGTCCATCT	GTGTCCTCCT	540
GCGAGCCCTT	CAAACACACA	CCACCCCAT	TCTCGAG			577

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 415 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GAATTCGGCC	TTCATGGCCT	ACATCTTCAT	TGCTGAGGTT	GCAGCTGCTG	TGGTCGCCTT	60
GGTGTAACCC	ACAATGGCTG	AGCACTTCCT	GACGTTGCTG	GTAAGTGCTG	CCATCAAGAA	120
AGATTATGGT	TCCCAGGAAG	ACTTCACTCA	AGTGTGGAAC	ACCACCATGA	AAGGGCTCAA	180
GTGCTGTGGC	TTCACCAACT	ATACGGATTT	TGAGGACTCA	CCCTACTTCA	AAGAGAACAG	240
TGCCTTTCCC	CCATTCTGTT	GCAATGACAA	CGTCACCAAC	ACAGCCAATG	AAACCTGCAC	300

CAAGCAAAAG GCTCACGACC AAAAAGTAGA GGGTTGCTTC AATCAGCTTT TGTATGACAT 360
CCGAACATAAT GCAGTCACCG TGGGTGGTGT GGCAGCTGGA ATTGGGGGCC TCGAG 415

(2) INFORMATION FOR SEQ ID NO:396:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GAATTCGGCC TTCATGGCCT ACTAAAAGAT ACTTCAAAGT GACAAAAACG TGTTCCCTTC 60
CCACTTAGAG ACAATGATTA ACAGGGCCCT ATATGTTCTT ACCACATACA GAGGATGCAT 120
TTATTTTTC TCTATGACAC TTGCAAAAT CTCTACTGTA ATTAATTTGG GTCTATTATT 180
AACTCTCTGT TCCATCATAG AATGTGGCCA GGCCTTACAA TGGAGAGCCA GAGTTAAAC 240
TTCAAGTTGC ATCTGTTTTT GGGCTGAGTC ACCACCGGAC CTCGAG 286

(2) INFORMATION FOR SEQ ID NO:397:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GAATTCGGCC AAAGAGGCCT AAAAATGAAA ACCTCTGCAC TTTAATTTTT TTCAGTAATT 60
TCCAGCTATT TCTAGGTATA AAGAGCAGCT CGTTTCTCTT ATTTATTTTA GTCTCATGTG 120
TCAATACTTT CCGATGCTTT GCTTAATTCA TGTATGTGTG CAGTGCTGCA ATGCCCAGAC 180
AAACGTGAGC ACACCCACCA ATCTCGAG 208

(2) INFORMATION FOR SEQ ID NO:398:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 452 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GAATTCGGCC AAAGAGGCCT ATGATGAAGC TGGGCATTTA TAACTAGATT CATTAAAGGAA 60
TACAAAGAAA ATACTTAAAG GGATCAATAA TGGTGTCTTC TGGTTGCAGA ATGCGAAGTC 120
TGTGGTTTAT CATTGTAATC AGCTTCTTAC CAAATACAGA AGGTTTCAGC AGAGCAGCTT 180
TACCATTTGG GCTGGTGAGG CGAGAATTAT CCTGTGAAGG TTATTCTATA GATCTGCGAT 240
GCCCGGGCAG TGATGTCATC ATGATTGAGA GCGCTAACTA TGGTCGGACG GATGACAAGA 300
TTTGTGATGC TGACCCATT T CAGATGGAGA ATACAGACTG CTACCTCCCC GATGCCTTCA 360
AAATTATGAC TCAAAGGTGC AACAATCGAA CACAGTGTAT AGTAGTTACT GGGTCAGATG 420
TGTTTCCTGA TCCATGTCCT GGAACGCTCG AG 452

(2) INFORMATION FOR SEQ ID NO:399:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```

GAATTCGGCC AAAGAGGCCT ATCTTCCTGA AGAGCAATGG AGCCGCTTTT ACTTGGAAGA      60
GGACTAATCG TATATCTAAT GTTCCTCCTG TTAATAATTCT CAAAAGCAAT TGAAATACCA      120
TCTTCAGTTC AACAGGTTCC AACAATCATA AAACAGTCAA AAGTCCAAGT TGCCTTTCCC      180
TTCGATGAGT ATTTTCAAAT TGAATGTGAA GCTAAAGGAA ATCCAGAACC AACATTTCG      240
TGGACTAAGG ATGGCAACCC TTTTATTTC ACTGACCATC GGATAATTCC ATCGAACAAT      300
TCAGGAACAT TCAGGATTCA CAAACTCGAG      330

```

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

```

GAATTCGGCC TTCATGGCCT AAGCAAACCC AGAGGTGGAT GTTATGAACA GCTGTGTCTG      60
CCAAACACAT TTACCTTTTG GCCCACTTT GAAGGGCAAG AAATGGCGTC TGCTCTGGTG      120
GCTTAAGTGA GCAGAACAGG TAGTATTACA CCACCGGCC CCTCCCCCA GACTCTTTT      180
TTGAGTGACA GCTTTCTGGG ATGTCACAGT CCAACCAGAA ACACCCCTCT GTCTAGGACT      240
GCAGTGTGGA GTTCACCTTG GAAGGGCGTT CTAGGTAGGA AGAGCCCGCA GGGCCATGCA      300
GACCTCATGC CCAGCTCTCT GACGCTTGTG ACAGTGCCTC TTCCAGTGAA CATTCCCAGC      360
CCAGCCCCAT CCTCGAG      377

```

(2) INFORMATION FOR SEQ ID NO:401:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 311 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

```

GAATTCGGCC TTCATGGCCT AGGCAAGGTC TTCGGCTCGT GCGTTCTAA GCCGGAGAAT      60
TCTCGCGGGA GCAGGGTTAC GTCTCTGTGG GATTCGTTGG CCGTGGCTGA GGTCTCCAG      120
CAGCCTGACC TGAGTGGGTT AGTGATCCAG AGAAACCAGC AGGCCAACTT GGTGAGGAAG      180
GTTCCGGAAG CTGTTGGAGC AGTGTGGGGA ATTTCCACC AGGATGAGTA TGATTGGCTG      240
TGATTTTAGA TGTAAAGCT GAAAATTGAA ATCATGAAAG TAGACAGGAC TAAACTGAAG      300
AAGAACTCGA G      311

```

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

```
GCATTGATGG AAAAGCATAA TGTCTTAGAA AAAGGCTTTC TAAAAGAAAA AGAGCAAGAG      60
GCCATTTCTT TTCAAGATAG ATACAAAGAA CTTCAGGAAA AACATAAACA AGAATTGGAA      120
GACATGAGGA AAGCTGGTCA CGAAGCCCTC AGCATTATTG TGGATGAATA TAAGGCACTA      180
CTGCAGTCTT CAGTTAAGCA ACAAGTAGAA GCTATTGAAA AACAGTACAT TTCTGCAATT      240
GAGAAACAGG CACACAAGTG TGAGGAGTTG CTAAATGCTC AGCATCAGAG GCTCCTTGAA      300
GTGCTAGATA CAGAGAAGGA ACTGTTAAAA GAAAAAATAA AGGAAGCCCA TCTCGAG--      357
```

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

```
GTTCTAGACC TGCCTCGAGC GTTAATGGTA TAAATCACTT GTTTGTAAAG TATTGTTTTT      60
AAATATTGCC AGATTTGATA TCTTAGTATT GTATTTTAT ATTTGTCTTC ATGTGTTTTT      120
GTTTTCTCAT AAGTGTCTGT ACCCCCCTTT TTTTCTTT AAAGAGAAAT AATGAGAGAG      180
ATTGTCTGTC TTGAAGTTCT CAGTGCCTGT GCATTGCTGC CACTACACAG CTAGTATCAT      240
GACAGCAGCT TCAGAACCAG AGCTGGCTTC CAGGCAAGGC TGGGTGGGGA AGAAAGAGAA      300
AAACAAAGA ATTATTCTC TATGCCGAGA CCAGCTCGGT CAGGGAGACC CTAACCTAGC      360
GGTGTAGAG GAATTAAAGA CATAGACACA GAAATATAGA GGTGTGAAGT GGGAAATCAG      420
GGGTCTCACA GCCTTCAGAG CTCAGCCACG AACAGAGATT TACCCACGTA TTTATTAACA      480
GCAAGACTCG AG                                         492
```

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

```
GAATTCGGCC TTCATGGCCT ACTTCCTCT AAGGTCCCA AATGCCTCTC ACGTGCCTAG      60
CATTTAGCTG CTGCACCGAG CATGCTCACT GACAACTTT TGGCCAAGAA GAGCCTTTTG      120
GTCTCTCTTG GTCAGATCTA GGAGGGCTTC AGGACTCTCC AAAACTCACC CACTCAGAGA      180
GCCTGCCAGG AACACTCAGC TGAGCGATGG CATTGTGGAG CCTGGGTTTT CAGAAGGGAG      240
CCCATAGTGA GTGGTAGCAT AACCTTGTTA AGGTTGTATT TTCCTTAGAT ATAGAAACAA      300
ATCAAAATGCT GCTAAATTGG TAAGGGATGG AGTTTTCATA TCACGTCACA TTTTGCTGAG      360
CGTAACCGAG ACAGGGAAAA AGCAGAGACC TCGAG                                         395
```

(2) INFORMATION FOR SEQ ID NO:405:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

```
GAATTCGGCC TTCATGGCCT ACCAAGTTCT AACTGTAAAA TGGGGACATT TTACCTTTCT    60
TTCTTTGGAT AGGATCAGTT CTTAAGAGCA GCCCCGGTAA CTGGAGGAAT GGGAGCCGTT    120
TTGATGAGAA AAATGGGCTG GAGAGAAGGA GAAGGATTAG GAAAAACAA AGAAGGCAAT    180
AAGGAACCCA TCCTAGTTGA TTTTAAGACA GACCGAAAAG GTCTTGTTGC AGTAGGRGAA    240
AGAGCACAAA AGAGGCCTCG AG                                     262
```

(2) INFORMATION FOR SEQ ID NO:406:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

```
GAATTCGGCC TTCATGGCCT ACCCATTTGT CAATTTTTC TTTGTTGCAA TTGCTTTTGG    60
TGCCTTTGTC ATGAAACCTT TGCCTACAGG TGCTGTTTAT TTACACCCCT GTCCCAACCT    120
CACCCCCTC CCTTCTTTT GCTGGTGGGA AGTCAGTAAG AACTGTGGGT GGGGTTCTGA    180
GGTAATCAAT ACAAAGAAGA AGGTAAGAAA TTGGAGGGGA CTCAGGGGAG ATGGCAATGC    240
TGACAAGGGG TTGGATGGAA TTTGTTCTGT AAAGTGAAG CAGCTCGAG                                     289
```

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

```
GCTCCTTCTG TATCCTTCCT TTCCCATCTG TCTGCTTCTA ACAAATAAGA CAAGCTAAGA    60
AGCAGCTTGT TTCATGATTC TATACTCACT TCCAAGCTTT CTCTGCATAG ACTTTCCTAG    120
TTTGCCACTT TATCTTTTCT CCATCCCTCC AGCCAGTCAT GAGATTCTAC TCCCCATTCA    180
TACATGCATT TATTTATCCA GACTTTACTG AAGGCTTACT CTTTGAAGTT TGCAAAATGC    240
CAGTGAGGCA AAGCATGCAT CCTGTACAGG AAAAAGTCTAG TCTAGAGGGG AGAGATAAGC    300
AAACAAGTGA TTACCACACC AGGCTCGAG                                     329
```

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

ATTGAATTCT AGACCTGCCT CGAGAGCTTT TGAGATTGTC TATTTGTCT GAGTGAGTTT	60
TGGTACTTTA TTGTTTTCGA TTGGTCCATT TCTTCTACGT TGTCAGATCT CTGAGTGTCA	120
AGTTGTTTCA AGTACTCCGT TATTATCTTT TTCATGACTG TAGGATCTGT GGTGATATTG	180
ATGATTGTG TCTTCACTCC TTTTGTGTTGG CCTACACTCG AG	222

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GAATTGGGCC TTCATGGCCT AAACCTGCAG AAATGAAGAC TAGAGTACAC AGCACACTCA	60
GAGCCACAGC AGACTTCGTC CCAGGACATC ATCTGTTCTT GATGCCCATT CTTCTCTCCT	120
AAACATCATT TACTTTTTCC TCTAAAAGTG CCTGCAGACC CCCACTACTC TCTCCCATGG	180
AGAAGGGCAT ATAAGCTTCG AATCTCACGG GGTATTGGG CACTCTGTCT CTGTGTATGC	240
TCCTATGCAT GTAATAAATT TATGTGTCCT TTCTCCTATT AATTGGTCTA ATGTCCATTT	300
ATTCCATAGA TTCAATTATC AAACCTCTCAG AGGGCAGAGG GAAAATTTTC ACTCCCTTAT	360
ATCATCAGAA ATATAAATAA AAATAGCACA ACACTCAGTA AATGATTATG TTATTATTGT	420
TATGTTTGTA ATATCTTGGT GTCGTGTTAT TTAAATCAT ATCACTTAAA GAAACAGTGT	480
TCCTTAGGCC ATGAAGGCCG AATTG	505

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 650 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

GTATGAACAT TGAGGGCCCA GATCTCAATG TGGAAGGTCC GGAGGGAGGC TTGAAAGGTC	60
CCAAATTCAA GATGCCTGAC ATGAATATCA AAGCTCCCAA GATCTCCATG CCTGACATTG	120
ACTTAAACTT GAAAGGCCCC AAGGTGAAAG GTGATGTGGA TATTTCTCTT CCCAAACTTG	180
AAGGGGATCT GAAAGGGCCA GAGGTTGATA TCAAAGGCC TAAAGTGGAC ATCAATGCCC	240
CAGATGTGGA TGTTCATGGT CCAGACTGGC ATCTGAAGAT GCCCAAAGTG AAAATGCCCA	300
AGTTCAGCAT GCCTGGCTTC AAAGGAGAAG GCCCTGAAGT CGATGTTACC CTCCTAAAG	360
CTGACATTGA CATTTCTGGT CCAATGTAG ACGTTGATGT TCCAGACGTG AATATTGAAG	420
GTCCAGATGC AAAGCTGAAG GGCCCCAAGT TCAAGATGCC TGAGATGAAC ATCAAAGCCC	480
CCAAGATCTC CATGCCTGAC TTTGACCTGA ACTTGAAGGG ACCCAAATG AAGGGTGATG	540
TGTTTGTGTC TTTGCCCAA GTGGAAGGTG ATCTAAAAGG CCCTGAGGTG GACATCAAGG	600
GCCCCAAGT GGACATTGAC ACTCCTGACA TTAACATCAA GAGGCTCGAG	650

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

```

GAATTCGGCC TTCATGGCCT AGGGGCTGGA GGGTGGCCCG AAGCAGATGG GGCCGGCCTT      60
GCAGGCACTT CTAAGGCCTT GGGGTTTGCT TCCGAGGGAG TAGGGAAGGA GAGCGATGTC      120
ACCCTGTGAG GCTTGGTCAC ATACCCAAT GGATTGGTA GCACAGCCA CAGTGAAGGT      180
ATAAGCTACT GTCATCACAC GTAATTATT CATGAAACAG AAAATTTTAA AATPAAAGAA      240
AATAGAAGTT TCCCTATTTT CTTCTCCTGC ACTATTGGAT CATCCTGTTT AGCCCTCTTT      300
TAAGACAAAT GGACTTAGCA AACGAGTGTA AATAGGAATG AATGGTTTGT TGGGGTTTAT      360
TTTATTTTAT TTTATTTTAT TTTATTTTAT TTTATTTTAT TTATTGAGAC AGAGTTTCAC      420
TCTTGTGGCC CAGGCTGGGC TCGAG                                     445

```

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```

GCCTGCCTCC AGGCCTTTGC TCCCACTGTT GNCTCCACTT AGAATAACAT TCCACCCCAT      60
CTCTATAAAT ATCCTACAGA CAAATACTAC CTTCCCCTTA AGGCCAGTTC TAACCCTAAC      120
TGACAACAAA TCATCTCTAC ATGATCTTTT CCTTCTGGGA ATGCCTGCAG CACTGTTTAA      180
TCCTGCCCCA CCACCATCCC CTCACCCAGC ACCCTCTCCC AGACCAGACA GGGTGGCTCA      240
TGCTGCAAT CCCAGCACCT TGGGAGGCTG AGGCAGGAGG ATTGCTCGAG      290

```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```

GAATTTGACA TCTTAGAACA TTCTGCAACC TTTTGCCTGG GAAATGGAAA CAGATCTAAT      60
CTTTACCACC CTCATGGCTC AAGGACCTCA TCTGGCAGCC TGGCTCATGT TTTTCAGCCA      120
AGTAGCTTCC AGCTTACAGC AGCCCTCAA TTTGGACCTG CCACCAGCTC CAGAGCTTGA      180
CTGGATGGAG ACAGGACCAT CTCGTGACATT CATTGGCCAT CAGGATATAC CAGGAGTTGG      240
TAACATCCAC TCAGGTGCCA CACCTCCCTG GATGATCCAA GATGAAGAAT ACATTGCTGG      300
GAACCAAGAA ATAGGACCAT CCTATGAAGA ATTTCTTAAA GAAAAGGAAA AACAGAAGTT      360
GAAAAAATC CCCCAGACC GAGTTGGGGC CAACTTTGAT CACAGCTCCA AGGACCTCGA      420
G                                     421

```

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GAATTCGGCC	TTCATGGCCT	AAGCCAGTCA	ACCAGCAGTA	TTAGTGCTGT	TTTCAAAGAT	60
TTAAGCTCTA	TAAAATTGGG	AAATTATCTA	AGATCATTTT	CCCTAAGCAT	TGACACATAG	120
CTTCATCTGA	GGTGAGATAT	GGCAGCTGTT	TGTATCTGCA	CTGTGTCTGT	CTACAAAAAG	180
TGAAAAATAC	AGTGTTTACT	TGAAATTTTA	ACTTTGTAAC	TGCAAGAATT	CCAGTTEAGC	240
CGAGCCACTT	CGAG					254

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GCAAACAGAC	AAGGCTTACA	GGTTAGTTCA	GGATCTGGGC	CTTATCAAGC	AAATTGTTTT	60
GCCTATCCAA	CCTGCGGTGC	CAAACCCATA	TACTCTCCTA	TCCTCAATAC	CTCCCTCCAC	120
AACCCCTCCA	TAACCCATTA	TTOGGTTCTG	GATCTCAAAC	ATGCTTTCTT	TGCTATTCCT	180
TTGCATCCTT	CATCCAGCC	TCTCTTGCT	TTCAGTTGGG	CTGGCCCTGA	CACCCATCAG	240
CCTCAGCAAC	TTACCTGGGC	TGTACTGCCA	CAAGCCTTCA	CGGACAGCCC	CCATTACTTC	300
AGTAGCCCTC	GAG					313

(2) INFORMATION FOR SEQ ID NO:416:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GCCTGCCCCC	ACCTTACAGG	TCTGGGATGT	ACCTTTCCAT	CTGTTGCTGC	TTTCTTCTAT	60
GGGCCCTGTC	CCTCACTCTC	AAGAACCCTCA	ACTACTCCGT	GCCGGAGGAG	CAAGGGGCCG	120
GCACGGTGAT	CGGGAACATC	GGCAGGGATG	CTCGACTGCA	GCCTGGGCTT	CCGCCTGCAG	180
AGCGCGGCGG	CGGAGGGCGC	AGCAAGTCGG	GTAGCTACCG	GGTGCTGGAG	AACTCCGCAC	240
CGCACCTGCT	GGACGTGGAC	GCAGACAGCG	GGCTCCTCTA	CACCAAGCAG	CGCATOGACC	300
GCGAGTCCCT	GTGCCGCCAC	AATGCCAAGT	GCCAGCTGTC	CCTCGAG		347

(2) INFORMATION FOR SEQ ID NO:417:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

```

GAATTCGGCC TTCATGGCCT AGCAGATGAT TGACATTGCT ATCGATGGTT TCCTTTTGAC      60
TCCAGTGCAG AAGATCTGCA AGTATCCCTT ACAGTTGGCT GAGCTCCTAA AGTATACTGC      120
CCAAGACCAC AGTGA CTACA GGTATGTGGC AGCTGCTTTG GCTGT CATGA GAAATGTGAC      180
TCAGCAGATC AACGAACGCA AGCGACGTTT AGAGAATATT GACAAGATTG CTCAGTGGCA      240
GGCTTCTGTC CTAGACTGGG AGGGCGAGGA CATCCTAGAC AGGAGCTCGG AGCTGATCTA      300
CACTGGGGAG ATGGCCTGGA TCTACCAGCC CTACGGCCGC AACCAGCAGC GGGTCTTCTT      360
CCTGTTTGAC CACCAGATGG TCCTCTGCAA GAAGGACCTA ATCCGGAGAG ACATCCGTA      420
CTACAAAGGC CGCATTGACA TGGATGCTCG AG                                     452

```

(2) INFORMATION FOR SEQ ID NO:418:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

```

GATAACTTGA GATCAAATCA GTCATATTG ACTCTTCTCT TTTTCACTCC TTTTATATCT      60
GATCAGTCAG CAGTTTTTTG AAACCCCTGT CGAAGCAGTT CTCAACACTT GTGCACCCAT      120
TCTTTCTCCT ACACCACTCA ATCTAGACCC TCACATGTGG CTGTCCTGCT TTCCTTCTCT      180
CCTACTTCTA AGCTATTCTG TGGAGAGATG TCAAAGTAAT CTTCACAAAA AATCTGATTG      240
CATCACTTCA CATCTCGAG                                     259

```

(2) INFORMATION FOR SEQ ID NO:419:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

```

GAATTCGGCC AAAGAGGCCT AATTAGAAAT GGCTACTCCC CAGTCAATT TCATCTTTGC      60
AATCTGCATT TTAATGATAA CAGAATTAAT TCTGGCCTCA AAAAGCTACT ATGATATCTT      120
AGGTGTGCCA AAATCGGCAT CAGAGCGCCA AATCAAGAAG GCCTTTCACA AGTTGGCCAT      180
GAAGTACCAC CCTGACAAAA ATAAGAGCCC AGATGCTGAA GCAAAATTCA GAGAGATTGC      240
AGAAGCATAT GAAACACTCT CAGATGCTAA TAGACGAAAA GAGTATGATA CACTTGGACA      300
CAGTGCTTTT ACTAGTGGTA ACGGGCTCGA G                                     331

```

(2) INFORMATION FOR SEQ ID NO:420:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GAATTCGGCC AAAGAGGCCT AAGAGCATTT ACCTGTCTGA CAATTGTATT TTTAATGATA	60
GTTTGCTTTT ACTTGGTCTT TATATATTCA ATTACAAATT ACTGATATTT TGTTTAAATC	120
TACCACATTT TTCCATTGA CTGTTTATTT TTATGTCCTT TCTTTCCTTT AGATTAAGTC	180
TTTTTTCTTC TCACCCCTC ACCCTCCCC CCTGGTTATA CATTCTTTTA CTATTCTTTT	240
TGTTATTCCA TAGTTGCAGC ACACTCGAG	269

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GAATTCGGCC AAAGAGGCCT ACATTGAGGT AAGAGATATT TAAAAGGTTT TTAGGTGAAA	60
TTTGAAGCAG GGATGAGATT GGGATTCCAC CTTTGTGTTCC ATGCATACCT GTTGATAATC	120
AGCTGTTCTT GTATCGACTC CGTGTCAACT CCAGAGCAGG GGGTATCCTC CTGTAGTGCA	180
CCTTCTCTCT TGGCCTGGAG GCAGCACTTT CTGTGCCTGG GCAGCAGAAA TGGGGAATGT	240
TCTTTGGTCC GTTGGAAAAA CGGGCCCCAA CATCTAGCCC TGTTGCATAA GGCATGGAAT	300
TGCCCCAGTTG GGGAGGACCT GTGCTGAAA GGGATCATCA AACTCCATCT GCCCCATCAG	360
ATGCCTGAAC TCTTGATACA ACTCCTGCCA TCCAAGCTAC TCGAG	405

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GAATTCGGCC AAAGAGGCCT ACTCGTACTT ATTTATAAAA AAAGTTAACT GTAAAACAGC	60
CTCAGGCAGG TCCTTCAGGA GGTACTCCAG AAGAAAGTAC TGTTATCATA GATGACAAC	120
CCATATGTGT TATTGCACCT GAAGACCTTT CACCTGGACA AGATGCCGAG GTGGAAGACA	180
GTGATACAGA TGATCCTGAG TATCTTAGTT TTTTGTGTTT TGTTGAGACG AAATCTCACT	240
CTTGCCCCCA GGCTGGAGTG CAATGGCAOG ACCTGGGCTC ACTGCAACCT CTGCCTCCCG	300
GGTTCAAGCG ACTCTCCAAG CCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```
GAATTCGGCC AAAGAGGCCT AGAATAATAC ACTAGTAAAA AAAAATGTAT GTCAGGCACT    60
GGGAAGGGCA GTAGGAATAT AGAAATGAGA AGCCGTGGAT TAGAGACTCA CAGTCTACTG    120
GGTAAAAGAA TACGAAAGCC AATGTATTAT ACTGTGGTAG CTGCTTTAGT AGATGTATGG    180
ATAGAAAAGT AACAAAGAGAA GAGAATGACT ATCTCTGCCT AACAGAAAGA TATTTTAAAA    240
GAAGGGTTTT GGGGCTGGAT TTTGAAGGCT CAATAGGCTC CTACCATATA GAGAACTAGG    300
AAGCGAGTCC TCGAG                                     315
```

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

```
GAATTCGGCC AAAGAGGCCT ACTATCCAGG TTTACATTTT AAGGCAGTCG AGACCTTATT    60
CAGGTGGTAT ATAAACAACC ACATTTCTCT TTTATATGGA ACAACACTTT TCATTGCGG    120
CTGGCCTTCT CACTAGCTTA TGCTTTTTTT TTTTAAGACC TTTCTTAGCA CTCGTGAAC    180
TCCTCCCCTT CACAATCAAT CTCAGCAACT CAGCAGAGTC GCTTCAGTTC ACAGCTCTTA    240
ATCCTTCACT CCAGACTAAA GCTAATCTTA TGTCCTCAAA CAGCTACAAC TCAGTGTAT    300
CACAGTCCG ACAGCAGAGA CTCGAG                                     326
```

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

```
GAATTCGCCA AAGAGCCTAT AGAAATAATA CCACGACCTG CGCATTCAAA GCTGTTGTAT    60
CTGGATTGTG ACTGCGTGGA AGGTCGAGGC GGAAGACAG GGGCTGTTGC TTTTCGTTAT    120
AAACTCTGCA TTAATTGATT TTTGCACTAC GTACATTTAC TTTGATAACA CTGGAAAGAA    180
TAAATTGGCC ATGTAGTGTA GCTTCCAAAA AAACTATTG CTTGGGTTTC AAGGTCAAGG    240
AAATTTTATT CTCATCAGTT TCTTGGGAAA GAGGAAGTGG AATGATGTTG TCAGAAAGTG    300
AAACCATGGG TCATTTTCAG AACTACTCAG AGTAATAAAT ATTTTGTGTC AGTTTGTTC    360
TTACAAGTGA AATGGTCCCC TCGAG                                     385
```

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GAATTCGGCC	AAAGAGGCCT	AAGAGATTTT	TATTATGATT	TTGATTTCTT	TACTACAACA	60
TTGCATGTGT	CTGGAGTATA	GCCATTACAC	TTTATGAAAA	AGGCAAAATG	GTCATTTGGG	120
GTGTTTTAGG	AAGTTTGCCA	AAAGGCTCCT	TTGTCAATTAT	AATCCTTCCT	AAGCTGCCAT	180
CCACGGGTTT	AGGTCATGGA	TATGAAAAGT	GAAAGGGTTT	AGAGATGAAG	TAGTGTCCCC	240
TGAGTGCTTA	CCAACCTGTT	AATCTTTTTG	AGATGTTAAT	TTTTTCATAT	AGAGCCCCCT	300
AAAACTTTGA	TGGCTCTAGA	TCAGTCAAGC	CTAAGAGAAG	ACGTATTAT	GGAAAAAAC	360
AAAAAACAAA	AAACCTTGCT	TGGATTGCTA	GTAATATCTA	CTTCTTGGA	ATTAATACTT	420
CATATTTTTT	AAAAAAATTA	TTGATGCATT	AGGACTCGAG			460

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GAATTCGGCC	AAAGNGGCCT	AGGAAAAACA	TGAAATACAT	AAATGGATTA	ATTTTGCAAA	60
TTAATCTNGC	AAATTAATCT	ATAGCTCTTA	ATGTTTCTTC	CAAATTAAAG	GAAAAATGGA	120
TAAGGAAGTA	CTTTCTTGCC	AAACTGTAGA	TGAATACTGA	ATAAAAGTCA	TTCTTTCCTA	180
AAGAAGAAAA	GTGCATTTTA	GTTTTTTAGA	AAAAATGTAA	TTTAGAAAG	TCTCTTCTAT	240
GCAGATTTTA	GAAAGTCTTT	TCTATTTTAA	GAAAGTCTTC	TTGTATGCAG	ATTTTGTTCA	300
ACTTCCCAT	CTGTACTTAC	CAAAGGAAAA	ATAAACAGTT	TATAGAATAT	TAATAGAATA	360
ATTATGTGCN	ATGTAAATA	TGTTGAATCT	CCCTAATTTA	TATTTACTAT	GTGAATATAA	420
ACTACAGAAT	AAAGAACTG	TTCTCCTTT	TATCCATTAT	TTTGTGAAA	ACAACTAAAG	480
AAATCTTACA	GATTAAATGT	CATATTAAAA	GGACTCCTCG	AG		522

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

GAATTCGGCC	AAAGAGGCCT	AGGTAGTTAT	CAAGAGATTT	TAAAACTTCA	ACCCTTTTTC	60
TCTTATAGTT	AGTGAAGAGA	GTAGAATATC	TCCAGTTTGT	GCTGACATCT	CTACAACCTG	120
AACAATTGGC	TTAAACTTCA	CTTGGGATTC	CCGGTTGCTT	GTTTTAGCAT	GGCNAATTTT	180
GGCGTTTACA	GAATCCTTCT	TCTGGCTATT	TCTCTGACAA	AGTGTCTGGA	GAGTACAAAA	240
CTGCTGGCAG	ACCTTAAAAA	ATGTGGTGAC	TTGGAATGTG	AAGCTTTAAT	AAACAGAGTC	300
TCAGCCATGA	GAGATTATAG	AGGACCTGAC	TGCCGATACC	TGAACCTCAC	TAAGGGAGAA	360
GAGATATCTG	TTTATGTTAA	ACTTGCAGGA	GAAAGGGAAG	ATTTGTGGGC	AGGAAGTAAA	420
GGAAAGGAGT	TTGATATTTT	TCCCAGAGAT	GCAGTCCAGA	TTGAAGAGGT	GTTCATATCT	480
GAGGAAATTC	AGATGTCAAC	GAAAGAATCT	GACTTTCTTT	GTCTTCTTGG	AGTAAGTTAC	540
ACATTTGACA	ATGAAGATAG	TGAATTAAAC	GGTGAACCTG	AG		582

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

GAATTCGGCC	AAAGAGGCCT	ACTGATCAAG	TGACCCATTA	CTGCGGGAAA	AAACCACACA	60
TACAAAAGCC	TTTGACCCCA	GTAATTTGT	ATTGGTATAT	TTACCCTGAT	CTTAAACTGC	120
AAGGAATGTC	CGCAATTAGA	GTTTTTCTTT	GTTTTCTAAG	TCTGAAACTT	GATAATCCAT	180
TTCTGCCTTC	CCATGACGAG	TGGACATTCC	TCCAGCCAGT	GGTGAGTTCC	TCTTTCCTTC	240
GCTCTCAGCA	AGAGCATGGG	TTGCCCTCCC	ATCTCGTAAG	CAGAGCCTAC	CACAAACGCA	300
GCTCAAATCT	CGAG					314

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GAATTCGGCC	AAAGAGGCCT	ATTGGGTCCT	ATTTACAAC	TTAAGAATGG	AGGCATACTT	60
CAGGAAAGAA	AGCACCAGTG	CAGTTCCAAT	TTATTATTGT	ATCTGCTGTC	TTGAGAGTAC	120
AGGGTGTATG	AGAGTGCACA	GTGGTTTAGA	ATCACTATGG	AATTTAAAAA	GACCCAGAGA	180
CATTAAACAAG	AATCCACATT	CTAAGTCGTC	AGAATCCACA	TTTCTGACCT	TGTCGTCTGG	240
GGCCTGCTCT	GTTTTTGATG	GCTCAAAATA	TAATCTTTTT	ATTGAAATAC	ATGTTCTCTCA	300
TCCTGTTTCA	GGGCTTCTGC	CTGGAATGTT	CCTCCCCCTA	GCATTGTAG	GGCTGGCTCC	360
TTCTGTTCAT	GCAGGTCTCA	GCTCAGATGA	CCCCATCTCA	GAGAGGGCTT	CCCTGACCAA	420
CCAATCTACA	GCCCTTCCTA	GTCACTTTTT	TCCACATCAC	CCTCTTTATG	CATGGAGGCA	480
GATAGGTGTT	TTACCCTGTT	TATTTATTAT	TATTATTTTT	TTGAGACAAA	GTCTTGCTCT	540
GGCACCCAGG	CTCGAG					556

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

GAATTCGGCC	AAAGAGGCCT	AGAAGTAACG	GAAGCTACCT	TGTATAAAGA	CCTCAACACT	60
GCTGACCATG	ATCAGCGCAG	CCTGGAGCAT	CTTCCTCATC	GGGACTAAAA	TTGGGCTGTT	120
CCTTCAAGTA	GCACCTCTAT	CAGTTATGGC	TAAATCCTGT	CCATCTGTGT	GTCGCTGCGA	180
TGCGGGTTTC	ATTTACTGTA	ATGATCGCTT	TCTGACATCC	ATTCCAACAG	GAATACCAGA	240
GGATGCTACA	ACTCTCTACC	TTCAGAAACA	CCAAATAAAT	AATGCTGGGA	TTCTTCAGA	300
TTTGA AAAAC	TTGCTGAAAG	TAGAAAGAAT	ATACCTATAC	CACAACAGTT	TAGATGAATT	360
TCCTACCAAC	CTCCCAAAGT	ATGTAAAAGA	GTTACATTTG	CAAGAAAATA	ACATAAGGCT	420

CGAG

424

(2) INFORMATION FOR SEQ ID NO:432:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 418 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

```

GAATTCGGCC TAAGNGGCCT ACATAAAAGT AAGAAAATAT CTTACTAAAA TCTCTTTTCT    60
TATAACATTT AGNTTACGTA TATATTTTAT CTCCCTTTTT TTGNAATATA TATAAATCAA    120
ATAACAGCTG AATAAACCTT TGGTCTTTTT TTTTTTTTTT TGTCTCAGGA TTGTCTTTAT    180
CTGGGACCCG AGATTAAATG CTTCGTTTTT GCTTTGGCAA AAGATTGTTT TTACAATTTT    240
TAGTCTTTTA AAGTTGACAC AGATTGTGTC AGTCTTGCTC ATTCTAAAAG CACACAAAAG    300
TTGAGCATAA AAATAGGATT AAATTTAGCA ATAAAGAATT ATAAAGACTA AAAGATACTG    360
AGTAAGTTGT TTGACAGAAA CCTGATTATC CATGATGATT ATTTGCAGGC TTCTCGAG    418

```

(2) INFORMATION FOR SEQ ID NO:433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```

GAATTCGGCC AAAGAGGCCT AGAACTCCAG AGGCAAGTGT TATATGAATT ATGCATTGTA    60
TTCTACATGT TTATTAGACA TGTATGGCAG ATACATTTAT ATTTTACTAA TGTTATGAT    120
GACTTTAATA ACTTCAAAG GATTATGGGG ACTCGAG    157

```

(2) INFORMATION FOR SEQ ID NO:434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 440 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

```

GAATTCGGCC AAAGAGGCCT ATGTTTTTAC TACTATTATT TTTTTTTACC CAAGGGAGAA    60
AGACAAAAAA ACGTGGGGAT TTATTTAACA TGATCTTGGC AAACGTCTTC TGCCTCTTCT    120
TCTTTCTAGA CGAGACCTC CGCTCTTTGG CCAGCCCTTC CTCCTGCGAG GGCCCCGAGC    180
TCCACGGCTG GCGCCCCCA GTGGACTGTG TCGGGGCCAA TGAGCTGTGT GCCGCCGAAT    240
CCAACTGCAG CTCTCGCTAC CGCACTCTGC GGCAGTGCCT GGCAGGCCGC GACCGCAACA    300
CCATGCTGGC CAACAAGGAG TGCCAGGCGG CCTTGGAGGT CTGTCAGGAG AGCCCGCTGT    360
ACGACTGCCG CTGCAAGCGG GGCATGAAGA AGGAGCTGCA GTGTCTGCAG ATCTACTGGA    420
GCATCCACCT GGGTCTCGAG    440

```

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

```

GAATTCGGCC AAAGAGGCAT AAACATAGAG AAATTGGTGA TGTTAAACCT TCTGAATTTT    60
GTTTAAAGTG CACTGGGAAG TGATGGAAGG GTTTGTAGCA TAGCAGTAAT CTGATCTGAT    120
CTGATCCGGT GTGAATGTCT TTTTAGCAGA TGATTTCATT TTACCAGCTC TCTNGAAAGT    180
TTAATCAATG TGATAGCCAT GACAGTTTAT TAAACTACTT ATTTGAGAAA GTAAGTGCCT    240
GTGGGAATCC AGATTATTTG TTTACTTCAT TTTAGATGTT AGTGCTAGCA CCCTTGTTTA    300
ATATTTGTTT TAACACTTAT ATACTTAAAA GCAGGAAATC TCGAG                      345

```

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

```

GAATTCGGCC AAAGAGGCCT AAGAACTCAC AATAAAGTAT CATATTCCTC TCTTTTGACC    60
TAGAATTCAT AGCCCTAGTA ATCTCGTTTT GATTAGATGC TTTGATTGGC AGTTATACAT    120
CTTTGATAAC ATTTTCAATG TGAAATGAAT TATTCTTTTCG TTAAAGCCAT TTTAAGCAGA    180
ATGTCATAAA ATGAGGGCCC ACGAGAAGGA ATAACAAAGC AGGGGTGTTG GGGATGGTGG    240
CTGGGAGCTT TTGGTGTATT TATTAACTTG TGGTTGAGTT TTGCGATGTG TGCAAGTACA    300
CACAGCCCCG AACRACTCGA G                                           321

```

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

```

GAATTCGGCC AAAGAGGCCT AGTTTAAAAA CGTATTGTTT AATTTTCNAA CATTTAGGGA    60
TTTCCAGAT ATCTNGTTG TNGGTTTCTA ATTTGATTCC ATTATGGTTA GAGACCATAC    120
TTGGTATGAT GAATTAAAAA AAAAAATNTA GAGGTTTGTA TATGGCCTGA AACATTTTTT    180
AGGTGAGTGT TCAGTTTGTA ATAGGAAAGA TGTGTCCTGC TGCCGTTAGG TAAAGTGTTT    240
CATAAGTAAT AATTAGGTCA AGTTGGTTGA TCGTGNTAAG GTCTGCTCTA TCCTTGCTGA    300
TTTCTGTCT GCTTGTCTA GTGATTACTG AGAAAGGAGT GTTGAAGTCN ACAACGATTG    360
TTATGGGTTT GTTCTCTTTC TCCNTGAAAT TCTGTCTGNN TATGCGTCCT GTATTTTGAG    420
GACCCCTCGA G                                           431

```

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

```

GAATTCGGGC TTCATGGCAT ANGAGAGGT TCCGGGNCCA GNNCANGCNC GGGACAAGNT      60
CAGAGATGAN GTTGCCCAANA GTNATGNGGA ACTCCAGTNC CCGNTGTCCC CGGNTTTTCT      120
CTCTTGTTGN ACATGGGGAN NTNTGGANTC CAGCTCCCAG NACTGGAGTG CTATTCAANT      180
GATCAGGAN GGAAGTGACA NAAATGTTTT TTTTTTTNTT TTTTAAAAAA GNAGNNNCNN      240
GGGGATCNGA AGNAGATGAA TGCCCTCAAA GGCCATGNAT GTACTTCAAA NGAAGTGGNT      300
NTTGAAAACA GNTNNAANAA TGTAANCGA NAGTNAAAAT NNATGTTGNG GANGAAGGAA      360
NTTGGTGGNN AGTNAAAAAA GAAGTAANCC GA                                     392

```

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

```

GAATTCGGCC TTCATGGCCT AGGTGTGCTT CCCTTTCCCC ATTTCCCATTT ATTTCCAGCT      60
GTATAGTAGT GTAGTGAAAA TCACTTGAGA TGTGGAAGAG TAGTCTGGTC TAGGAAGAGA      120
GAGGGAAAAG TAAGTTTCCC AGGATAAGAG GGGGAAAAAA GGCCCCAAAG CCTTCTCAAT      180
GAGGAATGGG GAAGGAGGTT TTGCTGCCAG GTTTTACTAA GTGCATTTGA ATGAACCTGT      240
CTATTGTAGT CCTCTTTTAT TAATGCTTTC CTGACATTTA CCCTGTTAGT TGAGGCTACT      300
CGAG                                     304

```

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

GAATTCGGCC TTCATGGCCT AATCACNGNA GTGACTGACA TTATATATTA NGGATCAAAT      60
TATGTCCACA AGCAATATTA TATAATCTAC GTAGAAGTGT AATAACAAAC AAGAGTACAC      120
TTAAAATTAC TTAAAAGAT GTCTTTAGTT CATTCCAATA TAATTCTTGA TTAAAATTAG      180
GATTATTTCT ACATTTTAGG ANNTACAAAG GATCACGGGT AACATGGATT GGGNCCANAT      240
ATTTTTTTAA AGTTTCGAAT TGGTATCTGT AGTAGTGGAA TGTATAGAT TTGAAGTAAC      300
TCTCCACGGA CAGTGCTGCT TCGTGTAGA GCAATTAAAT TGGAGAAGTG GCCATTCTTA      360
CTTCAGGGAT GCAAAGATGG TCTCATACCA TTTGGATAAA TGTCGTGGTA TCCATGCTTT      420
TTTTCAACTA ATAACATCAT CTCTTTCAT GACCAGTTAA TTGGGCTATT TGGCAGCCCA      480

```

GTGAACCTAT GTACTAATGC CAAGTTAGGG GCAAATGGAA ATGGACACAT CCGATAAAGT 540
TGAAATGTAT GTTTAATCT TTCACAGAAG TCCCTCGAG 579

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GAATTCGGCC TTTATGGCCT ACCTACGGTA CCTGAAAACA ACGATGGCAT GGAAAACACC 60
TCCCATTTAC CTGTTGTTGC TGCTGTCTGT TTTCGTGATT CACCAAGTTT CNTCTCAAGA 120
TTTATCANNCC TGTGCAGGGA GATGTGGGGA AGGGTATTCT ANAGATGCCA CCTGCAACTG 180
TGATTATAAC TGTCAACACT ACATGGAGTG CTGCCCTGAT TTCAAGAGAG TCTGCACTGC 240
GGAGCTTTCC TGTAAGGCC GCTGCTTTGA GTCCTTCGAG AGAGGGAGGG AGTGTGACTG 300
CGACGCCCAA TGTAAGAAGT ATGACAAGTG CTGTCCCGAT TATGAGAGTT TCTGTGCAGA 360
AGTAAAAGAT AACAAAGAAGA ACAGAACTAA AAAGATACCT ACCCCCAAAC CACCAGTTGT 420
AGATGAAGCT GGAAGTGGAT TGGACAATGG TGACTTCAAG GTCACAACTC CTGACACGTC 480
TACCACCCAA CACAATAAAG TCAGCACATC TCCAAGATC ACNACAGCAA AACCAATAAA 540
TCCAGGACC CTCGAG 556

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

GAATTCGGCC TTCATGGCCT ATTATTTTGG CACCAGCGTC AAGACAAATA ATATCCTCTC 60
CCATTATTTT CATAAGTAAC ACAGATTCCC TGATTTTAA AACTAAAAA TACAGCTAAA 120
CCTTCTTAT GTATAAAGTA TGCCTATCAT ATACAGGGAG AGGTGGGTAA TAACTTCCT 180
GTAATGACAG TGTTTGGCAT TTCTTTATGG ATGGAATTGG AACATGAACA AGACCATGTC 240
CAGCGTTTTT ACTGTGAATG TAAATGGAAC AGCAGCCCAA AGCTGTTGTC TGTGCCCCAG 300
AGGTGCTACC TGTAGACAGG GACCAACTCC ATGTGTGTGT GTTAAGTGT TGAATCCAAT 360
TAAGACTCCC AAGCAAATCC TGCATATTCC AAATGTAAAG AGTACTCAGT GGGAAAAAGG 420
TTGTTACCTC AAAGTCATTG CTTCTTTCCT GGCTGGGTCA CAGGGTGAAG AGATGAAGGT 480
GTCTGATGTA TATAGCAAT TAGGGAAAAA TGAGCGGCTT TCCTCGAG 528

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

GAATTCGGCC TTCATGGCCT ACTGGAATCT GCAGCCCCCA CATGCATCTG TCTAACGCAT	60
GCCTCGTGTT CGTTTTGCAA ACATGCCTGT GGTGGAGGGT GGTCAAGTGT AGCCCTGTGC	120
GTCTCAAGGC TGCCTTGTA GGCCATTCCC AGTGCCTGCC CTTGAGCTCC TTACCACCCC	180
TTTTCCTGCT CGGCCCTTTA ATCCCTGACA GACCTGGACT GTGTGGCTGA AGGGGGACCT	240
GCAGCACTGC AGAAATGCCT CTGCGTGGTG CCATGAAGGA AAGAAACCTT GGCCTGGTCT	300
CGAG	304

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

GAATTCGGCC TTCATGGCCT AGGGCAGGGG GAGGGGTGCA NAGTGGGACC CTCACCACAG	60
GGTACTGAGA CAGGTCAATG TAGGTCCGCC CCGCAATGGT GTTGAGTTGC ATCAAGTACT	120
CGAAGTTGGA TATCTCACGC TGTACCCATT TCTGGGTAAG GCCTGAGGCA CGCACCATCT	180
CCTGGGGGGA GCGGCTGCTT AGGTAGCCAA GAGAGGGGGG CCGTAGGCGC AGGANCCACG	240
AGTACACCTG GCCCCATCCC ACCCCATCCC TCGAG	275

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

GAATTCGGCC TTCATGGCCT AACCAGCTTT AATTTCAATT GAGGAATAAT AACAACCCTA	60
GAGATTCATA GGAAAGAGCA TTGAAATACA TTTTTGCAAT AAAGATACCT AAAACCATCT	120
ACCCAGCTTA GGGTTGAACT GAATTTCTGT GAAATAAATT TGTTTTAAAT ACTAATTATT	180
TTAAACTAC TTAATTCCTA AAAACAATGT CATCAGTTTC AAAAGTTTCA CTTTGGGAGG	240
ATATTCCTTA AAAGGCATAC ATAGATGGTA AAGTATAAAA TATTTCTGAC AGAATTATTTC	300
AGTATTATTTC AACATTACT TTCATGTTTG TTATTGTACC ACAAAGATAG TGTCATTGTT	360
GGGTTAAAT GTTGGCTGTT TTGTTAATA TACTTAAAC TGTAACCACT GGCTCGAG	418

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

GAATTCGGCC TTCATGGCCT ACTACATCAA GCACCAGAAC CGCCAGCTGC GCGCCCTGTT	60
GCTCAGCCAC CAGTTCAAGC GCCGGGAGGC CGACCAGACC CACGCACAGA ACTTCTCCTC	120

```

CGCCGTGAAG TCCCCGGTCC AGGTCATCCT GCTCCGTGCC CTCGCCTTCC TGGCNTGCGC      180
CTTCCTACTG ACCACCGCGC TGTATGGGGC CAGCGGACAC TTCGCCCCAG GCACCACTGT      240
GCCCCCTGGCC CTGCCACCTG GTGGCAATGG CTCAGCCACA CCTGACAATG GCACCAGGCT      300
CGAG                                     304

```

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAC ATCAGTTCCT TTTGCCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAATCGAG                                     380

```

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

```

GAATTCGGCC AAAGAGGCCT AAACAAATGA GGGTAGTAAT TTTTATCTG CTAAACTTA      60
TATTATATC ACATACTTGT TGCAATGATT TCAGTGTCTA CATAAATGGT GGCTTAGCTG      120
AGGCAGGTCT AGAATTCAAT CGAG                                     144

```

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

```

GAATTCGGCC AAAGAGGCCT ACTAGACGTT TGTACAAACT ATTCCCTTGA GTTATTTTCT      60
CTGGCTCTTC AGCTCCTTCC TCCCACCCCT TCCCCTGCAC CACCAATCCA TTCTTTTGCT      120
TAATTTCTCT CCATCCTTCA GGTTCAGCT TTAAGAGGTC ACTTCTTTTA GGAGACATTG      180
CCTGAATCCT CTCACCTCCA CCCACAAAAA AGGCCTCTCC AGATGCCCTT CTTTCTGCT      240
CAACCTCAT CTGCTTCCTT TATCATATGC TTATCGTTTT GGATTGTAAT TATTTATTTA      300
ATTGCATGTC TTTCTGCTAG TTTTGTGTT AGCAACAACA AGGATCTCGA G          351

```

(2) INFORMATION FOR SEQ ID NO:450:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```

GAATTCGGCC AAAGAGGCCT AGATGATGGC AGGAATGAAA ATCCAGCTTG TATGCATGCT      60
ACTCCTGGCT TTCAGCTCCT GGAGTCTGTG CTCAGATTCA GAAGAGGAAA TGAAAGCATT      120
AGAAGCAGAT TTCTTGACCA ATATGCATAC ATCAAAGATT AGTAAAGCAC ATGTTCCCTC      180
TTGGAAGATG ACTCTGCTAA ATGTTTGCGT TCTTGTAAT AATTGAACA GCCCAGCTGA      240
GGAACAGGA GAAGTTCATG AAGAGGAGCT TGTGCAAGA AGGAAACTTC CTAAGTCTTT      300
AGATGGCTTT AGCTTGAAG CAATGTTGAC AATATACCAG CTCCACAAAA TCTGTACACG      360
CAGGGCTTTT CAACACTGGG AGTTAATCCA GGAAGATATT CTTGATACTG GAAATGACAA      420
AAATGGAAG GAAGAAGTCA TAAAGAGAAA AATTCCTTAT ATTCTGAAAC GGCAGCTGTA      480
TGAGAATAAA CCCAGAAGTC TCGAG                                     505

```

(2) INFORMATION FOR SEQ ID NO:451:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```

GAATTCGGCC AAAGAGGCCT AGTCGTAAGT TACCATAATA GGTGCTTGCA GTCATTGATA      60
TAATCCAGAA AGCTAACGAA ATGCAAATGA TCAGGCTCAG TATAACTATA TTAGTTATCA      120
TCTTTATATA TCTTTTGCAT ATATTGTCGT TAAGATCTGT CATGGAAAAT AAGGATATGA      180
GCTCCTGCGG GAAAGAATAT TTAGCGTTTC GGAGAGAAAG TCATTACGA TGTGAGCAAG      240
ACACTGTGTC AGAGGCAAAC ATAAATCCCA ACATATTCCA CCGACCAAAC AAGCATAAAA      300
ATCACAAAAA TTCAACTCC TTCCGAAAC TCCTACTGGC CCTCGAG                                     347

```

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```

GAATTCGGCC AAAGAGGCCT ATCTTACTAT TTTTATGTCA TTGGTTTTTT CTCTTTTCTT      60
TCTTTCTTTT TTTTTTTTTT TTTTGTAGGC AGAGTCTCGC TCTGTGGGGA CACTGTTCCG      120
TTCAGAGGCC CCTCCAGCC ATGGGGTGGG GGACAGTGGT GGGCGTGGGA ATCCAGCGA      180
GCATCCTGGA GGGTGGCTCG TCTCCATGTA TTTTGCTCTT CCCCATCTTT TCCATGGGGT      240
CCCCTGCCAG GGTCAAGCAC TAATATGTGG TGAAGGCAGC AAACAGCGTC GGCCTCCCTT      300
TAGGGGTGGG GAGAGGGCTG TAGCACAAG AACCCCTCC CCCGCCACG ACATCCCTGA      360

```

AAAGGAGACT AAAATAAAGC CCCGGCGCCT CGAG

394

(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GAATTCGGCC AAAGAGGCCT AGGAAAAACA GAGTAAAAAA TTGGAAAAGA AGAAGGAAAC	60
AATAACAGAG TCAGCTGGTC GACAACAGAA AAAGAAAATA GAGAGACAAG AAGAGAAACT	120
GAAGAATAAC AACAGAGAT : TATCAATGGT TCGAATGAAA TCCATGTTTG CTATTGGCTT	180
TTGTTTTACT GCCCTAATGG GAATGTTCAA TTCCATATTT GATGGTAGAG TGGTGGCAAA	240
GCTTCCTTTT ACCCTCTTT CTTACATCCA AGGACTGTCT CATCGAAATC TGCTGGGAGA	300
TGACACCACA GACTGTCCC TCGAG	325

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 422 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GAATTCGGCC AAAGAGGCCN AGGGTCACAG GGTGGTTATC TCACTTCGCA GCTTTCCTT	60
TCTGAGGCCA GAAAAGGAAG GGGTTTGCCT TCCTCTAGTA TTTATTCTTC TGGACTACAT	120
CAAGTACTCT AAGCCTGATG TTAGGCAATA ACTGCCATT AGCCATTGGC TACATTGGCC	180
TCTTCTTGT TCCAACAATA TTAGTGATCT GTGGNACAGG ACACACTCTT TGTTTGCTAG	240
CTACAAATTC TAACAAAGCT AAGTTTATT CATGTAGNTA TTCACAAATT AANACAACAC	300
ACACACCACA CACACACACA CACACACACA CACACACATA CCACAAAACC	360
CAGAGATCAC CAAATACTAT ATAAATAAAC AAGCCCAAAG TCACAGATCA GGGACACTCG	420
AG	422

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

GAATTCGGCC AAAGAGGCCT AGACGTCCAA GAAAAACAT TTGGTGAAAG TCAGGATTTA	60
CCTTTGAAAT CCGACTTGGG CACCAGGGAA GATAGTAGTG TTGCATCTAG TGATAGGAGT	120
AGTGTGGAGC GAGAAGTGGC AGAACACCTA GCAAAAGGCT TCTGGAGTGA CATTGGCAGC	180
ACGGACACTC CTTGCCAAAT GCAGTTATCA CCTGCTGTGG CCAAAGATGG CTCAGAACAG	240
ATCTCACAGA AACGGTCTGA GTGTCCTGG TTAGGTTNTCA GGATTAGTGA GAGCCAGAA	300

CCAGGTCTCA CTCGAG

316

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

```

GAATTCGGCC AAAGAGGCCT AGTCAGTCTG AGTTAGAAAA TCGACTCCAT CATCTAACAG      60
AGACTCTCAT CCAGAAACAG ACCATGCTGG AGAGTCTCAG CACAGAAAAG AACTCCCTGG      120
TCTTTCAACT GGAGCGCCTC GAACAGCAGA TGAAGTCCGC CTCTGGAAGT AGTAGTAATG      180
GGTCTTCGAT TAATATGTCT GGAATTGACA ATGGTGAAGG CACTCGTCTG CGAAATGTTT      240
CTGTTCTTTT TAATGACACA GAACTAATC TGGCAGGAAT GTACGGAAAA GTTCGCAAAG      300
CTGCTAGTTC AATTGATCAG TTTAGTATTC GCCTGGGAAT TTTTCTCCGA AGATACCCCA      360
TAGCGCGAGT TTTTGTAATT ATATATATGG CTTTGCTTCA CCTCTGGGTC ATGATTGTTT      420
TGTGACTTA CACACCAGAA ATGCACCACG GCCTCGAG      458

```

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

```

GAATTCGGCC AAAGAGGCCT ATCGAGGTTT GGTGACTGA TGAAGCTTT TATTTCTTTA      60
ACCATTTATG CATTTTCTCA ATTTGCTACA ATAAACATAG ATTGCACAGG GGTGAATACT      120
AAGGAACTCG GAGGGTTAGG GTTAATTTCT GTGAAAGACC AAATATGTTT CTCTGGTTCT      180
CTCGAG      186

```

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

```

GAATTCGGCC AAAGAGGCCT AGCATTATGG TATATTTTAA ATTCATCAAG CTCATCTGTA      60
TGTGTCCTTT TGTCTTTTCTA CTACTGAGAG GATTGGGGCT GGGATCATGG CAGCCTGCTC      120
TGATGTATTT CTCCTCACTC TATTTTATTA TTTTAAAA GAGTTCTAAC TTAAATACGT      180
GGACCAGCTA TTGGATAACT TTAATTCATA TATTTATCAT TCTTCTATT CACTTTGCCA      240
CATACACACC ATGTGATGAT TTTAAACCCG ATTTCTGTAT AGAGAATGTT AAAAGGATAG      300
CACTCGAG      308

```

(2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

```

GACATGCTGT GGTTCACCG CGCACTCACC CTGCTCATCA TCCTCCGCCA CCTCACCAGG      60
AAGGACCCAC AGGGGCTGGG CGTGACGAGT GACGCCATCG CCGATGCCTG CCAGGCCCTG      120
GTGGGCCCCA CCGCCACAG CCGTTGCTGG TGATCTCCGG GATCCCCACC CACCTGGACG      180
AGGGCGTAGT CAGAGGCGCC ATCCGCAAGG CCTGCAACGC CCACGGCGGG GTCTTCAAAG      240
ACGAGATCTA CATCCGCTG CAGGAAGAAG ACACCAAGAA GCCAAAAGAC AAGGCCGAGG      300
GCG                                                                                   303

```

(2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

```

GAATTCGGCC TTCATGGCCT ACACTTTAAT TGCTGTTATC ATGGGCCTAA TTACAGTCAC      60
TGCACTGGCC ACCACTGCCG GAATGGCATT ACACCACTCC ATTCAAGCGG CTCATTTTGT      120
TAATGGTTGG CAAGCCAATT CCATCCAAAT GTGGAATTCT CAACAAGGCA TCGATCGAAA      180
ATTGGCAAAT CAAATTAGTG ATTTAAGACA GTCTGTTATT TGGCTTGAG ATCAGGTAGT      240
GAGTCTCGAG                                                                                   250

```

(2) INFORMATION FOR SEQ ID NO:461:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

```

GGTGACGCCT GCTTCACATC TCTAATGAAC ACCCTCATGA CGTCGCTACC AGCACTAGTG      60
CAGCAACAGG GAAGGCTGCT TCTGGCTGCT AATGTGGCCA CCCTGGGGCT CCTCATGGCC      120
CGGCTCCTTA GCACCTCTCC AGCTCTTCAG GGAACACCAG CATCCCGAGG GTTCTTCGCA      180
GCTGCCATCC TCTTCTATC ACAGTCCCAC GTGGCGCGGG CCACCCGGG CTCAGACCAG      240
GCAGTGCTAG CCCTGTCCCC TGAGTATGAG GGCATCTGGG CCGACCTGCA GGAGCTCTGG      300
TTCCTCGAG                                                                                   309

```

(2) INFORMATION FOR SEQ ID NO:462:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

```

GAATTCGGCC TTCATGGCCT AATGAAGAAA AGCAGAATTC CAAATTCAAA CTGTTGGAGT    60
GAGCCAAGTG GACAGACCCT CCATGAGTGC ACTTTCTTCC AAGAAATCCC CAGATTTACC    120
CCATAGAGGT CTGGGATTAC CTGGAATATA ATATGAAAAA CATTITTTAG GCTGGGTGTG    180
GGGCTCACAC CTGTAATCCC AGCACTTTGG GAGGCTGAGG CGGGCGGATC ACCTGAGGTT    240
GGGAGCTCGA G                                     251

```

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

```

GAATTCGGAA CAATGGGGGT TCAAAACAT AAAAGTGAAA GTCCTTGTA ATCTCCTTAT    60
CCAAATGAGA AAGACAAGGA AAAAAATAAG TCAAAATCTT CAGGCAAAGA AAAAGGCAGT    120
GATTCAITTA AATCTGAGAA GATGGATAAA ATCTCCTCCG GTGGCAAAAA GGAGTCCAGG    180
CATGATAAAG AAAAGATAGA AAAGAAAGAG AAACGGGACC TCGAG                                     225

```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

```

CTCGAGGCGT GTGGGATCAT GAGGCAAAGA AAGTCCAACG AGGGAGAGAG GAGAGTGAGG    60
GATGAGAGGG GACACTTGCT CCATCCTAGT CCCCACGCGG CCCAGCTGGC TTCCTTTTCC    120
AGAATATCTC CTTGCTATAA CCTGGCAGCA GGGGAGCCAA GGTCTTCTC CATCCTTACA    180
GGCACTGAAC CAGGATGTAG GCGCACACTG CTGTGTTCTC TCTGGCCCAT CCTCTCTAAT    240
TGTCTTTCCC TTCCCAGGTC ACAGGATGCT TATTCTCATC TCCAGGCCTT TGCACGGGCC    300
GGGCCTGCTG CCAATCCCCG CACTCTCCCC TTCTTAGGGC CAGGCTAACT CTTCCCCATC    360
CCCGGGGCTC AAGCGTTTCA GTCTCTTCCA AAAGCAGTCT TGGTGGTCCC TGCCACGCGT    420
TACCCTCCTC TCAAGTCACC CGGGAGGTGG AGGTTGCTGT AAGCCAAGAT CGCAGTGAGC    480
TGAGATTGCA CCATTGCACT CCAGCCTAGG CCATGAAGGC CGAATTC                                     527

```

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GCACTCATAA AAATCTTACT CAGAAATCTT CAGAGGTTTG CTAAGGATAC AATTTGATTC	60
TTACACATTT AATGCTCACC AGCTGCTTAG GCCCACACCA TTTATCCACC CTGATTTGCT	120
ACTGCTCTTT GAAATACAAC CAGTGTTTCA GCCAGACTGT TTTCTGCTT CTGCTCCCT	180
TCTCCTCCTC CCAGCACATC TGTGAATTCT TTGACTGGTT TACCACTCCC AAACCTCTCC	240
CCAGCAATGC AGATCTTCTA CACCCTTTAG GATCTAAGCT AAGTCTGCTT CCCAGATATC	300
CTCCCGAACA GCTCGAG	317

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GGTCATTCTT TCCATCGCTG CGGACACGGG AGTCAGAAGT GAAACAGTCC TGTCCTCGTG	60
GGGCTTACGT TCCAGGCGCA AGAGCCACAG GTAGTCGAAT TGGGAACCG CCTCGGATGT	120
CACATAAGCG CCCAGGGAGG ACAGGGCAGG ACAGGGCCTC CCTGGGGAGG TGACTTGAGT	180
CAAGACTCAA AAGAGGGAAG CGAGGGAACA AGCCATGCGA GGAACAAACG AAGGAACATT	240
CCAGAAAGAT TTCACATCCC AAGCCTAAGG TCCAGGGGCA GCAGGCATTG AGGCGGATGT	300
GGCTGGAGTG GAGAGAAAGA GGAATTAAAA GGATGGCATG AGCTCGAG	348

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

GAATTCGGCC TTCATGGCCT ACGAGGAAAG ATCTAATTAT CATGGACCTG CGACAGTTTC	60
TTATGTGCCT GTCCCTGTGC ACAGCCTTTG CTTTGAGCAA ACCACAGAA AAGAAGGACC	120
GTGTACATCA TGAGCCTCAG CTCAGTGACA AGGTTACAA TGATGCTCAG AGTTTTGATT	180
ATGACCATGA TGCCTTCTTG GGTGCTGAAG AAGCAAAGAC CTTTGATCAG CTGACACCAG	240
AAGAGAGCAA GGAAAGGCTT GGAAAGATTG TAAGTAAAT AGGCTGGCTC GAG	293

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GAATTCGGCC	TTCATGGCCT	AATAAATTGC	CAGCATANTA	AAAAACTGCC	TTACTACTCAA	60
TTGCTACACC	TTTTACAGG	CAAAAGGTTT	TATTCTCTCC	TAAATTAAT	TTATCCCGTT	120
TTTTTTTACC	ACCTAACTTT	TGCCTTTTAT	TCAGAACTAA	TGTATTTTTT	TCTTATTGTC	180
GTTCCTTTT	TCAAAATTCC	CTCCTCGGTG	GAAAGTAAAG	GAGTAGGAAC	ATACTATTAT	240
TCAACCAACA	TGCAGCAACC	CTTACGTACG	GTCTCGAG			279

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GAATTCGGCC	TTCATGGCCT	AAGTTTGA	AAAAAAATC	TTTAAGTGA	TTGTGAGTAG	60
ATTTTTTTAA	GGAGCATTTT	TATAATATT	TTCTGAATC	CTTGCAATT	TGACAGTGTC	120
TTTCTATTGT	GTTTATGTGT	GGCAGCAATT	TACTTTATAT	CAAAGTTTTT	TGTTTTTGT	180
TTTGTTTTGT	GAGACACAGT	CTCACCTAT	CACCCAGGCT	GGAGTGCACT	GGCACTATCT	240
CGGCTTACTG	CAGCCTTGAC	CTCCAGACT	CAAGTGATCC	TCCACCTGC	CTCGAG	296

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

GAATTCGGCC	TNCATGGCCT	ATGTTTTTTA	TATATGGATT	TATTTTTGCT	TTTTTAGGCT	60
GATTCAGTGT	GAATATGAGG	TAGGGAAATT	GTGTTTATC	ACAGAAATCC	CAGAATTAAT	120
ACTGGAAGAC	CCCAGTGAAG	CCAAAGAGAA	CCTCATTCTG	CAAGAAACAT	CTGTGATAGA	180
GTCGCTGGCT	GCAGATGGGA	GCCCAGGGCT	AAAATCAGTG	CTATCTACAA	GCCGAAATTT	240
AAGCAACAAC	TGTGACACAG	GAGAGAAGCC	AGTGGTTACC	TTCAAAGAAA	ACATTAAGAC	300
ACGAGAAGTG	AACAGAGACC	AAGGAAGAAG	TTTCCTCCC	AAAGAGGTGA	GAAGGGACTA	360
TAGCAAAGGA	CTCGAG					376

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

GAATTCGGCC	TTCATGGCCT	ACAAGATTGG	CAAGATGCTT	ATTTTGGTG	CCATATTGG	60
CTGCCTTGAC	CCAGTGGCAA	CACTAGCTGC	AGTTATGACA	GAGAAGTCTC	CTTTTACCAC	120
ACCAATTGGT	CGAAAAGATG	AAGCAGATCT	TGCAAAATCA	GCTTTGGCCA	TGCGCGATTC	180
AGACCACCTG	ACGATCTACA	ATGCATATCT	AGGATGGAAG	AAAGCACGAC	AAGAAGGAGG	240
TTATCGTTCT	GAAATCACAT	ACTGCCGAG	GCTACTCGAG			280

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GAATTCGGCC	TTCATGGCCT	AGCAGTAAGC	CAGGATTGCA	CCACTGCACT	CCAGCCTGAG	60
TGACAGAGTG	AGACTCTGTT	TCAAAACAAA	ACAAAAAACT	TTACAGCAAT	CCTGGTCCCT	120
ACCATGGAGC	ATGTGTTACA	GGAAAACAGC	CAGTCCACTC	TGCAACCAAT	TTGGACATGG	180
CCCTGAAAAT	CCTTTTTCGA	CAGAAAGGGG	AAAATAAGAG	TACTGGCAGA	AAGTCAGATG	240
CTGGGGATGC	CTCACCTCT	AGTCTCATGA	CTATCACACA	TGAGACGGTG	TTCCGCTGTA	300
ACTTTTCCCC	CCCCCCCCC	CGTTTGTTGA	TCTGAATCTG	GAAAAGAGCT	TGGAGAGATT	360
TACAGGCCTC	CTCTTCTGCA	ATCAGTAAGA	GTACCATGTG	GAGGCAGAGA	GCCAGAATAG	420
GTTGTGGGGC	TTCTCGAG					438

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GAATTCGGCC	TTCATGGCCT	AGAACAGCTC	TCCAATTAC	ACTTATCTGT	ACAATGTACA	60
TTAATAACTA	ATTTGTTAGA	TGATTAAATC	CAATAATTAA	CTTGCTAGAG	GACCCAGGAA	120
ACAGAATATC	TGCAAGGCCC	AGAGTAGATC	ATAAATAAAT	AGGAATGCAG	ACATAAGATG	180
TTCACTTTTG	GAACAGTAAA	GCTATAATGA	GTTTCTTTA	AAATCAAACA	ATTGTACAAT	240
GCATTATAGT	CTACAACTTA	TTCTGTAGTT	CAAATAAATA	AACTTTCCC	CTGTTACAGA	300
AAGACAGCCC	TCCTCCAGC	AACATTTCAG	ACTGGATGGA	TTGATTCTC	ACCTGACATA	360
ACTCTAAAAT	CCTCACTGAA	GAAGCCAGGA	AGTCAAATG	AGGCTGAAGA	CCTGAAAGTA	420
CAGGGGACTA	AACCCAGAAA	GCAGTAGGCC	ATGAG			455

--(2)--INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

GAATTCGGCC TTCATGGCCT ACATGGACCT CCTGCACAAG AACATGAAAC ACCTGTGGTT	60
CTTCCTCCTC CTGGTGGCAG CTCCCAGATG GGTCTGTGCC CAGGTGCAGC TACATCAGTG	120
GGGCACAGGA CTGTTGAAGC CTTCCGAGAC CTTGTCCCCTC ACCTGCGCTG TGAATGGTGA	180
GCCCTTCAGT GGTATTCTT GGACCTGGAT CCGCCAGNCC CCCGGGAAGG GCCTGGAGTG	240
GATTGGGCAA ATCAATTATG ATGGAACCAC CAAGCACAAAC CCTCCCTCG AG	292

(2) INFORMATION FOR SEQ ID NO:475:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GAATTCGGCC TTCATGGCCT AAGGGTGGGC TTAAATGGCA GCTGGGGTAA AAGGAAACAA	60
AAACAGTAAT TCTGAAGAGC ACAGGGAACA GGCAGCCAGG ACCAGCCTGG CCCATTCCAG	120
GCCAGCTGAG CTGAAATGCT GATTCTGTCC AGGGGGCTGC TGTATGTGTA GACTGGTGGC	180
AGTCTTGGGG ACTGAGGCCT CTTGGAGAGA AGGGAAGACT GTCGGCTCAG AAGTCCATGG	240
AGCTGTGGGC CAGGTAGTCC TTGCGACCGA TGTGTCTGAC CTGCTTGGTC TGCATAGCCT	300
CGAG	304

(2) INFORMATION FOR SEQ ID NO:476:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GAATTCGGCC TTCATGGCCT ACCAGCTCTC TTCTAAAAGA GAAGTGGGTG GGCACACTGA	60
ACTGTTTGGT GGCCCCAACC ACAGGAAGCT GCAATTCTCT GGCTTAGGGT GATACTTTTG	120
CCCTCCTTGT GCCCTCTCTT GGACGCTCTG CACCAACCCC AGGCTACTGA GCCACCTTCC	180
CTCCTCATGC CTTCCCTGAG CTTTGGTGCA TCTCATCTGG ACTATGGGTT GTACTGTGAC	240
CATCCCAACA CCTCACCTC TGTCTACAAG GAAATGGGAG GTGGAGCCTC CTGGCTGAGA	300
AATTGTTTTG CAAATGGATC TCGAG	325

(2) INFORMATION FOR SEQ ID NO:477:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GAATTCGGCC TTCATGGCCT AAGCTCATCA ACGAGAAGCT CATCAGAACC AAGGGGCTGT	60
GGGGCCCCGT CCATGAGCTG GGCCGCAACC AGCAGCGGCA GGAGTGGGAG TTCCACCAC	120

ACACCACCGA	GGCCACCTGC	AACCTGTGGT	GTGTGTATGT	GCATGAGACG	GTCTTGGGCA	180
TTCTCTGAAG	CCGTGCCAAT	ATTGCTCTGT	GGCCCCCAGT	TCGGGAGAAG	AGAGTCAGAA	240
TCTACCTGAG	CAAGGGTCCC	AATGTGAAAA	ACTGGAATGC	ATGGACCGCA	CTGGAAACTC	300
GAG						303

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GAATTCGGCC	TTCATGGCCT	AGTTGTTT	CAG AATCCACACA	GCTCTGAATT	ACCAACGCTG	60
AATTTCCAAG	ATACTGTAAG	CACCCTGACC	AACAGTCCAG	CCATCCCATT	GGAAACATCT	120
GCATGTCAGG	ACATACCCAC	TTCTGCCAAT	GTACAAAATG	CAGAGGGTAC	CAAAATGGGA	180
GAGGAGGCAT	TGAAAATGGA	TCTTGACAAT	AACTTTTATT	CAACTGAGGT	GTCAGTTTCT	240
TCCAATGAAA	ATGCTGTCAG	TTCTGACCTC	CGGGCAGGGG	ATGTACCTGT	TTTATCTTTG	300
AGTAATAGCA	GTGAGAATGC	CGCCTCTGTG	ATCAGCTCGA	G		341

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

GAATTCGGCC	TTCATGGCCT	AAGTTTGTAA	AAAAAAAATC	TTTAAGTGA	TTGTGAGTAG	60
ATTTTCTTAA	GGAGCATTTT	TATAATATTT	TTCTGAATC	CTTGCAATAT	TGACAGTGTC	120
TTTCTATTGT	GTTTATGTGT	GGCAGCAATT	TACTTTATAT	CAAAGTTTTT	TGTTTTTGT	180
TTTGTTTTGT	GAGACACAGT	CTCACCTTAT	CACCCAGGCT	GGAGTGCACT	GGCACTATCT	240
CGGCTTACTG	CAGCCTTGAC	CTCCAGACT	CAAGTGATCC	TCCCACCTGC	CTCGAG	296

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

GAATTCGGCC	TTCATGGCCT	ACAGAGATGG	ATTATCCTAC	TTTACTTTTG	GCTCTTCTTC	60
ATGTATACAG	AGCTCTATGT	GAAGAGGTGC	TTTGGCATAC	ATCAGTTCCC	TTTGCCGAGA	120
ACATGTCTCT	AGAATGTGTG	TATCCATCAA	TGGGCATCTT	AACACAGGTG	GAGTGGTTCA	180
AGATCGGGAC	CCAGCAGGAT	TCCATAGCCA	TTTTCAGCCC	TACTCATGGC	ATGGTCATAA	240
GGAAGCCCTA	TGCTGAGAGG	GTTTACTTTT	TGAATTCAAC	GATGGCTTCC	AATAACATGA	300

CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA 360
CTTACCCATG GGAACCTCGAG 380

(2) INFORMATION FOR SEQ ID NO:481:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

GAATTCGGCC TTCATGGCCT AAGTTTGTAA AAAAAAATC TTTAAGTGGG TTGTGAGTAG 60
 ATTTTITTTAA GGAGCATTTT TATAATATTT TTCTGAATC CTTGCA/TATT TGACAGTGTC 120
 TTTCTATTGT GTTTATGTGT GGCAGCAATT TACTTTATAT CAAAGTTTTT TGTTTTGT 180
 TTTGTTTTGT GAGACACAGT CTCACCTAT CACCCAGGCT GGAGTGCACT GGCACTATCT 240
 CGGCTTACTG CAGCCTTGAC CTCCAGACT CAAGTGATCC TCCCACCTGC CTCGAG 296

(2) INFORMATION FOR SEQ ID NO:482:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC 60
 ATGTATACAG AGCTCTATGT GAAGAGGTGC TTGGCATAAC ATCAGTTCCC TTGCGGAGA 120
 ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA 180
 AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA 240
 GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA 300
 CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA 360
 CTTACCCATG GGAACCTCGAG 380

(2) INFORMATION FOR SEQ ID NO:483:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

GAATTCGGCC TTCATGGCCT AGGCTGGACA GACTTTCTAA TGAACCCAAT GGTATGATG 60
 ATGTTTCTTC CTTTATTGAT ATTTGTGCTT CTGCCTAAAG TGGTCAACAC AAGTGATCCT 120
 GACATGAGAC GGGAAATGGA GCAGTCAATG AATATGCTGA ATTCCAACCA TGAGTTGCCT 180
 GATGTTTCTG AGTTCATGAC AAGACTCTTC TCTTCAAAAT CATCTGGCAA ATCTAGCAAC 240
 GGACAGCTCG AG 252

(2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 304 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

```
GAATTCGGCC TTCATGGCCT ACTACATCAA GCACCAGAAC CGCCAGCTGC GCGCCCTGTT      60
GCTCAGCCAC CAGTTCAAGC GCCGGGAGGC CGACCAGACC CACGCACAGA ACTTCTCCTC      120
CGCCGTGAAG TCCCGGTCC AGGTCATCCT GCTCCGTGCC CTCGCCTTCC TGGCCTGCGC      180
CTTCCTACTG ACCACCGCGC TGTATGGGGC CAGCGGACAC TTCGCCCCAG GCACCACTGT      240
GCCCTGGCC CTGCCACCTG GTGGCAATGG CTCAGCCACA CTTGACAATG GCACCAGGCT      300
CGAG                                     304
```

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

```
GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTGGGCATAC ATCAGTTCCTC TTGCGCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACCTCGAG                                     380
```

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

```
GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTGGGCATAC ATCAGTTCCTC TTGCGCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACCTCGAG                                     380
```

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAC ATCAGTTCCC TTTGCCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACCTGAG

```

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAC ATCAGTTCCC TTTGCCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACCTGAG

```

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

```

GAATTCGGCC TTCATGGCCT AGGTTTACAG GCATACCTCA TTTTATTGCA CTTCACTTTA      60
TTGTGCTTTG CAGATAATTG TGCTTTTAC AAATTGAAGG TTAGTGGCAA CCTGTGTTG      120
AGCAAGTTCA TTGGCAACAT TTTTCAACA GCATGTACTC ACTTGTCTCT ATGTCACATC      180
TTGATAATTT TCATATTTC AACTTTTTC TTATCATGAT GATGATTAGT GATCTTTGTT      240
ACTGTNGTAG TTGTTTTGTG GGCACCACAC TGTATGCAGN AAAGCTCGAG      290

```

(2) INFORMATION FOR SEQ ID NO:490:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

```
GCTACCTTAA AAAATAGATA CTCCACTAGA GGCTGTGCTT AATTCAAATC CATGTGTGTG      60
CCTGCATTAC ATGTGTGAAC ACGTGTTCCT GTCGTGTGTG TCATGCACAT CTGTGTGTGG      120
CATAGCATAA GCCAAATGAA AATCATTGTG TCATGGGATT CATATGAGGA ACAAATTTAA      180
ATTGAATAC AGTCAGATAA CTGCCACGCA GGGCATTGCG GGAACCATCC CCGAATGCCC      240
TGATGTGATT TCCCTCAGAA AATCCTTGTG ATTAGAGGAG AAGGTCTGGG CAGGGGCGAG      300
AGCATCTCAG ACATCAAGTC AACTTTATCA TCTACTACAT CAGCACTGAA GTCCAACGGC      360
ATCCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:491:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

```
GAATTCGGCC TTCATGGCCT ATGCTTTTTT CTTTATTCTT TGATGTTGTT TAGGAGTGGG      60
GGGCCTCGCA GAACACCTAG TCCAGCCACG TGCCCAGAGC AGGTGTGTCC CTTTCATACT      120
TCAGTCCACT TTAACACAGC CTTCCCCACG CCCCTTCTAT GGTAGCAGTT CTCCTCGGGG      180
TCTCCATGGA CACCCTGTGC CCCAAGCCGA TGGCCCCACC CAGCAGCATC AGCAGAGCTG      240
CCCCCCTTCT CCGCAGAGCA GGCTCTCCTT TACGGGACTC TCCTCTTCCC TCCCACCCCC      300
CCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:492:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

```
GGAATAAGAA GAGAAAGCCA AGGAAGACAA GGGCAAACAA AAGTTGAGGC NGCTTCACAC      60
ACACAGATAC GGAGAANCCA GAAGTGCCAG AGTCAGCATT CTGGAAGAAA ATCATAGCAT      120
ATCAACAGAA ACTTCTAAAC TATTTTGCTC GCAACTTTTA CAACATGAGA ATGTTAGCCT      180
TATTTGTGCG ATTTGCTATC AATTTTCATC TGCTCTTTTA TAAGGTCTCC ACTTCTTCTG      240
TGGTTGAAGG AAAGGAGCTC CCCACGAGGC TCGAG
```

(2) INFORMATION FOR SEQ ID NO:493:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GCCTTGGGCC	CTCGCAAAGT	CTTGGAGAAG	CAGTTTACT	TCCCTTCCTT	CACTTAGACC	60
CCATTCTTTA	GCATTTCCTC	TGAAGCTCCC	ACAAGACCCA	AGAATGGCTG	CTGCAGTGTC	120
TCCTCTTCAG	TCAGGGACCC	TGGTTGAGGT	TTGTGTATTG	TTCATTATTG	CTCTGTTTTG	180
CAGTTGTTCA	AAGTTGGAAG	ACTTGCCTGC	GGAGCAGTGG	AACCATGCCA	CAGTCCGCAA	240
TGCCTTAAAG	GNACTGCTCA	AAGAGATGAA	CCAGAGCACA	TTAGCCAAAG	AAACCCTCGA	300
G						301

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 389 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GGAAGATGTC	TACAGAAAAG	GTAAGACAAA	AGGAGGAAGC	TGGGGAAAAA	AGAGTGTGCG	60
GAGACCAGAT	CAAGGGACCG	GACAAAGAGG	AGGAACCACC	AGCTGCTGCA	TCCCATGGCC	120
AGGGGTGGCG	TCCAGGTGGC	AGAGCAGCTA	GGAACGCAAG	GCCTGAACCT	GGGGCCAGAC	180
ACCTTGCTCT	CCCGGCCATG	GTCAACGACC	CTCCAGTACC	TGCCTTACTG	TGGGCCCAGG	240
AGGTGGGCCA	AGTCTTGGCA	GGCGTGCC	GCAGGCTGCT	GCTGCAGTTT	GGGGTGCTCT	300
TCTGCACCAT	CCTCCTTTTG	CTCTGGGTGT	CTGTCTTCCT	CTATGGCTCC	TTCTACTATT	360
CCTATATGCC	GACAGTCAGC	GCACTCGAG				389

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 438 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

GTGGCGATTG	GTCCTGTCAT	GGTTTATTCA	GCCATGTGGT	GGATGGCTAC	TTGTCTTCTA	60
AGCCACTTGC	CTTCTGATCG	CTGGACTGAC	TCTCTGCCCC	TCTCTTGGTG	CAGTCCTCAG	120
GAGGCTCGGT	CACACTCTCC	AAGAGCACAG	CCATCATCTC	CCACGGTACC	ACAGGCCTGG	180
TCACATGGGA	TGCCGCCCTC	TACCTTGCAG	AATGGGCCAT	CGAGAACCCG	GCAGCCTTCA	240
TTAACAGGTG	ACCTCGGGGC	ACAGGGCAGG	GCACCGAGGC	AGGCTTACCC	TGGTGCAATC	300
GAAACACCGG	TCCCCTTTCC	TCCCGCCAGG	ACTGTCTTAG	AGCTTGGCAG	TGGTGCCGGC	360
CTCACAGGCC	TTGCCATCTG	CAAGANGTGC	CGCCCCCGGG	CATACATCTT	CAGCGACCCT	420
CACAGCCNGG	TCCTCGAG					438

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

GAATTCGGCC TTCATGGCCT AGGTAAAATT TGTATAACAA AAAATTAACC GTTTTAAACT	60
GAATAATTCA GTGAGATTTA GTGAATTCAC AATATTGTGC AACTGCCACC TCTTCTACT	120
TCTAAACCAT TTTCTCATA CCAAAGTAA GCCCGTACC TATGATGCAG TCCCTTCCCG	180
TTTCCTTCTC TCCTCAGTCC CTGGCAACCA TCACTCTGCT TTCTGTCTCT GTGGATTAC	240
TTATTCTAAT ATTAAATTC AGTGGGAATC CTGCCTCGA G	281

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 570 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

GAATTCGGCC TTCATGGCCT AACTTAGAG AGGCAGTCGG GATGGAGGGT CGAGTTGAAG	60
ACAGGGAGGG GTGAGGAACG AGCAGAGGCC AGTTGTTTGG CCACTTGAGG GAGTTTGGAC	120
TTGTCCCGAG GGCACTAGGG AGCCGTGAAG GGCTTCAAGC CGGGGAGGAT CATGAACATT	180
TCCCCAGAGG AGCTCAAAAT GGAGTTGCCG GAGAGACAGC CCAGGTTCGT GGTTTACAGC	240
TACAAGTACG TGCATGACGA TGGCCGAGTG TCCTACCCCTT TGTGTTTCAT CTTCTCCAGC	300
CCTGTGGGCT GCAAGCCGGA ACAACAGATG ATGTATGCAG GGAGTAAAAA CAGGCTGGTG	360
CAGACAGCAG AGCTCACAAA GGTGTTGCGA ATCCGCACCA CTGATGACCT CACTGAGGCC	420
TGGCTCCAAG AAAAGTTGTC TTCTTTTGGT TGATCTCTGG GCTGGGGACT GAATTCCTGA	480
TGTCTGAGTC CTCAAGGTGA CTGGGGACTT GGAACCCCTA GGACCTGAAC AACCAAGACT	540
TTAAATAAAT TTAAATGC AAAACTCGAG	570

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

GAATTCGGCC TTCATGGCCT AGGTGCATGC CATCAAATAC TCTAACGAGA CATTTTAAAT	60
GAAAGACTTA AACCAGATAG GCCACAATGA ACCAAATTAG AAATCTGAAC ATGTCACCAC	120
TGTCAGCATA AAGGAATATA AAAGGGCAGA GCAAAGTCTT TTTTCCTAAG GTGAATATTT	180
CTAAGGTAAG TATTCATTTG TAAAAGTTTT TTTTTCAN CANGTCTGAA NNCTTTTAC	240
CANNNGNGA GNATTACAAC AAAACATCCC TNGGTTAAAA AAAAAAATA CCATCTTGCA	300
ATTGAGCACA CACCNGCAGC TGGTGTGCTC ATCCAAACCN ATCAGTAGGC TAAGAGNATT	360
TNAAATTCCA TACATATGAG TTAGGTATT AATGCCGATT ACACAGTACA CAGTACAGAG	420
GGAGGTCCTT ATATCCACAC ACACACACAC CCCATCCAGC ATTTACACCN AAAGCCTTAC	480
CCTCGAG	487

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

```

GAATTCGGCC TTCATGGCCT AACAAATCAA AGAAACTTTT TTCTGAACCA TTTGAAATTT      60
GCCAGCCTGA TGTCCTATCA CCCCCAAGT ATTTTAGCAT CTATGCAACA AAACATTTTC      120
TCTGACAAAA CCACATCAGA ACTCTCAAAT CAGGAAACAA ACATTGATAC ATGTCTATCA      180
ACTAATCCTG TCTTCAATGA CATTTTACCG ATTGTTCCAA TGATGTCAGC ATCACGGGTC      240
ACATTTAATA GTTGGCTCCT TCAGTCTCGA G                                     271

```

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

```

GCACTTCTGG ATGTTGGTTC TCTTTGTCAT TTTCAACAGT CTGCAGGGAC TTTATGTTTT      60
CATGGTTTAT TTCATTTTAC ACAACCAAAT GTGTTGCCCT ATGAAGGCCA GTTACTACTGT      120
GGAAATGAAT GGGCATCCTG GACCCAGCAC AGCCTTTTTC ACGCCCGGGA GTGGAATGCC      180
TCCTGCTGGA GGGGAAATCA GCAAGTCCAC CCAGAACTCT ATCGGTGCTA TGGAGGAGGT      240
GCCACCTGAC TGGGAGAGAG CATCCTTCCA ACAGGGCAGT CAGGCCAGCC CTGATTAAAA      300
GCCACGTCCA CTCGAG                                     316

```

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

```

GACAAAGACC AGCAATGGAT CACTTGGAGT CCTTTATTGC TGAATGTGAT CGGAGAACTG      60
AGCTCGCCAA GAAGCGGCTG GCAGAAACAC AGGAGGAAAT CAGTGCGGAA GTTCTCTCAA      120
AGGCAGGAAA AGTACATGAG TTAAATGAAG AAATAGGNAA ACTCCTTGCT AAAGCCGAAC      180
AGCTAGGGGC TGAAGGTAAT GTGGATGAAT CCCAGNAGAT TCTTATGGAA GTGGNAAAAAG      240
TTCTGTCCGA GGAAAAAGGA GNACTCGAG                                     269

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

GAATTCGGCC TTCATGGCCT ACTTGTCTCA CTCTGCATCA TCCCTTAGTC TACAACAGGC	60
CTTTTCTGAA CTTAGACGTG CCCAAATGAC AGAAGGACCC AACACAGCAC CTCCAACTT	120
TAGTCATACA GGACCAACAT TTCCAGTAGT ACCTCCTTTC TTAAGTAGCA TTGCTGGAGT	180
CCCAACCACA GCAGCAGCCA CAGCACCAGT CCCTGCAACA AGCAGCCCTC CTAATGACAT	240
TTCCACATCA GTAATTCAGT CTGAGGTAC AGTGCCCACT GAAGAGGGGA TTGCTGGAGT	300
TGCCACCAGC ACAGGTGTGG TAACTTCAGG TGGTCTCCCC ATACCACCTG TGTCTGAATC	360
ACCACTACTT TCCAGCGTAG TTTCAAGTAT CACAATACTC GAG	403

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

GTTTGGATGA TTGGTGGCGT GTACGCAGCT GCTATGGCCT GGGCCATCAT CCCCCACTAT	60
GGGTGGAGTT TTCAGATGGG TTCTGCCTAC CAGTTCCACA GCTGGAGGGT CTTCTGCTCTC	120
GTCTGCGCCT TTCCTTCTGT GTTTGCCATT GGGGCTCTGA CCACGCAGCC TGAGAGCCCC	180
CGTTTCTTCC TAGAGAATGG AAAGCATGAT GAGGCCTGGA TGGTGTCTGAA GCAGGTCCAT	240
GATACCAACA TCGAGGCCAA AGGACATCTT GAGCGACTCG AG	282

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

GAATTCGGCC TTCATGGCCT ACTGAGAAAA AAAATCAAAT CTAATTTTAA AATGAAGGTA	60
TTTAAAACCA TGGCACAAGG GAGCCTTATT TATGGAGCTG GTGGGAAGCC AGGATGTTTC	120
CAATCCGCTG CTCTTACAGG AGCCTGTGCC TCGCCAGTTC TGTGCTGCAG TGGGCAGCCA	180
ACTGAAGTGC ATGAGTCAAA TGCACGAAGC AGCAGACTCG AG	222

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GAATTCGGCC TTCATGCCCT AGTGGTGCG TTTTTCAGGA TTGTAGAGAT GCTAACAAAT	60
TACAGGTTCT CTCATGCAAA CACTTTGCTA GGAATTATAT ATATCAAGTT TATATTGGC	120
AATCAGGCTT TAGAAGCAGA AGGTCTAGCT ATCTCAAACCT ACCACCTACC TCCCTCACCA	180
AAGCCGCTCG AG	192

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GAATTCGGCC TTCNTGGCCT AGTAAAATTG TTAAAGTTGA CAGGATCAGT TTTGGAAGAT	60
GCTTGAAGG AAAAAGGAAA GATGGATATG GAAGAAATTA TTCAGAGAAT TGAANACGTT	120
GTCCTAGATG CAACTGCAG TAGAGATGTA AGACAGATGC TCTTGAAGCT TGTAAGACTC	180
CGGTCAAGTA ACTGGGNCAG AGTCCANGCA ACTTCAACAT ATAGAGGNGC NACACCAGAA	240
AATGATCCTA ACTACTTTAT GNATGNACCC ACATTTCATA CATCTGATGG TGTTCCTTTC	300
ACTGCAGCTG ATCCAGATTA CCANGAGAAA NTCCAAGAA NACTTGAAAG AGANGATCCT	360
CGAG	364

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GAATTCGGCC TTCGATTGAA TTCTAGGACT TGACAGAATT CGAGTTATCC TTCTCAGAAC	60
ATGTGCAGAG TCTCTTTTTC CCTCACCATG TGGTCCTGTG CTCTTTCAGG TGGGAGTTT	120
GGGGCCTCCA GGGCAGCAGG CACCACCTCC ATATCCCGGC CCACATCCAG CTGGACCCCC	180
TGTCATACAG CAGCCAACAA CACCCATGTT TGTAGCTCCC CCCCAGAGAC CCAGCGGCTT	240
CTTCACTCAG AGGCCTACCT GAAATACATT GAAGGACTCA GTGCGGAGTC CAACAGCATT	300
_AGCAAGTGGG ATCAGAGCAA TCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

```

GAATTCAGTG AGTGGGCATG GCTGATCTTG TGCAAATTAA AAGTTATGGG GCATAAGAAT      60
AGCAAAAGTT GAACCTCTTT TAAAAAGGAA AGTACCCTGA GAGCCAGTAT TGGTTGAGGC      120
TCTTCAGTAT GCCCAGGTTG GCAGCACTGA GAACCGCAGG AACGGCCTGT TGTACAAAA      180
AGGAGATTGA CTCAGCTGCC CTTGGTGCAT CTGACTGACT ATGACTGCTG AGAGATTCCA      240
AGGACCCCTTA ATGCCAGGGC TAACCTCTCC ATGTGCAGTG AGACCTCTGG AGGAAGTGTC      300
ATCCTCTGGC TTTGTGTGGT ACTCATTATG GTGCAGTGCG GGCATGAAAT GAAGACACAC      360
AAATAGGCTC GAG

```

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

```

GAATTCGGCC TTCATGGCCT ACTCTTCCTG GTCCTTCTC AGCCTTGTTG CTGTAAGTGC      60
TGCTCAGTCC ACCATTGAGG AACAGGCCAA GACATTTTGT GACAAGTTTA ACCACGAAGC      120
CGAAGACCTG TTCTATCAAA GTTCACTTGC TTCTTGGAAAT TATAACACCA ATATTACTGA      180
AGAGAATGTC CAAAACATGA ATAATGCTGG GGACAAATGG TCTGCCTTTT TAAAGGAACA      240
GTCCACACTT GCCCAAATGT ATCCACTACA AGAAATTCAG AATCTCACAG TCAAGCTTCA      300
GTGCAGGCTC GAG

```

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

```

GAATTCGGCC TTCATGGCCT ACTTGAACAA TTAAATATA GGAGAAGACT ATTTTTTAGA      60
AATGTTTTCC GTCGCCAACT TGTAAAGCT TTATAGCACT TTGCATATTT TGGAGAATGT      120
CACTATATT TTTATCAGAG CTGATTGTGTT CCAGTGGAAC AACAGTGGCG TAGACATCGC      180
CCACAAGGTT CTGCATACTC GAG

```

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

```

GAATTCGGCC TTCATGGCCT ACGTGGTATT AAGGAGACAA TCTGAGGCAT TCCCACCAGT      60
CAATTTGACA TGCGGTTGGC AAGGTTCCCTC TTCCCTTCCC ACTTTAGATC GTGCCCTGTC      120

```

```

CCAGGTCAGA CCCGAAAGAT TCATAGGCAC ACTTACAGCC TTCATAGTCT CAGCCATAGT    180
CATCCTAGCA ACTGCTAGTG TGGCTGTAGC ATCTATTACT GAATCAGTAC AAACAGCTGC    240
TTTTGTAGAT AATTTGGCCA GAAATGTTTC TAATGAACTT CTCTTACAGC AAGGTATAGA    300
TCAAAAGATT CTTGCACATC TGCAAGCCCT CGAG                                334

```

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

```

GAATTCGGNC TTCATGGCCN AAAGCTCTNG AAGGAGTATT AGAGTACAGA GTCTGAGNCT    60
NTGANAAATG GTGGTCAGAA GCCNTCTTCA TCAGATANAT TTCTCAGATG TGCCCCCTCC    120
GCGGCAGAGG NGGATATTCA TCTCCTAGTT CATGTTTCTA AACATGTCAG TANGCAGATN    180
ANTCACTACC AGTATCTGCT TCTACTTTTC CTGCATGAGT CACTTATCCC TGCTTTTCTA    240
GAACNTAAGG AAAGATGTAG AAGCTGTAACT TGGCAGTCTT GCTAGTCAGA CATCCATTG    300
TATTGGAATT TTAATTAGAA GTGCAGAACT GGCTCTTTTG CTCCATCCAG TGGATCAAGC    360
AAATACTCTT AAGTCTCCTG TTTCTGAAAG TGTGAGCCCA GTGGTACCTG ANTATTTGCC    420
TACAGAAAAT GGGGATTTTT TGNCTCAAA AAGAAAACAA ATTAGTAGGG ATATAAATAG    480
AATTAGAAGT GTAAGTGTTA ATCATATGTC AGACAACAGA TCTATGAGTA TCTCGAG      537

```

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

```

GAATTCGGCC TTCATGGCCA AGGTGCTTAA TATTAAAAAA AAAAAAAGTA TATCCAACCA    60
CAGATATACA GTTCTGCCCT TTTTTCCTTT TTACCTAAAT ATACTCCATA AACAGTTTCC    120
ATGTTGTGTA ATATCTTCAT GTTCTACTT TTCACTGATT GCTTAAATGT CCATTGGGCT    180
GATAGGTCAC AGTTCGCTAA CCCATCTCAT TGTGTTCAT TGGGATCTCC ACTTCCCTC      240
GAG                                243

```

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

```

GAATTCGGCC TTCATGGCCT AGTCTCAAAA AAAAAAAAAA GATTATCCAC AAATGCAGTG    60
GNCCCTGGGA CAAGCCCTTT AAAGGAGTCA TNGAGAATCG TCTGTTGCTC ACAGCATCAA    120

```

TCNGGTATTT AGTTCTCAAG CTTGAGGATT CTAGTTTTC	TCAGAGGGTC GGGTTCAGTC	180
TCTAAAAGAC GCTCTGAAAG CAGACCAGGC TGTTTTCTTG	GAGCTTTTCA GGTTAGATT	240
TCATGTGTGT ATCTTCCATC TACCACGATT ATTTGGCTAC	CAGATGCCTT AGCAAGCTGA	300
ACAGTGAGCT CAGAAGTGCC ACCATCTATA GTAACATTCT	CGAG	344

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GAATTCGGCC TTCATGGCCT AAGAGTATCC GCTTACAGAA	AAGACACTTC ATCACCTAGC	60
ACTGATTAT GCAGCTTTGG TTTCAATTGG GCTAAACTCT	GAAGAACTGG ATGTAAAGCT	120
TATAATTGCC CCAGGAGTAG AAGCAACTGC CTTGATAATT	CGACAAATTG CTGACCACAG	180
TTTAATGACC TCAAAGAGAG ATCCTCATGA ATGGTTGGAT	AAATCCTGGC TTAAAGTTTC	240
ACCATCTGAG GAAGAAATGT ACTTACTTGA TTTTCCATGT	ATTAACCCAA TCGTGGCTCG	300
AG		302

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGGCC	TTCATGGCCT AATCCATAAA	60
AGGCTTTTGA GATGCTCTG CTGAAAATAA ATGGAGCTCT	AGTAAATGTT AGAGTTTTTG	120
CTAGTAGAGT TTTGATGCTT TTTGTCTTTG TTCTACTACT	GAGCTTGCAC CTAGGATGCC	180
TTCTTATAGT GCCATTCAAC ATGCAAGTTT CTTTTCTGG	GGCTGTGTGT CCAGGTGACT	240
TTATGAGTTA GGCTTTGGCA AATGCCAGAC TTGTTTCATC	TAACACTAGA ATGTAGGGAT	300
CCTGCATTCA GCATGACCCT CGAG		324

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GAATTCGGCC TTCATGGCCT ATAGGCCANG AAGGCCGGCC	TTCATGGCCT ATAGGCCATG	60
AAGGGTTGGT TGTGTTTTCC TAACAATGAA TAAGACAGAA	ACCCTTGATA GCTAAATTCA	120
TCTGCAGTCA AACTAAGTTT TGCAGTGTCT TTTTAAGAGC	CAGGCAATTC TACCACAAA	180
TAAATATAT TTTTAAATC CACATTACTA TACCACTGAC	AAGTCTTTAC TTCAGAACTC	240

ATCATTGAGA AATGTGTAGC TGCTTCCAGA GTGTGTCTAA TACTGTTGGA ACAGGCGTTT	300
CAGAAAGAAA TGAGAGGCC AGTCTCAGTA ACTCCATGAA GGGTGCCGAG CTCCTCTGTT	360
GAGGATTTGG CTTGTGAGAG GCAATGTTCC TATCATTGTC CAATTTGGCC TTTGTTATTC	420
CCACATTGGC TCGAG	435

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GAATTCGGCC TTCATGGCCT ACCAGGTTGG CCAGGCTGGT CTCGAACTCC TGACCTCAGG	60
TGATCTGCTC ACCTCGGCCT CTCAAAGTGT TGGGATTACA GGAGTGAGCC ACCGCACCGG	120
GCCAAAAAAT CCAATTTCTT AGAGATTAAA TAACCCCTCA GGATTATCAA AGGAAATAAT	180
TAGGGAAAGG TAGATGTTCT GTCCAGTAA GAGAAGAAAG TGGTCCAGAA ATTTTATCTC	240
CCATCAAATG ATCCATTTTA CTTAAGTATT AAACCAAGTG ACATTCTTCA GTTTAACTCT	300
GATAAATGAA TCATATTCCT CTTGAAAAT AACTTTTGTA TTTCTGCTC TAAAAAGAGA	360
ACCACCCCTC GAG	373

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GAATTCGGCC TTCATGGCCT AAACAATTAA TTGTGGGTGT CTGAGGGGGA AGGTCGCAGC	60
TTTGGGCAGC TTTGAGAAGC GGTACAAGAG TTCTGTGCCT GTGTGTCCAG CCTGGAGCC	120
AGCCAGTGCA TTTATTTTAA GCTCTTAGAA GCAACTCCTT GGCCAGGAA TGGGTGACCC	180
CTGAGATGGG TCCACGCATC TCTTACACT TCCTTCTCTC CGTGGGATAC TGGACTCGTG	240
CCTCTGCGCC CATTCTCTTC TCACGCATAT CCATGAGCTT TAATTTCACT TTCTGATCAC	300
GGTACGTCCA TAAAGCCAGT ATTACACTTA AATGAAGTAT TCITTTTTGT AATCGTTTTT	360
TTTAGAAGGT AAACAAATTT AATAAGCTA TCTCGAG	397

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GAATTCGGCC TTCATGGCCC ACATGAATCT NGTAATTTGT GTCCTACTTT TGTCATTG	60
GAAAAATAAT TGCACTACTA CAAACCAAAC CAATGGATCT TCTACTACAG GAGATAAACC	120

```

TGTGGAATCA ATGCAGACAA AATTGAACTA CCTTAGAAGA AATCTACTCA TTTTAGTTGG      180
TATTATCATC ATGGTTTTTG TCTTTATCTG TTTTGTGTAT CTCCATTATA ATTGTCTGAG      240
CGATGATGCG TCCAAAGCAG GAATGGTCAA GAAAAAAGGC ATAGCAGCCA AGTCATCTAA      300
AACATCATTC AGTGAAGCCA AGACAGCCTC TCAATGCAGT CCAGAAACAC AACCCATGCT      360
ATCTACTGCA GACAAGTCAT CTGATTCATC GAGTCCAGAA AGGGCATCCG CACAATCCAG      420
CACAGAAAAA TTAATCAGAC CCTCAAGTCT ACAAAGCCA TCCAACCTCG AG              472

```

(2) INFORMATION FOR SEQ ID NO:521:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

```

GAATTCGGCC TTCATGGCCT ACACCTCTTC TTAGGGCTGT TTTTAAAC ACAATGATAT      60
TCTAAGGAAC AAGAGGTTGG CTATGGACTT TTGTATACCC ATGCCTATCA TATTGCGCTA      120
AATGTTTGAT TATATAGAGA CATTTCTTTG GAACTTTGAG CTGTGTGAAG ACAACACAAA      180
CCTGGCCATT CATGGCTGAC AGAAGGTTGG CCCTAACCTT GCTCAGGCCC ACACAGATTG      240
TGTAATATTC TTTGGATCTG GCTCTAGTCA GCAAAGTCTT GGTGTTGTAG GATACAGGTG      300
TCTTCATGCA TTCCATTTTA TACTCGAG                                328

```

(2) INFORMATION FOR SEQ ID NO:522:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 313 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

```

GAATTCGGCC TTCATGGCCT AGAAAAAGAA AAAGTAGCTG ATGAAGATGA TGTGGACAAT      60
GAGGAGGCTG CACTGCTGCA TGAAGAGGCT ACCATGACTA TTGAAGAGCT GCTGACACGC      120
TACGGGCAGA ACTGTACAA GGGCCCTCCC CACAGCAAAT CTGGAGGTGG GACAGGCGAG      180
GAACCAGGGT CCCAGGGCCT CAATGGGGAG GCAGGACCTG AGGACTCAAC TAGGGAAACT      240
CCTTCACAAG AAAATGGCCC CACAGCCAAG GCCTACACAG GCTTTTCCTC CAACTCGGAA      300
CGTGGAATC GAG                                313

```

(2) INFORMATION FOR SEQ ID NO:523:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

```

GAATTCGGCT TCATGGCCTA GCGTTGTGTG CATGCGAGCG CTCCTGCAGG CGTGTGCATG      60
GGGCCAGGTG TGCACGTGGA TGCCCGGGTG AGTGTGTGTG CATGCACGTG TGTGCACGCA      120

```

```

TGTGCACATG CCTCCAGCCC CACCTTCCAA CCCCTCAGTG CCCCCAGGAC AGGGGCCCCCT    180
CTTAGCTATC AGGGTATGGC CGGACCGGCC CTTCTGCCCC AGCANGTTGC AAGCACTTGG    240
CCAGGCCGGC CCTCCAGGNT GCTGCTGCGT GGGGGCCCCG GTGCCCCCAG GTCCATGCAG    300
ACTGGGGATT CGGTGGGGAG GGGCGCTTCT AAGGAACCAA ACTGACGCTC ACTCTGGGCT    360
TCCCAAGCAC CCTTAGCACG GAGCCACCC CTAGCTCGAG                                400

```

(2) INFORMATION FOR SEQ ID NO:524:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

```

GAATTCGGCC TTCATGGCCT ACCCACCCTG TAGTCAACCC CACTCGTACT GTAGCGAGAC    60
AAAAACATGC CATTGTGAAG AAGGGTACAC TGAAGTCATG TCTTCTAACA GCACCCTTGA    120
GCAATGCACA CTTATCCCCG TGGTGGTATT ACCCACCATG GAGGACAAA GAGGAGATGT    180
GAAAACCACT CGGGCTGTAC ATCCAACCCA ACCCTCCAGT AACCCAGCAG GACGGGGAAG    240
GACCTGGTTT CTACAGCCAT TTGGGCCAGA TGGGAGACTA AAGACCTGGG TTTACGGTGT    300
AGCAGCTGGG GCATTGTGT TACTCATCTT TATTGTCTCC ATGATTTATC TAGCTTGCAA    360
AAAGCCAAAG AAACCCCCCT GCCTCGAG                                388

```

(2) INFORMATION FOR SEQ ID NO:525:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

```

GAATTCGGCC AAAGAGGCCT AATTGAATTC TAGACCTGCG TCGACCGAAC CGAGTTGTAC    60
ATTTTTTTTG TGATGGGTTA TTTTATTATT TAATTATTAT TGTGTGTTTG GTTTTTTTTT    120
GGTTGGTTTT NGATTTATGA CAATNCCACT CTTGGCCCCA GTGTGCTGCC TGTCACCTCC    180
TCCCCTGTCC ATCACCTGG CTCCAGACC AGGCTCAGCA ACACATTGAG TCTTGGGTTC    240
CAGGAACCTT GCCAACCTCA ACCCTCCAGC CCGTGCTCCA CTGGCTATGG CTCAGACCAA    300
GGGCTCCTCC TCTCCNTCT TGCCCTATGG AACAGCCCCG GTGCTCCAAG GGGGCCAGGA    360
GGGCATGGCT TGGCTCCCAA GATAAGGGGT CCGGGGCCAG GACACCCAGG CAAGGTGGCC    420
CCTCCCTGCC TAGCCCCCTT CCCCCACCC AAAGTCGAG                                459

```

(2) INFORMATION FOR SEQ ID NO:526:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

```

GAATTCGGCC TTCATGGCCT ACAACCTGGA AAATTCTCTG ACTTAGAAAT TTAACAAAA    60
CCTCCCTTT TCATTGAATC TCCATTGTCT GGAGTTTGCT TGTTTAAATC TAGCCTGTTT    120
CTCCACTATG GGCTCCCTTT CAAACTATGC CCTGCTTCAA CTAACCCTTA CTGCTTTTTT    180
GACAATTCTA GTACAACCTC AGCACCTGCT TGCTCCAGTT TTCCGGACAC TATCTATCTT    240
GACTAATCAG TCTAATTGCT GGTATGTGA ACATCTAGAT AATGCAGAAC AACCCGAACA    300
CCTCGAG                                           307

```

(2) INFORMATION FOR SEQ ID NO:527:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

```

GAATTCGGCC TTCATGGCCT ACCAATACTA AGCTTATTTT ATTGTAATAC AGTTATTTGT    60
ACCACTTAG AGCAATCTTT TGAAGAACAA GAAACACATA TTGAGCCACC ACGCCCAGCC    120
TTTTTTCAGT TTATTTTAA TCTTTTGCTG TTCATTGGCT CATTCTGTGT ATAAGCATGT    180
TAAATTTACC CAAATATGAA AATAGCCTCC CCTTGGCCCT GAACTCCTCT ACAAGCAACT    240
ACCTCATGAT TTTATCTCTT TATCCTCAA TTCTTTGGAA TATAATTTAT ACTTGTTTCA    300
TCCCTACCAC CCTCGAG                                           317

```

(2) INFORMATION FOR SEQ ID NO:528:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 405 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

```

GAATTCGGCC TTCATGGCCT ACAGCAGTGT GCTTTCATCC AGTTTGCCAC ACGGCAGGCT    60
GCAGAAGTGG CTGTGAGAAG TCCTTTAATA AGTNGATTGT AAATGGCCGC AGACTGTATG    120
TGAAATGGGG AAGATCCCAG GCAGCCAGAG GAAAAGAAAA AGAGAAGGAT GGNACTACAG    180
ACTCTGGGAT CAAACTAGAA CCTGTTCCAG GATTGCCAGG AGCTCTTCCT CTCCTCCTG    240
CAGCAGAAGA AGAAGCCTCT GCCAACTACT TCAACTTGCC CCCAAGTGGT CCTCCAGCTG    300
TGGTGAACAT TGATNTGCCA CCGCCCCNTG GCATTGCTNC ACCCCCACCC CCAGNTTTTG    360
GGCCACACAT GTNCAACCA ATGGGACCAC CCCCTNNNAC TCGAG                                           405

```

(2) INFORMATION FOR SEQ ID NO:529:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 283 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

```

GAATTCGGCC TTCATGGCCT AAGAAACCAA ATTAGCAGAC GGATAGAATA TAAAGCAAGA    60

```

GGCAATACTT ATAGTGTATT AAGAACTTG CTAGACCCCA TCCAAATTAC TCAGTCTACT	120
GTGGTTGAT AGAATTACTT TAGGAAGAGT ACGTTTTTGC CTTGGAAATA CACTGGAAGT	180
GGTACCAAAC AAATCTAATA AAATGATGTT AAAGAGATTT GCAGTAATTT TTATCAACTT	240
TCAGTTTGCA AACTTTTATA AAGATATGAA CGGGACACTC GAG	283

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

GAATTCGGCC TTCATGGCCT TTCTATAAAT GAGTCTTTA TAAGAAGCTT GTATCATTCT	60
CACAAATTAA AAATAATAAT ATTTTAGCAA GCTATTTTTT AAATATAATT TAAGCCCACA	120
CTTCCACATT TGGGGTAAGT GATAATTTTT TCCTCTGAAA GACAACAAAT ACTAACACAG	180
GCCCAGACTT GGCTTTTGTG AGTCAATTAG TGATCCGAAG GTGAGTGGTA TTTAAACGTA	240
TGATGAGGGT AAGATTGAT TTATTTTACA TATATATCTT CTGGTATCTG TGTGTGTGTG	300
TGTGTGGTGT GAAGCTCGAG	320

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

GAATTCGGCT TCATGGCTTG GGGGTGACAG TTAATATATN CGGTCATTTT AGATTGCTTC	60
CACTAATATT GGTATTATCCA TATTATAAAA TATTTTAGTG AGTATAAAAT TGCTGCATT	120
CATAAAGATG CATAAAATTA ACTACAGAAC CAGCTTGAGT AATGCTTTTC TCTTCTTTTC	180
TTCTTGTCAA TCAGATATTA TCTTTATACA TTGTTTAGA GTATACATCT ATCAAAATGC	240
AACATTGTTG AAGGATATGT AATTTATACA GCAAACGTGT AATGGATAAA AATGTGCAAA	300
AACAATCCTT AAAGTATTGT ATTTGAACNA AAACAATCTT AAACCACATA ATCTGAAAAA	360
AAGGGGTACA TATTTTACCA AATATACTAA TCCATACAAG ACTGCTTGAG AAAAAGAATA	420
TGCCACCTAC TCGAG	435

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GAATTCGGCC TTCATGGCCT AAGCCATCAG ATTGAAATTA ATTTAGACAG GAAGAATCTA	60
TATAAATTTG ATGCATAGCA AACTCTGACA TAATTTGGTT TATTTTGAAG TCTGGCATAT	120

TTTTCATCAC	TTTTTATTTT	ACGGGTAAAT	CATAATATAT	CATATTTTCA	ATAAAAGTAT	180
TTTCTTAAAA	ATCTGCCATT	TGCTTCACAG	ATTTTAAATC	TTCTAACAGA	AAAAGAAGTA	240
AATATTGTTT	TGCCAACACA	GTCCATTGTT	CCAAGAAGTT	TTGTGCTTAA	ACCAGGAATG	300
GTCTGTGTTT	TGGGTGCTAT	AGGCCGCATA	GCCCTCGAG			339

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

GAATTCGGCC	TTCATGGCCT	AATGTGCTCC	AGGAGGCGCT	GGGGGATGGT	GACCTCCCAA	60
GGCGGGCAGA	NGACTTCTGC	CGTCAGGGTC	GCCTGCTGCT	GAGCCTGGGG	GATGAGGCGG	120
CGGCCGCAGG	GTCTGGATCC	CCTGTGCCGT	CGCCTCTTCC	TTTTTCGACG	CCTCCGCCGC	180
CGCCTGAGGA	GGCGAGCTAG	CCGGGAGTTA	CACCGCCACC	GCCAGGATGG	ATAGAATGAC	240
AGAAGATGCT	CTTCGCTTGA	ATCTGTTGAA	GCGGAGCTTG	GACCCAGCAG	ATGAGCGAGA	300
TGATGTCCTG	GCAAAGCGAC	TCAAATGGA	GGGGCATGAG	GCCATGGAAC	GTCTGAAAAT	360
GTTGGCATTG	CTCNAAGGA	AGGANTTGGC	AAATCTTGAG	GTGCCACATG	ANTTACCCAC	420
CNAACAGGAT	GGCAGTGGTG	TCAAGGGCCA	TGAAGAAAAA	CTTAACGGGA	ACAACCTCGAG	480

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

GAATTCGGCC	TTCATGGCCT	ATATGTATTT	TTAATCTATG	ATGGTTTATG	TGAATAGGAT	60
TTTCTCAGTT	GTCAGCCTGG	GCGACAGAGC	GATACTCCAT	CTAAAAA	GNAAAAAA	120
GAGGTGACTA	GGCCATGAAG	GCTCTGTCCT	CACAGATGGA	TTAATGCCAT	TGTTGTGGGA	180
GTGGTTTTCT	CATTGAAGGA	TGAGCTTGAG	CTTGGCCCCC	TTCTTCTCC	CGCCTCATTC	240
CCCTCTATGT	NGCCCCCTATG	ATGCCTAANG	CCATGTTATG	ATGTGGCAAA	AAGGCCCTCG	300
CCAGATGCCA	GCCCCCTGAC	CNTGGAATTC	CCAGCATCNA	GAACTGTGGA	CCNAATGNAT	360
GTTTTTTCCT	TATAAANTAA	CCNGCCACNG	GTATTTTGT	AAAGCNGCAC	CNAGCAGACT	420
CGAG						424

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

GAATTCGGCC TTCATGGCCT ACGTTGACTT AATCAGAGGG TCAACATTTG CCAAAGCAAA	60
ACCTGAAATT CCATGGACAT CTCTGACTCG GAAGGGGCTT GTTCGAGTTG TATTTTTC	120
ATTGTTCAGC AATTGGTGA TTCAGTTAC CTCTTAAGA ATCTTTGTTT GGCTGTTACT	180
ACTTTATTTT ATGCAAGTTA TAGCAATTGT CTTATATTG ATGATGCCTA TTGTGAACAT	240
AAGTGAAGTA CTTGGACCCT TGTGCCTTAT GCTACTCATG GGAAGTGTCC ACTGTCNAAT	300
TGTGTCTACT CAGATAACAA GACNTCAGG AAACCTCGAG	340

(2) INFORMATION FOR SEQ ID NO:536:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 446 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

GAATTCGGCC TTCATGGCCT AGGCGCTCGC TGAGGCAAAA GGAGGCGCTC GGCCCGCGGC	60
CTGACAGGGA CTTAGCCCGC AGAGATCGAC CCGCGCGCGC TGACCCACA CCCACCACT	120
CATCCACTTA TCCACTCCCT GCGCGCCTC CTCCCACCCT GAGCAGAGCC GCGGAGGATG	180
ATAAACACCC AGGACAGTAT TTTGCCTTTG AGTAACTGTC CCCAGCTCCA GTGCTGCAGG	240
CACATTGTTC CAGGGCCTCT GTGGTGCTCC TGATGCCCT CACCACTGT CGAAGATCCC	300
CGGTGGGCGA GGGGGCGGCA GGGATCCTTC TCTCTAGCT CTAATATATA AGGACGAGAA	360
GCTCACTGTG ACCCAGGACC TCCCTGTGAA TGATGGAAAA CCTCACATCG TCCACTTCCA	420
GTATGAGGTC ACCGAGGGTA CTCGAG	446

(2) INFORMATION FOR SEQ ID NO:537:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

GGCAAATTAC ATCACCAAT CAGCATATTC TCCACTGGAA AGGAGAGGCC CACATAGCCA	60
AATTATAATC TGCAGGTTTC TGAGCCAGTG TTAAATCTGA ACAGAGAAAA GATTTTTTTT	120
TCAATTGGCA AATTTTAATG ACATCACTCA TTGATACCCC AAAATCTCCA GTTCTTACCA	180
AGCTTGGCCT TGCCAGTGG TTCCTCTGTT CCCTCAACAA TGTTTCATGG NATCTAACAA	240
CTTCCCTACC CACTAACCTT CTCAGCTTTC ATGGTGAACC AAGCCTCCTC TGTCGCACTA	300
ACCTTCCCAG CTTTCATGGT GAACCAAGCC TCCTCTGTCC CGCTATTCTC GAG	353

(2) INFORMATION FOR SEQ ID NO:538:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

GAATTCGGCC TTCATGGCCT AAGAAGGAGN AGCAAGCGGA TTTCAGAGAG GTTGTCTTTC	60
AGAAAAAAT GGTATTCTTCT TTGAACTCAT GCCTGAGCTT TATTTGTTTA TTGTTATGCC	120
ACTGGATTGG GACAGCATCA CCTCTGAATC TTGAAGACCC TAATGTGTGT AGCCACTGGG	180
AAAGCTACTC AGTGACTGTG CAAGAGTCAT ACCCAGATCC CTTACTCGAG	230

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

GNGAACCAGA GATCCCCATA GATGGAACAG AATTATCCCA CTACCGTCAG CGTGCCCTCC	60
TGCAATCACA GCCAGTTGCG CGGACGCCTC TCCTCCACAA TTTCCTGCAC ATGCTGTCCT	120
CCCGCTCTTC TGGCATCCAG GTGGGAGAGC AAAGCACAGT GCAAGATTCT GNTACCCCTC	180
CACCCCCACC GCCTCCCCCT CAGCCCTCCA CGGAGCGCCC CAGGACTTCC GCTTACATCA	240
GGCTCCGACA GCGGGTCAGT TACCCACAG CTGAGTGCTG CCAGCACCTT GGGATCCTGT	300
GCCTTTGCAG CCGCTGCTCT GGCCTCGAG	330

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

GAATTCGGCC TTCATGGCCT ACTCCGACTT TCGTCTTGA TTAATGAAAA CATTCTTGGC	60
AAATGCTTTC GCTCTGGTCC GTCTTGCGCC GGTCCAAGAA TTTCACCTAG TTACCCTCTA	120
GAATTATTGC ATTGGGGCCA GGTGGTGTCT AGTACAGTTT TTTACTTTGG AGAATTTATT	180
GAAATTTTCT TTGGCTGAGA ATGCCCTCAG TGTTTGTGGT TATTCCTTGG ATACTTGCAA	240
ATCGATTGTA TTTTCTCTGG GACACGGGGT TTCAGATAGA TCAGTTAAAT GAAGCTTGAT	300
TATATCGTAT TTCACGTGCG ATGCCATGTG TCTTGTCTGT TGGACTGTCA GGTCTCAAGA	360
GACGGGCTTG GGTTCCTCTG TGTGGCTGCT GCCTTGCCCC TTCCCGGATC CACACTCGAG	420

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

GTGGGCAAAG AAATGAAGTA CATTAAAGGAG GCCTTTTTTT TCCTCCAATG GCTGTTAGAT	60
TGTGTATTGC AACCAGGAGT TGTCAAGCTC CTGATCCTAA TCCAAGCTGG GGACTGTGGT	120
ACAGTGTGGC CAGCTGCCTT GCCAGCTGCC TTACCAGGCA GGTCTGCGAT CTGCCATTGT	180

CATCCCATG	GAATCAAGTT	GCAAGCCAGT	GAACCTGCTG	GGGTGTGCCC	AGGTCAGAAC	240
AGTTACAGCT	TAAAAGCCTT	TGCTGCCCTT	TTTCAGATCC	TGTTCTGGG	AGAGTCTCCC	300
ACACTAAGTT	CAGTGTGGT	ACCAGCTGTG	GTGAGGGTGT	GCTGCCACTG	CAGCTGCTGT	360
CTGGGCATCT	GTGTTAGGGC	CAATACTTCA	AGAAGTGTGA	GTCATTGTGA	AGTGACTGTA	420
GGCAGCTGGG	AAATAACAGC	TGTGAACAGA	GAACAACCTG	AG		462

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

GAATTCGGCC	TTCATGGCCT	ATGGGAGATA	GGGGACTTAA	TTATTTTGTG	GGTTTTTTCT	60
TTTTTAGGTC	TTAGGAAGGT	CTTTGTTCCA	TAGGTATCTG	TATAATACAA	TTTTATTAGG	120
TGTAATAGAG	ACAGTTTGT	GGAAACAGAA	TGCTGACACT	GATTAAAATT	AAGGTGTATA	180
TATGTTTAGT	CTTTGAGATG	ATCTGTATGC	TACATGTAGG	TGTACATTGT	AATTTTCTGG	240
CTTGTAATTT	TTTGTATCAT	ACTCTGTTTC	GGGAATTTGC	AAATGCCTAT	GACCAGCCTA	300
TGACATCTGA	ACCATACCAA	CTGACCTTAG	AAACAACGAC	ACTCGAG		347

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

GAATTCGGCC	GCCTAGCAAA	AGTGAAAAA	TAAATAAAAC	AAGCCACAGA	TTGGGACAAA	60
ATATTTGTGA	AGGATATATC	TGATTAAGAA	GTTATATCCA	GAATATATGA	AGAAGTTTCA	120
AAACTAAAGA	AAACAATTCA	TTTTTTTAAT	TGGGCAAAAG	ATTTAAACAA	ATATTTTACT	180
AAAGAAGATA	TCCAGATAGC	AAATAAACAC	ATGATATTCA	CCGAAATTAT	TAATTAGGAA	240
AATGCAAATT	AAGATGAATA	TCATTATATA	CCTACTAGAA	TGGCTATATT	TTAAAAGTTT	300
GACACTGCCA	ATTACTGGTA	AAGATGCAAA	TCAGCGGAAG	CTCGAG		346

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GAATTCGGCC	TTCATGGCCT	ACTTCTTCC	TACATTAGTG	GCATACTCTG	AATGACCTAG	60
TGAACAGACT	GAGAAGAGGC	CTCTGAATTG	CAGAGTCTCG	TCTGTAGGAG	AAGGTTTCAGG	120
AGAGTATTGA	ATTTTAGGGA	CTAGAATCCA	TCTTACCTAT	GCTGTTGCAA	TCCCATGCTG	180

```

ACTGGAAGTG TGGGAAAGAG ACTTACAAGT AAGGACATGG GTTTGTTTTG TTTTGTGTTT 240
TTTGTGACAG AGTGAGACCC TGTCTCGNAA AAGGAAAAAA AGTAATAGAA CATTAAATAC 300
AGTATCACAC CATTATGGT TAAAAAAGNA AAAAGACAAG AACTATATG AAGTGAGTGT 360
CTTTTAAAGT TAAAAAATT AAATGAAAAC AAATCGAG 399

```

(2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

```

GAATTCGGCC GCCTCCATCT CCCTGGCCAT GTTCTTCTTG AAGACCCTGA CAGTGGCTTC 60
TCTTTGTGG CAGCTGGCCA ACAGCCAGAC CCTGACAGCC AGCCCCAAG CACCTGGGTC 120
CCCAGAGGAT TCTGAGGGTG TCCCCCTCAT CAGCCTGCC CGCGTGCCAC AGGGAGGGAG 180
TCAGCCTGGG CCCAGCCGGG GATTAAGTCT CATGTCCAGT CAGGGCAGTG TGGACTCAGA 240
CCACCTAGGT TATGATGGTG GCAGCAGTGG CTCAGACAGT GAGGGTCCCA ATGACACCCT 300
TGGTGAGAAG GCCCCCTTCA CATTGCGGAC TCCACCTGGG CCAGCACCTC CACAGACTTC 360
ACTCGAG 367

```

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

```

GAATTCGGCC AAAGAGGCCT AACCGCGGNC GCTCTACAAC TAGTGATCC CCCGGGCTGC 60
AGGAATTCGA TATCAAGCTT AATTAAGAAT TCGGCCAAAG AGGCCTAAGC GAGAAGAGTC 120
CCCGCTCCGT GCCCTACCAC TACTTTGAGA AGGGCCGGCT AGATGAGTGT CAGATGTACC 180
GTTTGCATGA GCAGGCTCCA AGGAGCGCCC ATCGCTTCAT TACCGAGAAC CCTGTGTTCT 240
CCCGCTGGGC CAAGAAGCGA CCCATCGTGT TCGCCACCC GTCCTGGAGG GCCAAGTAGT 300
TCCTGTTGCC AGTGAAGTCC AGGCCTCAGC CAGGCCTGTG ACCCATTCCA GGCCAACACG 360
GCTCTAATGT GAGCATTTAT GACTCACCTT CTACCTGACA CCAGGTAGAA CATGAAGTCT 420
CTATTACCCA AACTGGGTA CACTCGGAGG TCGAG 455

```

(2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

```

GAATTCGGCC TTCATGGCCT AGTCATTTTG TCAGCTTTCA CACAAGAATC TTTGATCCTA 60

```

TTGTAATAGT TAATAAGGAA GTTCTTCTCT TGCTCAAAGA AGTCATCTAC CTCCTTAACT	120
CCAGTAAAAA GGACTTCATC AGCACTTTTC ACCACACTTT TGAAGAAGCC ACCAAACATT	180
TCTTTAGTAT TTTTCCGCCT AACACTTAGA TCCTGATCAT ATTCCAGGAA AACATGAAAG	240
TTGCGATCTT TACTGAGAAC AGGGTGAGAA GAAAGCCGCT GAAGAAAGAC TTCATGGGAG	300
GACACAGTCT TCTTAAACAC AGCGAGATAC TCAGCTTCCA GTTCTTGTTT CATCTGGGCT	360
TATTATTCCA CTTTCTCCCA GTTCTGTCAT CTTCTCTCGA G	401

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GAATTCGGCC TTCATGGCCT ACAAGCCCCT CTTACCTCTC TGGATGCTTT CTTTAACT	60
AACTCACCAC TGTGCTTCCC TGCAGACACC CAGAGCTCAG GACTGGGCAA GGCCAGGGA	120
TTCTCACCCC TTCCCAGCT GGGAGGAGCT TGCCTGCCTG GCCACAGACA GTGTATCTTC	180
TAATTGGCTA AGTGGGCCTT GCCCAGAGTC CAGCTGTGTG GCTTTTATCA TGCATGACAA	240
ACCCCTGGCT TTCCTGCCAG ATGGTAGGAC ATGGACCTTG ACCTGGGAAA GCCATTACTC	300
TTGTGTCTGC TACTGCCCTC CCACAGTCAC CCAATATTA CAAGCACTGC CCCATTGGCT	360
CGAG	364

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

GAATTCGGCC AAAGAGGCCT ATGCTTTTCT TTGCAGCACT TAGCACAAAT AGTAATTTT	60
ATTTTACTTT TATAGATGTA TTTTATGTCC CTCCACCAGA CTGTATACTC CATGAGGACA	120
AGGATATTGA TGTTTATGTT AACTCTTGTA CACTCAGTGC CTGGCACCAT GCCTGACCCA	180
GAAGAGGGAC TCGAG	195

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

GAATTCGGCC AAAGAGGCCT AACATAATGC GCTAGCAGAC TTGGGAATTA GGGGCAGAAT	60
GCTGCTCTAA ATTCAGGAAA TCATGGCAGG GTTTCATATT GAACATGGTC TATTCCTACC	120
ACTAGCGCTT TCCTGGCTGA TTTCTTCTCC AGCTGGAGAC TTCTTTCTGG TTTTCCAATT	180

TATGCTCCAC	CCTCACCCCA	ACCCACCCAT	AAACCAGTGG	CTGCCGGAAG	CAGTATCTTT	240
CATAGTGGTG	AGTTCTGGAT	TTTCAGCAGT	AATGGCCGAG	AGTCAGGGAC	CAGATGAGTG	300
TGTGTGAGCT	GGTGAGAAAA	GGTAGATTCC	CTCGA			335

(2) INFORMATION FOR SEQ ID NO:551:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 662 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

GCCAAACATG	TCTCACCNA	NNCCAAATGT	CCCCNGGGG	AGCAAAATCT	CCCCTGGACA	60
ACTGTGGAAT	CACTGTNNGG	AAGTGTTTAC	TTGAGTGGTT	TNCTGGCCTG	GGCCTCATAC	120
TCTGAATTTT	TGAAGTAAAT	GGTCTGGGGG	TGCTGGGGGT	GGAGAGCAGA	GCACTGGTAT	180
TTTTAGGAGA	TCCCCCTGTC	ATTCTAAAGC	ATATCCAGGG	TTAAGCACCA	TTAATCTGAN	240
GATCTNCNGT	CTGATCTGCG	GGCCCCCTTT	CATCTANGTG	CAGTATTTT	CTCTATGCTT	300
TTTAAAATAA	TGAAAGTTTC	TNGAACTCCA	TCTGGACTTG	AAATATAGCC	TGCCACACAG	360
TTAGCAAATA	TAGCAAGAAT	AACAAGTGTT	CTAAATGGAT	TTTTAATTTA	TTATGGCAAT	420
AGTACATTCC	AANAGGGTGG	CATTTTTTAA	AATGAGATTT	TTCTTTTGGG	CCTAAGATTA	480
CAGTCACATG	GTTCCAAATT	CAGAGGGTTC	AAAAGGACAC	AGAAAAGCCT	GCTTCCCACT	540
TGNGCCCACT	GGCCTCCCT	TTTTTCGCAT	AAATGGCAGT	ATATAGCTTT	GTCTGTTCTT	600
TGTTTNNNGA	GCTTAATACC	TTAGAGACAG	ATTTTNGTAT	ATCTGTACCT	ACAGAACTCG	660
AG						662

(2) INFORMATION FOR SEQ ID NO:552:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

GCTGTTTTAA	AAGAGTTGGG	GGAAGAGGTA	GAAATGAATC	TTTTGGTTTA	GTTTTTTAAT	60
TCTCTAAGGA	CAACATTGGG	GAAGTGAGCT	TTAGAGTTAT	ATTTGCAGTA	TTTATTTTTA	120
TCATGAAATA	TTCAAGTCTA	GGCCCTTGGT	GAAATTGAGG	CTGGTGAGTA	TTTCTGCTTT	180
CCCCCTGGAG	AGATTGAGAT	GTTTCTGAT	TGGGAGCTTT	AATTCTGTGG	GCATTGTGTT	240
GACTTACCAA	AGAGGTATCT	AGAGTTCCTT	TAAAACCCCC	GCCCTGTCCC	TGCCACAAAA	300
CTCGAG						306

(2) INFORMATION FOR SEQ ID NO:553:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

GTCAAAAGAG GAGCTAGGAC CAGATCTCTA AGTCTTACNG TCCAGGTCAA AAAACAAGTA	60
CTTTCCTATC TGGTTATACA GAAATCTGGA AACAGTCACT CCCAGCCTCA CAATTAAAAA	120
AACTTGGACA TACAGAAAGT TCATAGTTT CTTGAACTC ATGATAGTGC TGAGATTTCA	180
CGGCAACCAA CTGGCCGAGA TACTCCAGAG TCAAAGACAC TGTAAGGAGA GTTGACATNT	240
GAGCATTAGA CAAGACACAG ATGGTANGAG TTAAGCTAGG GTTACTCGAG	290

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

GAATTCGGCC TTCATGGCCT ACTCTATGGG GATGAGGTAG AGGAGAGCAA GATATTTCCG	60
CAGCAGGGAA AAGGGTAGAA CAGAATAGGG TGACACAATT TACACTTGAT ACTGCATTAA	120
CATCTGGTAG AGTGTCTAGG GCAAAGGTTA GCCAAAATAT AGCTGGATGG TTGAGGGATT	180
TAGAAGGAGT TGGGTGAAT CCATAGTCTC AATGAATGGA GAAAAAGTAA CTCAGGAAAG	240
TAAATGCTGG TGAATTATCA GCGGGTGGCT GGTGATGTTT GGTTTGATT GTGAAAGCTG	300
CTTAGACCAA GATGGGCTGA GGGAAGGGGA GGAGAGTGAG CATGTAGAGG TTGAGGCACT	360
TGGTCTCGAG	370

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

GAATTCGGCC AAAGAGGCCT AATTGCCAAT CAACAACTTT TCCTAATCCA CCTTGATCCT	60
CAATCATAAT ACTCAAAAAC TGCCAAAAAC AAAATCTTCC TGACAAAAT ACAGGCCCAA	120
CTTCCTCATC TGCTTCCAG GTCTTCTGTA ATCTTATCCC AGCTTATTTA CAGTCCTCCA	180
TTTACTAAGA AAACCCAAA TAATCTTTTC CTGCCCAA TTCAATGTTCT TCCTTTCTCT	240
TTTGTTTATA CTACCATACA TATCTAGAAA TGATACTCAA ATATTCATCC TCAGCACCT	300
CGAG	304

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

GAATTCGGCC TTCATGGCCT AGAGGGGAAA GCATATCACT AGGACTGTGA CCCCTGTGCC	60
TACCCATCTT ACTCTCTACC TCTAGGAAA GTTCACTGT GTTACTTGG GACTTCTGGA	120

CTAGCTGCCG TTTGCAACAG TGGACTTACC AGTTTGCCAC TACTCTGCTA CCTTTCTACT 180
 GGTGCACACA CCTTAGTAAG GCAGTTTGAT TACTAAATGC AGCTGTCTCC AGAAATGGAA 240
 TGATGCTATA GGCCACTTAC TAAATGAATG ATCAGGAGTC TCGAG 285

(2) INFORMATION FOR SEQ ID NO:557:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 409 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GAATTCGGCC TTCATGGCCT AGCTGGATCT GCCCACTGTG CACTCCATCA TCAGCAAAAT 60
 GATCATTAAAT GAGGAGCTGA TGGCCTCCCT GGACCAGCCA ACACAGACAG TGGTGATGCA 120
 CGCACTGAG CCCACTGCCC AGCAGAACCT GGCTCTGCAG CTGGCCGAGA AGCTGGGCAG 180
 CCTGGTGGAG AACAAACGAAC GGGTGTGTTGA CCACAAGCAG GGCACCTACG GGGGCTACTT 240
 CCGAGACCAG AAGGACGGCT ACCGCAAAAA CGAGGGCTAC ATGCGCCGCG GTGGCTACCG 300
 CCAGCAGCAG TCTCAGACGG CTTACTGAGC TCTCCACTCT GTTCCCGCC TGGGCCATCC 360
 AACCTGAAG TCCTAAACCA CACCTCAGTC ACTAAAGGTC TGTCTCGAG 409

(2) INFORMATION FOR SEQ ID NO:558:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

GAATTCGGCC TTCATGGCCT AGGAAAAAGA GATATAAAAA AAAGAAAAAG AGGNGGTACC 60
 AGCCAACAGG AAGACCACGG GGAAGACCAG AAGGAAGGAG AAATCCTATA TACTCACTAA 120
 TAGATAAGAA GAAACAATTT AGAAGCAGAG GATCTGGCTT CCCATTTTGA GAATCAGAGA 180
 ATGAAAAAAA CGCACCTTGG AGAAAAATTT TAACGTTTGA GCAAGCTGTT GCAAGAGGAT 240
 TTTTAACTA TATTGAAAAA CTGAAGTATG AACACCACCG TCTCGAG 287

(2) INFORMATION FOR SEQ ID NO:559:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GAATTCGGCC TTCATGGCCT ACTTCTCAAA AATAGATGTA CTTGACTACT CTTTCTTGA 60
 TTCTTCTGGG AGTAACCATC TCTTTGGAGA TGGTTGTTAG TAAGGTTATA AAAATAACCT 120
 TACTGAGGAA CTCCCATGCA ATCCTCTGAA AATAATAAAA ATTTCCTTAT TTCAAGAACT 180
 CTTATTTAAC AAAGTAATTG TTAGGGTTGA ATACTCTAGG GGCAAATGAT TTATTGTGCC 240
 TTTTGTAAAA GTCAACACTT GGCAGGTGTG TGTTTGACAC TGGCTGATGC TGGGCTTATT 300

TCTCTAAGAG TATGGTAATT CTAGTAAAGT AAAGAAAATT GTTTATCAGA TATTAGGAAC 360
TGTACATAGG CCCCCTCGAG 380

(2) INFORMATION FOR SEQ ID NO:560:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

GAATTCGGCC TTCATGGCCT AAAATTGTTC ACGAGGGATT ACGTGGTTTA CTGTCTGTT 60
GTCCAGATAG CTTTATATTC TTTAAGATTC AGCTCGGATT CTTATCCTAT TTTTGCCATT 120
AACTTTCATT ATGATTTTGG CAAAGCCATT TTGTTTGCTT ACATTTTCA CTTTAAATGT 180
GGTGTCTGGC CTCCTCCCCA CACTCGAG 208

(2) INFORMATION FOR SEQ ID NO:561:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

GAATTCGGCC TTCATGGCCT ACAAACANTT TTTACTGNGT TATAAATAAA AACAGCGACA 60
CATCCTAAAT GTGCACCTGT GCCGTGGCTG AGCCGCTGCA GTGAGGGCTA GTGTGCAACA 120
CCGATGCTGT GCTGGACGCG TGCCAGCCG GGTCCCCTGA CAGGAGGCAN CCGGGGCCGG 180
TGCGTGTGTT TGCATGTTGC AGTCATGGGG CGGGGNCGGC AGANGCCTGT GTGATNGTNG 240
CGTCCCTGGA AAAAGAAGNN GGGNAGGCC CTCNCACNTG TANCCAGCC TGCAGANGGG 300
GNGTTNTGTG GGTCTTCCC CGTGCATATG CGTGTGATNT CACCCATCCC GTGTGGGTGC 360
GCAGGAGGGG CCGAGGGAGG AGGGTGCTGG AGGGCGGAAG TTACCTCTGA CTGGAGGAGA 420
NACCCGGCCC GTGTNACCAG CANAGGTGTG NTCGTTCTAA AACTGGGAAA AATTTGTTCT 480
TAATTTTAAAC CACAGTCCCC TCGAG 505

(2) INFORMATION FOR SEQ ID NO:562:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

GAATTCGGCC TTCATTTAAA AGATAAGTTA GAAAAGTCAA AGCGAGAACG GCATAACGAG 60
ATGGAGGAGG CAGTAGGTAC AATAAAGAT AAATACGAAC GAGAAAGAGC GATGCTGTTT 120
GATGAAAACA AGAAGCTAAC TGCTGAAAAT GAAAAGCTCT GTTCCTTTGT GGATAAACTC 180
ACAGCTCAAA ATAGACAGCT GGAGGATGAG CTGCAGGATC TGGCAGCCAA GAAGGAGTCA 240
GTGGCCCACT GGGAAGCTCA GATTGCGGAA ATCATTTCAGT GGGTCAGTGA CGAGAAAGAT 300

GCCCCGGGTT ACCTTCAAGC TCTTGCTTCC NAGATGACCG AAGAGCTCGA G

351

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GAATTCGGCC TTCATGGCCT AAAAACTGT CCATGGCATG AAAGACTTGG ACCGCCATCT	60
CAGAATCCAC ACGGGAGACA AACCGCACAA GTGTGAGTTC TGTGACAAGT GCTTCAGCCG	120
GAAGGACAAC CTGACCATGC ACATGCGGTG CCACACCAGT GTGAAGCCAC ACAAGTGTCA	180
CCTGTGTGAC TACGCTGCCG TGGACAGCAG TAGCCTCAAG AAGCACCTGC GGATCCACTC	240
TGATGAGCGG CCGTACAAAT GCCAGCTCTG CCCCTATGCC AGCCGCAACT CCAGCCAGCT	300
CACCGTCCAC CTGCGATCTC ACACGGGTGA GTCCCTGACC AGGGGTCCTC GAG	353

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

GAATTCGGCC TTCATGGCCT ATAGAAATCC TAGACTTTAC AGACTAATAG TTTGACATCT	60
ATCTCTGGCA AAATTCGAAA CTTAAACATT AAACAAGGGA AAATGAGGGG TGGAGGNAAA	120
GACTGCGGAT TTCTAGGAAC TAACAATTTG CTAAGNATCA TTCATTTTAA AACTAATGTT	180
ATTTACTTTT GTGGTAGATC AGGGNATATG CAAGATCTTT ACTTTTCAGC AAGACATTTT	240
TCTCATAATG TCCTTATGGA GAAGACTGCT CTATGGACTA GNATAGTTTG ATAAGAAAGG	300
GCTGAGTCCA GCGNATTCAT TAGTTCAAGC AAAATCTACT GGAGGCCAAC TAGATTTCCT	360
GCCATTATCG TACTTGGCAC TTTCNATACT TTGAATTTTA ACCACCACAC CTCGAG	416

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

GAATTCGCCC TTCATGGCCT AAGACGGGGT TTCACCATGT TAGCCAGGAT GGTCTCGATC	60
TCCTGACCTC GTGATCCTCC CGCCTCAGCC TTCCGAAGTG CTGGGATTAC AGGCGTGAAC	120
CACCACGCCC AGCCATATAT CAGGAACTTG AGCATCCATG GAGTTTGGTG TCCAAGGGAG	180
GTCCTGGAAC CAATCCGCCA TGGATACTGA GGGATGACTA TAATATGAAC CTTGTATGTA	240
TGTAATTTAC CATTTTCTAG TTAGCCACAT TAAAAAAGGA AAAAGAAACA GGTGAAAAAT	300
ATTTAAAAAA TACGTTAACA CAATATATCC AGAACATGAT TTCACATTGA AATCAATATA	360

AAAATTACTG AAATAGTTTA CAGTCTGGTG TGCATTTTAG ACTTAAAGCA TATCCCTTTG 420
GGCATGGTGG CCCATGCCTG TAGTCCTAGC CACTGAAGGC TCGAG 465

(2) INFORMATION FOR SEQ ID NO:566:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GAATTCGGCC TTCATGGCCT ACAGCGAGAA GGAGTGTATG AGTGTGAGTG TGTGTGCATG 60
 GAAGTTGGGC ACTGGGCGTC TGANTCCTTC CCCACCCAAG AGAGGAAGGA CCCCTCACCA 120
 CCCCCACTGG CGAGACAGTT TACTTTGCCG ACTTGCCATG TTTTGGCCAA AACCAAGATT 180
 TTGAAGGAAA TGAGTGGCCA GCGCCAGGGC CCAGGCCATG TGGCCTGCCC AGCCTCAATG 240
 TNACTTGGTG GCGGGGTGGG GTGGGGGTGG GCAGCAGCAT CCCAGCCTTG AGATGCTTCA 300
 CTTTCCTTCT CTGTAACCAG ACTTTGAAAA ATTGTTCGTT TCATCAGGCA TCTCGAG 357

(2) INFORMATION FOR SEQ ID NO:567:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GAATTCGGCC TTCATGGCCT ATCTGCACTG AATTAGAACA AAATTTAGGA GACTTCTAAT 60
 TTGAAGCCAG AGGTGCTGAC TTTTGAGTCT TTGGAGATTG CCTGTGGGAA ATATTCCTGT 120
 TGAGGGCCAA TGTCCCAATG GGCTCTGAAG ATGAGAAGGA TCCCTGCCCT ATGTGGATGC 180
 CACTGGATCT GGAATCATTT CTGTGGCTCA GATTCTGTGA CACATTCTGC CAGGACAGGA 240
 GCAGCCGTAT TGGGAAAAGA AGGGGGACAA TAACTAGAAA CGAACTAAGA TGTGGCCCTT 300
 GCTTTGTAC TTTTAATTTA ATGGGAAACA CTCGAG 336

(2) INFORMATION FOR SEQ ID NO:568:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

GAATTCGGCC TTCATGGNCT ACCTGGACCT TGGGTGGCAG GCCTGGGGCC TTCAGTCCTT 60
 AATTCAGGAG GTAGCCAGTC GCTGGAAC TAAGANTGAACT TCAGCTGTG TTGCCATAGC 120
 TGGAGGGAAG AGGGAAAGGA GCGCTGCAGG GGAGCAGAGA CCTCACCCCTT CCTCTGCCGA 180
 CATCAGGCTG CCGGTGCTGG ACGGGGCCCT GGCAACCGTG GCAGGAGTGG TGATGTCCGA 240
 TGATGGTAAC AAGGGCTTCC TGAGGACCCC GAGCTGTCTT AAGGGCTCTT TACCTGGAGT 300
 AAGTATCCCC TTTAATCCTC CCAACAACAC TGTGAAATTG ATTCTGTTGT TATTCCCAT 360

TCACCGATGA GGAACCCACA GCCCAGAGAT GTTAAGTAAC CTGCCCAAGC CTCCTCTGA 420
 GCATGGCAGA GGGAGGTCC GAATGCGGAA AGTCTGGCTT CAGTGCCCC ATCCTCTCGA 480
 G 481

(2) INFORMATION FOR SEQ ID NO:569:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

GAATTCGGCC TTCATGGCCT ACTCATCATT TGGAAAATAC TTGATGGCAG GAGAACTTGC 60
 TTAAACTAA AGGTGGAGAA AGAGTTAACT TCCAGGACAA CCCATTATAG CTCACTTCTT 120
 ACCAACAAAG CAGTTTTTAT ACAGCACCTT AGGACTCATT TCTAATGTCA ACCCAGATGG 180
 CCAGTAAAGG CAAGGGAAGA GGCTAAGTGA CTCACAAAAA TCTCTGATAT TGAGGTCTAA 240
 TGTGAAGGCT ATAGATAGGA ATTCCCACA AACTTCTAAT GAGGACTAAT ATGAACAGCA 300
 AATTGGAGAA GACACCAAGG ACCTAATTTT AGTTTCACTA GCCGTGGGAC CTTAGAAAAA 360
 AGACCATTG CTCTGGACTT TTGTTTCCCA AGCCATAAAA TGTGGAAGAA TCTTCACAAT 420
 TCAAGTTGG TCATGTATAT TTCCCTTTTA CAGAGAAAGC TGAAGCCTCG AG 472

(2) INFORMATION FOR SEQ ID NO:570:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

GAATTCGGCC TTCATGGCCT AGAAAGGATC AAGCTGATCA GAAGCGGGAG CTGCATTGAG 60
 GGAAAAATAT GGCCAGAGAA GGCCTCACTG AGGAGGTGAC GTTGGTGATG CTGGAGCTCA 120
 GATCTGAAGG GGAAGAAGGA AGCAGCCACA TATAGAAGTG AGGGAGGGGG CTTAGGCCAA 180
 AGGAACAGCA AGCGGAGAGG CCCTGAGAAA GGAAAGGCTT GGCTCGCTCA CCTGCAAGGG 240
 CCCCTGGCT TGACATAGTG AGAAAGGTGT GAAGATGAAT TTGGAGAAAG GCAGGGACAG 300
 ACCACAGGAG ACCTTAGATT TGATTCTGAG GGCGATGGGA TCCCTTGAGA GGATGCTGAG 360
 CAGGGGAGAG ATGTGATCTC CTTTTCATT TAACATGATC GCTGCAGCTG CTGCTGGAGA 420
 ATGTTTGAG GAGCGAGAGT AGAGACTGGG AAGGTCTGTG CATCCTCTAA GCNACAGGCG 480
 TCTCGAG 487

(2) INFORMATION FOR SEQ ID NO:571:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 456 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

```

GAATTCGGCC TTCATGGCCT AGAATAAATT GTGATACAAA AAAAAAAAAA AAAAAAGAGT      60
GTACACTATG AATGGGTTGG TCGTTTTCTT CCTGGCTTTT TTTCTTTTTC TTCAGAGTTA      120
GGAAATACTT TTATTTTTTA AAGGAAAATT CATCATAAAT TTGCGCTGGT ACTTTTTGAC      180
ACAGGATTCT TTCAGTGAAG CTTGCCCGG CCGAAATCTC CATGGCCGGC CTGCTCTCTG      240
CCCGGTCTTC ACTGAAGCCT GCTGGGCTCT CTCCACCTAC TTGGTCCATC AGTCTGTGCT      300
TGGTCATCC TAGCAACCTG GATCCCGCAC CCGCTATGGC ACCGTGCTTG GCTGGAGGCT      360
GGTCCGAGCG TCCGTGACTA GCTTCCACCT TCGGCGCCAG CTTTGGACA AGGGGAACGC      420
AGTGGCACCC AAAAACTCGG AGACATGAGA CTCGAG      456

```

(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

```

GAATTCTAGA CCTGCCTCGA GATGCCCCGAC TACTACAAAC CTCAGTACCT GCTGGACTTT      60
GAAGACCGCC TTCCCAGCTC GGTCCACGGC TCAGACAGTC TGTCCTCAA CTCTTCAAC      120
TCCGTCACTT CCACCAACCT GGAGTGGGAT GACAGTCCGA TTGCCCCATC TAGTGAGGAT      180
GGAGACCTCA CAGACACGGT CAGTGGTCCC CGCTCCACAG CCTCCGACCT GACCAGCAGC      240
AAGGCCTCCA CCAGGAGCCC CACCCAGCGC CAGAACCCTT TCAACGAGGA GCCGGCAGAG      300
ACTGTGTCCT CCTCTGACAC CACCCCGTG CACACCACCT CTCAGGAGAA GGAGGAGGCC      360
CAGGCCCTGG ACCCGCCGGA TGCCTGCACG GAGCTCGAG      399

```

(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

```

GAATTCGGCC TTCATGGCCT AGATTGGGT TAGTGGTTTT CTTTAGCAT GTTGAAAATG      60
TCACCCAAC TTTTCTGGG TTCCTTGAA AAGCCAGCTG TCTGTCTGTC TGGTTGTCAT      120
GTCTGAAGGT GATGTGCTT TACCTCTGGC TGCTTAAAGT ATCTTTTGCC TTTTCCCCCT      180
TTGTGAATGT TTTTGCTGAA GTGTAACATA TACACAAAAG AGTGTGCAA TCATCAATGC      240
TTGATGGATT CTCGAG      256

```

(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

GAATTCGGCT TCATGGCCTA GAATCATGCA TTTTCTTTTC TTTTITTTTT TCCCGTTGGC 60
 TTTGTCTATG CTGGTGGCAT CCAGGGCATT GCTTTGTCTC CCTGATTATG CCCAGGATTC 120
 AAGGTCTTCT TATTGTGGG GAGGCAGGCT GCCCACTGGG ACGGTTTTTA GTGTGTTTNC 180
 CATTCTGGC TCCCTCGAG 199

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

GAATTCGGCC TTCATGJCCT AGGATTTGAA GAAGTTGGGA AAGCATTATG TAGATTAATA 60
 TACTGGTTGG TTCCTATCT ATGTGGAAGG TCATATTAGC TGCAATTATT TAATTGCTG 120
 TGTATTTTG TGTATATAA CACAAATATA TTTGTATATT AACTTCATT TTACTGTCAT 180
 TTTCTCTGT GTATACAAA TGAACAAATC TTGTAATTAT TTTCAAATAT AGAAGTATAT 240
 ACATTAGATG GATTTCCAAG ATTTTGTAA NAAATCTTAA ATCAGTGTTC TGAGTTATTT 300
 AATTTTAAA TTAATCTACA AATTATGCAC NACAACTAG CAACTCGAG 349

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

GAATTCGGCC TTCATGGCCT ACAAATTTTG CTCACITTTCA TTAATCAGTT GCTCAGATAG 60
 AAGGAAATGA CATCTGGTTC TGTCTTCTTC TACATCTTAA TTTTGGAAA ATATTTTCT 120
 CATGGGGTGG ACAGGATGTC AAGTGCTCCC TTGGCTATTT CCCCTGTGGG AACATCACAA 180
 AGTGCTTGCC TCAGCTCCTG CACTGTAACG GTGTGGACGA CTGCGGGAAT CAGGCCGATG 240
 AGGACAACTG TGGAGACAAC AATGGATGGT CTCTGCAATT TGACAAATAT TTTGCCAGTT 300
 ACTACAAAT GACTTCCCAA TATCCTTTTG AGGCAGAAAC ACCTGAATGT TTGGTCGGTT 360
 CTGTGCCAGT GCAATGTCTT TGCCAAGGTC TGGAGCTTGA CTGTGATGAA ACCAATTTAC 420
 GAGCTGTTCC ATCGGTTTCT TCAAATGTGA CTGCAATGTC ACTTCAGTGG AACTTAATAA 480
 GAAAGCCCCCT CGAG 494

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GAATTCGGCC TTCATGGCCT AGGCACGTTA AATTTTAAAA GTTANAAAAA GAAAGATGCT 60

TTTTGCAGCA GTTCCAGGGT AAACGGCCCC ATGCAACACA AACCTCGGG AAGGGCATT	120
CAGCCTTGCA GTGGGCCACG GAGTGCACCA CGCGGCGCTC AGCCCCCAG GGAAGCGATG	180
CCCCACATCG GGCCAGAAAC AAAAGGGGT GAGATAAAGC ATGCTCGAG	229

(2) INFORMATION FOR SEQ ID NO:578:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

GAATTCGGCC TTCATGGCCT AAGGAGTTG AGATATATTT AGGAAGCAGA GCCTATAAGA	60
CATGCTGATC ACTTGCATAC ATAACTGAG AGAAGTAGAG GTATAGAAGA CTTCTAGAAC	120
TTGGAGAAAT TGGATGAATG GATGTATTGT TATTGATGTA ATGAACCTTA GAGGTGGGTG	180
GGATCAGAAA GATCTATTG CTTTCAAAGG AAATGGGGAG TGGACAGGTA TGTTGGCAGC	240
ATAAGAACTG GAATAACAGC ACATCTCATT CATGCCTTAA AAGAACGTGA AACTTTGAAT	300
GTACAGCAAT GGTATTCAAT AGGTATGACT TTGCCCCTAA AGGACATAGA CACCAGGGAT	360
GTTGCTAAAT ATCCTCCAAT GCACAACACA ACCCTCGAG	400

(2) INFORMATION FOR SEQ ID NO:579:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GAATTCGGCC TTCATGGCCT ACGAGGACGA GGACGTCAAG GATAACTGGG ATGACGATGA	60
TGATGAAAAA AAAGAGGAAG CAGAAGTAAA ACCAGAGGTA AAAATTTCAG AAAAGAAAAA	120
AATAGCAGAG AAGATAAAG AGAAAGAACG GCAACAGAAG AAAAGGCAAG AAGAAATTAA	180
AAAGAGGTTA GAAGAACCCG AAGAACCTAA AGTGCTAACA CCAGAAGAAC AATTAGCAGA	240
TAAACTGCGG CTAAGAAAT TACAGGAAGA GTCAGACCTC GAATTAGCAA AGGAAACTTT	300
TGGTGTTAAT CTCGAG	316

(2) INFORMATION FOR SEQ ID NO:580:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GAATTCGGCC TTCATGGCCT AAGCGAGGCC TGAGCCTCTG CGTCTAGGAT CAAATGGTT	60
TCAATCCCAG AATACTATGA AGGCAAGAAC GTCCTCCTCA CAGGAGCTAC CGGTTTCTA	120
GGGAAGGTGC TTCTGAAAAA GTTGCTGAGG TCTTGTCCTA AGGTGAATTC AGTATATGTT	180
TTGGTGAGGC AGAAAGCTGG ACAGACACCA CAAGAGCGAG TGGAAGAAGT CCTTAGTGCC	240

AAGCTTTTGG ACAGATTGAG AGATGAAAAT CCAGATTTTA GAGAGNAAAT TATAGCAATC 300
AACAGCGAAC TCACCCAGAC TCGAG 325

(2) INFORMATION FOR SEQ ID NO:581:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 353 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GAATTCGNCC TTCATGNCCT ANGAGAAGNA CCCAGACCCC CCCAAGAAGG AGGAGGANCN 60
CCNNGAGNC NCTNCTCCAG NCGGANGAGG AGCGCAAGGC CAAGTNGGCC AAGATNGAGG 120
CGGAGCNCGA GGCCNTGNNC CAGGGCATCC GAGACAAGTA CGGCATCAAG AAGAAGCAGG 180
AGCGCGAGGC CGAGACCCAG ACGCCGCCAA GAAGGAGGAG GAGCGGCAGG AGGCGCTGCC 240
CCAGGCGGAG GAGGAGCGCA AGGCCAAGTA CGCCAAGATG GAGGCGGAGC GCGAGGCCGT 300
GCGCCAGGGC ATCCGAGACA AGTACGGCAT CAAGAAGAAG AAGAACGCTC GAG 353

(2) INFORMATION FOR SEQ ID NO:582:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GARWWYKCSS YYTTNANGGC TAGTCAGTGG CAGGGCCACC CAGAAGCCCC GCAGATGACG 60
GAGCTGAGAA CAGGGAATTN ACCTNCACGT GTTGCCATTT CCTCANTGGA AAGTCCTTGG 120
GAGGTGGCTG GGCTCAGCCT GAGCTCAGGG CTTTTCGGTG GGGTTGGGGC AGGGGCAGGG 180
CGGGCNCNTTG CAGGTGGCAC AGGCTTCATC AAGGCAGGAC ACGGGNTTCA TCAAGGCAGG 240
AGCCACAGCG CCCGAGCCCT GGCAGGGGAG GTAAGGCCCA GGATGGGGCA GGGCCGTGTG 300
CTCCTGGNAC GGACATCCTT NTCTGCCAGA GACCTGCTCC CCAAGCCCTG TCCCTCCCAA 360
TCCCCAGGCA GCCCACTCTG CCCTCATAG ATGAATCTAA TATTGAATTT CTAGACCTGC 420
CTCGAG 426

(2) INFORMATION FOR SEQ ID NO:583:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GAATTCGGCC TTCATGGCCT AAGAAAAGAA AGTAAGATTA TCTCCAGCCA AAATGTCAAC 60
CAAGAATTCT ACAGATCTAG TTGAATATGT TGACAAGAGT CATGCTTTTC TCCCCATCAT 120
TCCAAACACC CAGAGAGGTC AGCTAGAAGA CAGACTGAAC AACCAGGCAC GTACCATAGC 180
TTTCCTTCTT GAACAAGCCT TCCGCATCAA GGAGGACATC TCTGCTTGCC TGCAGGGGAC 240

CCATGGCTTT CGAAAAGAGG AATCGCTCGC CAGGAAGTTA CTGGAAAGCC ACATCCAGAC 300
 CATCACCAGC ATCGTCAAAA AACTCAGCCA AAATATTGAG ATTTTAGAAG ACCAAATAAG 360
 AGCTCGAG 368

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GGAATTCGGC CAAAGAGGCC TAAACGACTC TTTGCCCTGT TTCTTCTTGG CTTCCTTGC 60
 GTAACAAGGA TGAAGGAGGT GGTTTAACTT TATTTTGTGCT CTTTAACTTT TTAAAGTCTA 120
 AAGTAAGTGC TTGAATCGGG TGGGTTTCA TTTTGTGCT TTCTCACCCC TCAGGTGGC 180
 CCCTAACTTG GCCTCTCACC CTGCTGTCAG CTGTTAGACA CTGACTCAGT GGCTCAGAAT 240
 ATGAAAGGCT CAGGAAGTAG CATGCTGGCC CCACCTCCCT GTCCCCATAC CTTAGCAGAG 300
 CAGCTGCCCA GCAGGGCCTC CTCTCTTTC CTAAGAGTTT ACTCCATCCA TGGTGGGTGT 360
 CTTGGTAGGC CCGAGATACG AGAGGGAGTG CTGCTGTTAC AAGAAATTAC AGTTGTTCTC 420
 TTCGGCACAA GCTCGAG 437

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GAATTCGGCC AAAGAGGCCT AGTGCAGAGT TGCAAGCAAG TTTATCAGAG ATACGCCATG 60
 AAGTTCGTCC CCTGCCTCCT GCTGGTGACC TTGTCCTGCC TGGGGACTTT GGGTCAGGCC 120
 CCGAGGCAAA AGCAAGGAAG CACTGGGGAG GAATTCATT TCCAGACTGG AGGGAGAGAT 180
 TCCTGCNCTA TCGTCCAG CAGCTGGGG CAAGGTGCTG GAGAACTCTG GCTTCGCGTC 240
 GACTGCCGCA ACACAGACCA GACCTACTGG TGTGAGTACA GGGGGCAGCC CAGCAATGTG 300
 CCAGGCTTTT GCTGCTGACC CCAAACCTTA CTGGAATCAA GCCCTGCAGG AGCTGAGGCG 360
 CNTTCACCAT GCGTGCCAGG GGGCCCCGGT GCTTAGGCCA TCCGTGTGCA GGGAGGCTGG 420
 ACCCCAGGCC CATATGCAGC AGGTGACTTC CAGCCTCAAG GGCAGCCAG AGCCCAACCA 480
 GCAGCCTGAG GCTGGGACGC CATCTGAG GCCCAAGGCC ACAGTGAAAC TCACAGAAGC 540
 AACACAGCTG GGAAGGAATC TCGAG 565

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

```

GAATTCGGCC AAAGGGCCTA CAGAATAGCG GTACCATGAT AGAATACTGC AATTGTGGTC      60
AGAATTACAG TATGCACAAA GAATTAATTA GCATTATTAA AGAGTCCTCA CTAAACATTT      120
CATATGATCA CACTGAAGAA CTGTAACATT CCATAGAGTG AAGTGGTTCA AATTTCCTTT      180
GGAATTTTTC CTTTGTGGT CCTTATTTTA TGATCCTTTT CATATTTCCT TTGACTTAGA      240
GTATTAATAC ATGGCCAAAA TAATTTAGTT ACTACCTCAT ACAAACAATA TAATGGTTAC      300
TCGAG                                         305

```

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

```

GAATTCGGCC AAAGAGGCCT AGTTGTTTTT AATGGCACAG GACTCTTCCA CTTTGTGGTC      60
CTCCTCTAGC ACAATACTGG ATGGCTGGGG CAAAAGATTA AAGGAAGTCT TTTCCACATC      120
ATTTTCTGTC TGTTCTCAA ATCTTTTAC TAAATTGAT ACAAATTCCT CTATTCTTG      180
ATGATATTGC TTTGAAATAG CATTGTTTAT GAATAGAATC TGTAATATAG GTCCATCTAA      240
CTTAGTATCG TTCACCAATA TTCCAATCGG TCGAGTCAGA ATGTTCAATT TTCGTTTAAAG      300
TTCTTGATTG TCGGCGCGGA GCTGCTCGAT GGTCTCCACG CACTCGAG      348

```

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

```

GAATTCGGCC AAAGAGGCCT ACTCATGACA GGATGACAGT CACATTTGGT AGACACCATC      60
AACCAATGAT CTCTAATTG CGGCCCCCAA CAAGCAATGG GGTCTGTGG GCTACATCTG      120
GAATTTGAAA TGTCTCATGG AAATCATGTT CTTACCCTGG AGAAGGGTGG CTGCTTAGGT      180
GCTACTTAGG AAACCACTCT GGCAGACCAG ATCTTCCCA ACTCAGGGGC TATGCGGGGA      240
GAAGTATTAG GAGCCCCTGA GCAGGAAGGA TGTACTTAGG AAGGCTACCG GGGATGGGGA      300
AGGGTAAAAG AGCTTAGAAG CCTGGGTGAA GTTTGGGTAG ACCAAAAACA GGAGGGAGGG      360
AGGGAGGATG TTCCCTTGA ATACAACTA GAGAAAAGCT TAGGGGANCA AGTCTTTTTC      420
TTGGGGGACA GTGAAGAGTT TCCTAAAAAT TCCCTGGCCC CCAGGCCTTG GCTAAAAACC      480
CTCGAG                                         486

```

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:


```

GAATTCGGCC AAAGAGGCCT AATTGATTGT GATTAACCAA GATGTATGGA AAACAGTTTT      60
AAGTGTTAG TGCATGTATC TCATAAGGTC CATTAAAGACG TTCATTATTT TTCAATTGAT      120
GCGTCTTAAG CCCCACTTGA TGTTTGTGT AGTGCAATTC CACAGAAGGA TTCTGCACTG      180
TGGGATTGAG TTCATTTTGT TAATTGCATA ATACAACCCC ATCGTGTTTC ATAGAAAATA      240
GTAAATACTC TTGCTTTTAT TCATTGGTAT TCTTTGATAT TACTGAAGAA ATACCAAAGA      300
AGCAAAGGAG CAAAGAAATA CCAAAGAAGC AAAGGAGCAA GTGAATAGTT CTTCAAACCT      360
TTACATATTA AGGGCACGAA TGTTTCTTGA AATGTGGACA CATACTCGAG                  410

```

(2) INFORMATION FOR SEQ ID NO:590:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

```

GAATTCGGCC AAAGAGGCCT ACGGCCAAAG AGGCCTAATT GAATTCTAGA CCTGCCTCGA      60
G                                                                    61

```

(2) INFORMATION FOR SEQ ID NO:591:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 211 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

```

GAATTCGGCC TTCATGGCCT ATCTAGACCC AAATATTTTG AATATGTTAT CTGTCTCTT      60
TTCTTTTGT TATATAGAGA GATTGATGCA TAAATCTGT GTTTGATGA CTGTAATTCC      120
AAGTTTAGCG AAATTGTCCC TAGGACAACA CACCAACGGC CATGAGCTGT CTCGGTCTGT      180
CAAGCTTAGT CTCCGATCCT GCCCACTCGA G                                                                    211

```

(2) INFORMATION FOR SEQ ID NO:592:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

```

GAATTCGGCC TTCATGCCTA GCCGGACCTG GTGCTCCTTT CCTTGGTGCT GGGCTTGTG      60
GAGCATTTTC TGGCTGTCAA CGCGTCATC CCTACCAACG TTCCCGAGCT CACCTTCCAG      120
CCCAGCCCCG CCCCCGACCC GCCTGGCGGC CTCACCTACT TTCCCGTGGC CGACCTGTCT      180
ATCATGCGCG CCCTCTATGC CCGCTCACC GCCCAGATCC GAGGCGCCGT CGACCTGTCC      240
CTCTATCCTC GAG                                                                    253

```

(2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

```
GAATTCGGCC TTCATGGCCT AAAGAAATGA AATAATATCT CTGAATTTTA GTCCATGTTT    60
TCAATGATTT CTGACTTTAT TATATTAACT CTTATTAATG ATCACAATTT ATTTTGTAAG    120
TTTGCAGCC AAAGGGACAA TTTATTTTGT AAATTGCGA TTCTATTTC AAAATAGGGA    180
TCGACTCGAG                                         190
```

(2) INFORMATION FOR SEQ ID NO:594:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 208 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

```
GAATTCGGCN TTCATGGCCT ACGGGGAACA GAGGATGGCG GAGGAGGGAA CACACAAGCA    60
GGAGCCCATG CAGCTGGGAG CCACTGAGAT CCCAGCTGGA GGAAGAGTGC CCTGGCACTG    120
AGGTCTAATG GCTGTCCAGC TGCTGCCCA GGATGTGAGG GCAGGTGGTA GGCCATGAAG    180
GCCGATTGAA TTCTAGACCT GCCTCGAG                                         208
```

(2) INFORMATION FOR SEQ ID NO:595:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

```
GAGCTATAAA ACAGAAATAC ATGCATAGCT GCAGAAACCA TGATAGGTAG AGGACTTTTC    60
TTTTGGTTTT GTTTGTTTT GTTTGTTTT GTTTTGGTT TTACAGAGAA GAGACTCGAG    120
```

(2) INFORMATION FOR SEQ ID NO:596:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

```

GAATTCGGCC TTCATGGCCT AAGAAACCAA ATTAGCAGAC GGATAGAATA TAAAGCANGA      60
GGCAATACTT ATAGTGTATT AAGAACTTG CTAGACCCCA TCCAAATTAC TCAGTCTACT      120
GTTGGTTGAT AGAATTACTT TAGGAAGAGT ACGTTTTTCC TTGGAAATAC ACTGGAAGTG      180
GTACCAACA AATCTAATAA AATGATGTTA AAGAGATTG CAGTAATTTT TATCNACTTT      240
CAGTTTGCAA ACTTTTATAA AGATATGAAA NGGACACTCG AG                          282

```

(2) INFORMATION FOR SEQ ID NO:597:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 184 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

```

GGCCTTCATG GCCTAGACAC ATACAAAGAT AAGGCTTTGA TAAAATTCAA GAGTTATTG      60
TATTTTGAGG AAAAAGACTT TGTGGATAAA GCAGAGAAGA GCCTGAAGCA GACTCCCCAT      120
AGTGAGATAA TATTTTATAA AAATGGTGTG AATCAAGGTG TGGCTTACAA AGACATTCTCT      180
CGAG                                  184

```

(2) INFORMATION FOR SEQ ID NO:598:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

```

GAATTCGGCC TTCATGGCCT ACTTTGAGTT AAATAGAGAG TTGATTAAAT GCATATATTG      60
ACAGTTACTG ACTCAGTAAG CTCATAATT CTAGGAATCA ATCACTGCTG ATTCATATGT      120
TTAGATATAT TCATTTCTGT CTTTCTGTTT CTTAGGCCAA AAAGAAAAAA GAAAACCAAT      180
ATTTAAGAGA AGAGAAAAAT GAAGACGCGA CATTTTGAAA TAGTCACCAT GCTGCTGGCA      240
ACCATGATTC TAGTGGACAT TTCCAGGTG AAGGCTGAAG TGTTAGACAT GGCAGATAAT      300
GCATTTGATG ATGAATACCT GAAATGTACG GACAGGATGG AAATTAAATA CGTTCCCCCA      360
ATCCCTCGAG                                  370

```

(2) INFORMATION FOR SEQ ID NO:599:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 376 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

```

GAATTCGGCC TTCATGGCCT AAGACTCTTA GATCTAAAAG GAAACTGACT TGCCACCTTG      60
CCAGAGGAAT TCTTGAAATG TTTCTGCAGC CACTTGGCCT TGAAAATAAA GGGTGCAACT      120
CTCAAATCTT GTTCTAACCC GGCTGGAGGA ACCACAAGAC CCAATGAAAT AGCATTTTCT      180
CTCCTTTTCC CAGCACTAGT ATATAACCTA TGAGGAACCC TTGTCTCTGA ATCTGCTCAG      240

```

CTTGAAATTT TGTCTCTGAA GGAAGAGAAT GATCTCAGCC CTAGTCTGAC AGTCCTAGAT 300
 TTCTGTGAAA TAAGAGTATT CTTCAACTTA GTGCTCACAC TCACATACCA TGAGGGTTCT 360
 CTGCAGAGGA CTCGAG 376

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

GAATTCGGCC TTCATGGCCT AAGTCACTAT TTGGTAGCTG ACTTTGTGCC CTGATTAGAA 60
 ACGTGGCTCC TTTTC..TGGT AGTTGTTCTT AGAACCTATC AACCTGCAGA GATTTTATT 120
 TTCATGGAAG GGAACGAGT GTTCTTTCTT TTGCTTCAGA CGGTCACATC TTTAGATCCT 180
 GAAGGGAGAG ATGCAGCTTG CTCTCTCCAG AGTCCAAATG CAGCAACAGA TTTTGCTTCC 240
 ANGCAAGCAA GATATGCTAT AAAAACCTGC NACATTCCTT CACCAGCTCC TCTCTTTGAA 300
 TTTTCGATGC CTCGATGGTC ATTTGAGAT GACAGCTTGT AGTGAGATAG CTGTGGCATT 360
 GGAAGGGGGG AAGCATGCAC CATTTCCCT AGGGCCTTCC TGCTTTTGCT TGATAAGCAA 420
 TTCCTTGAAT GGCATGTTCT CCACCTCTAG CCACTTTGTT TGTAGTCCCT ACTCTCGAG 479

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

GAATTCGGCT TCATGGCCTA CACAGGCATA ACAGTCAGTC GGGAAAAGGT CACTGAAGTT 60
 GCCCTTAAAG GTGAAGGGAC AGAAGAAGCT GAATGTAAAA AGGATGATGC TCTTGAAGT 120
 CAGAGTCACG CTAAGTCTCC TCCATCCCCC GTGGAGAGAG AGATGGTAGT TCAAGTCGAA 180
 AGGGAGAAAA CAGAAGCAGA GCCAACCCAT GTGAATGAAG AGAAGCTTGA GCACGAAACA 240
 GCTGTTACCG NATCTGAAGA GGTCAAGTAAG CAGCTCCTCC AGACAGTGAA TGTGCCCATC 300
 ATAGATGGGG CAAAGGAAGT CAGCAGTTTG GAAGGAAGCC CTCCTCCCTG CCTAGGTCAA 360
 GAGGAGGCAG TATGCACCAA AATTCAAGTT CAGAGCTCTG AGGCATCATT CACTCTAACA 420
 GCGGCTGCAG AGGAGGAAAA GGTCTTAGGA GAAACTGCCA ACATTTTAGA AACAGGTCTC 480
 GAG 483

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

```

GGGCCGTGCA GGCAGTGAAT CGGAAAGTGG AGATGATGAA TGAAAAGAAC TTGGAGAAAG      60
GACTGGGCGT GGACAGTGTG GACAAGGATG CCATGAACGC GGCCATCCAG CAGGCCATCA      120
AGGCCCAGCC GTCCATGTCT CCAAGAAGG CGCCCCCAGC GCCTGCAAAG GAGGCCAGGA      180
ATGTCGTGGC CGTGGGTACT GGTGGCCGTG GGACCCACGA CCGAGACCCG AGTGAGAAAC      240
CACCCCGCT CCAGTGGTTT GAACAGCAGG CGAAGAAGTT GGCAAAGCTA CTCGAG      296

```

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

```

GAATTCGGCC TTCATGGCCT AGAACTTTTT CATCTTTCCA AACAGAAATT CTATACCCAT      60
TAAACAGTAA CTCTCCCTTC ACCACTCTCC CCAACCCCGG AGACCTCTAT TCTATTTTCT      120
GTCTCTATAA ATTTGCCTAT TTTAGGTACC TCACATAAGT GAAATCATAT ATTTGCCCTT      180
TTGCATCTGG CTTATTTTAC TTAGCATGAT GTCTTCAAGG TTCATCCATG TGGTAGTAGC      240
AGAATTACT TCCTTTTAA GACTAGCATA CTCACACTGT TTTTGTGTTT GTTTGTGTTG      300
TTGTTGTTT TTGGGATGGA GTCTCACTCT GTTGCCCGG CTGTGGTGCG GTGGTGCCAT      360
CTCGGCTCAC TGCGGCCTCT GCCTCCCGG TTCAAGTGAT TCTCATACCT CAGCCATCCC      420
TCGG                                     424

```

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

```

GCGATTCGAT GTCCGTGCCC ACCTGGACCA CATCCCGAC TACACCCCCC CCTCTGCTCA      60
CCACCATCTC CCCAGAACAG GAGTCGGACG AACGGAAGTG TAACTACGAG CGCTACAGAG      120
GCCTGGTGCA GAACGACTTT GCCGGCATCT CAGAGGAGCA GTGCCTGTAC CAGATCTACA      180
TTGATGAGTT GTACGGAGGC CTCCAGAGAC CCAGCGAAGA TGAGAAGAAG AAGCTGGCAG      240
AGAAGAAGGC TTCCATCGGT TATACCTACG AGGACAGCAC GGTGGCCGAG GTAGAGAAGG      300
CACTCGAG                                     308

```

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

```

GGATGCTACA GAAATCACAG AAGAAAGCAG AACTTCTTGA TAATGAAAAA CCAGCTGCTG      60

```

TGGTTGCTCC CATAACAACG GGCTATACGG TGAAAATCAG TAATTATGGA TGGGATCAGT	120
CAGATAAGTT TGTGAAAATC TACATTACCT TAACTGGAGT TCATCAAGTT CCCACTGAGA	180
ATGTGCAGGT GCATTTTACA GAGAGGTCAT TTGATCTTTT GGTAAAGAAT CTAAATGGGA	240
AGAGTTACTC CATGATTGTG AACAATCTCT TGAAACCCAT CTCTGTGGAA GGCAGTTCAA	300
AAAAAGTCAA GACTGATACA GTTCTTATAT TGTGTAGAAA GAAAGTGGAA AACACAAGGT	360
GGGATTACCT GACCCAGGTT GAAAAGGAGT GCAAAGAAAA AGAGAAGCCC TCCTATGACA	420
CTGAAACAGA TCCTAGTGAG GGATTGATGA ATGTTCTAAA GAAAATTAT GAAGATGGAG	480
ACGATGATAT GAAGCGAACC CTCGAG	506

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GGTGGAATGA AAGATATACC TAGAACGCCA TCTAGAGGGA GAAGCGAATG TGATTCTTCC	60
CCAGAACCGA AAGCTTTGCC TCAGACTCCT AGGCCGAGGA GTCGTTCTCC ATCATCCCCA	120
GAGCTCAACA ACAAGTGCTT TACCCCCAG AGAGAAAGAA GCGGGTCAGA ATCATCAGTT	180
GATCAGAAAA CTGTGGCTCG GACTCCCCTG GGGCAGAGAA GTCGTTCTGG ATCTCTCAA	240
GAACCTGATG TGAAACCCAG TGCATCCCCT CAGGAAAGAA GTGAGTCAGA CTCTTCTCCA	300
GATTCTAAAG CCAAGACACG AACCCCACTT CGGCAGAGGA GTCGGTCTGG ATCATCTCCA	360
GAGGTTGACA GCAAATCTCG ACTATCCCCT CGGCGCAGTA GGTCTGGTTC CTCCCCTGAA	420
GTGAAAGATA AGCCAAGAGC AGCACCAGG GCACAGAGTG GTTCTGATTC CTCTCCTGAA	480
CCTAAAGCTC CAGCCCCTCG GGCCCTTCCC AGACAACTCG AG	522

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GAATTCGGCC TTCATGGCCT AGGCGCACCA AGAGCAGGGC TGTGTGTGGG AGGCTGCAGC	60
CAGGATTGCC TCAGCTCCTC CCCCTCAGGC TGGGAGGATA GCACAGGCTA GGGGCTCGGG	120
GTGGAGGGTC TCAGCTCTGC TGCCCCCACC CCAGTACTAG CCTAGCTTCC CAAGCTGTGG	180
CTTAGAGGAT AGTTGGCTTC CTGCCTCTCT CCTCTAAAT AGCAAGTCTG GGAAATCCTG	240
GGGTGAGTGG AGTCACCCCA CTCCCAGTTG CTGGCAGAGA CTGAGACTAA AGCATCACTT	300
AATAAACCCC CCAGCTCGAG	320

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

```

GAATTCGGCC TTCATGGCCT AGTTGTGTAT TCTTTTCTCT GTATCATATG TGATAGTGGG      60
GTAGTGCCAA ACATTGTAA CTCTGATGAA TAATGTCTCT TTTGGTTAGA TCATTCTTAC      120
CTTACTGGTA TCTCTACTG TTTCTTACC TAGTTATGCT GTTATGCCT ATGGCTGTGC      180
CAGCTGCCCG AAGCTAACTT GTGAGAGGGA AGGTTGCCAG ACTGAGTTCT GCTACCACTG      240
CAAGCAGATA TGGCATCAA ATCAGACATG CGATCTACTC GAG                          283

```

(2) INFORMATION FOR SEQ ID NO:609:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

```

GAATTCGGCC TTCATGGCCT ACACATGAGT GTGACCTCTG CCATGGGGAA ACACACACAG      60
AGATATCTAT ACATATATAC ATACATACAA ACATAGGCTA TCTTGGCACA CTAATGCTA      120
AGCACTGTCT TAAGAGGTAG AGCTGGTGTG AGTGAAATTA ATGTTACATT TTCCAGCTGT      180
AAACAGACAT CTGCATTTC TAGTGAGCTG CCAGGAGCCA GATTCGGGAA CCGTAACTGA      240
TGTGCCAGGA ATGTTGCATT GATTCCCACT TCCAGGGATC TCTCGAG                          287

```

(2) INFORMATION FOR SEQ ID NO:610:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

```

GAATGATAGG TCCTAGGTTT AACAGGGCCC TATTGACCC CCTGCTGTG GTGCTGCTGG      60
CTCTTCAACT TCTTGTGGTG GCTGGTCTGG TGCGGGCTCA GACCTGCCCT TCTGTGTGCT      120
CCTGCAGCAA CCAGTTCAGC AAGGTGATTT GTGTTCCGAA AAACCTGCGT GAGGTTCCGG      180
ATGGCATCTC CACCAACACA CGGCTGCTGA ACCTCCATGA GAACCAAATC CAGATCATCA      240
AAGTGAACAG CTTCAAGCAC TTGAGACACT TGGAAATCCT ACAGTTGAGT AGGAACCATA      300
TCAGAACCAT TGAATTTGGG GCTTTCAATG GTCTGGCGAA CCTCAACACT CTCGAG                          356

```

(2) INFORMATION FOR SEQ ID NO:611:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

```

GAATTGCGCT TCATGGCCTA ACCACATGAT CCTTCGTGTT TCTTGCCTTC CATTTCCCTT      60

```

```

GGGTGGATGG TTGGGTAGGT GGGGTTTCCT GGTTTGGGGT TTCTCAGACA AGGGCCCTCT 120
AGGGAGGGTG CCCTGGACCC CCCACCACTC CTGGGCTGAG GAGCGTGTC CATGATGCCG 180
TTGGTGAGGT ACTGGAAGCC GTCATAGAGT TTGGTGGTGA TAGACCGCAT ACTGCCATCC 240
ACCATCTGCT CCACCAGCAG CTGCAGCTGC TCCTCAGTCA TGCTCATGTG GAACCTCTCT 300
TTGAGGTTNC GAATGGTGCT GGAGCCATGG AAGCAAGGAA GCTGAGAACC TTGTCCATGT 360
GTTTCCGAGC GGCAATCAGC CCTGCAGCA TCA 393

```

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

```

GAATTCGGCC TTCATGGCCT AGGCGGGTTA AAGTCACATT TTAAAAAGG CTAAACTCTA 60
AATTGCTGTA TTGCTCTCT CTGGAGATTA ACAAAGTGCT TGGTTTGAG ATTTGCTGGT 120
ACGGTGATCT CAATGATATG ACCGAGGGTG GGAGGGATGT GAGGAGGGAA ATCGGCAAAA 180
CCCTGGCCAG CCAGCCAGCC AAGGTGACAC ACAGCCAGAG GGGGCTCCCC TCTCCTCTG 240
CCGTCCGGCC ACGGCTCACC ACGCTGTCCA CTGGGAACGC GGCCCCGCGG CCCGCAGAGT 300
CAGGCGTGAG CTTGCCCCTT TTCTGAAAGG GCCTCCGCTT GGGCAGGCGC CGGGGGGCAG 360
TCCTCGGGTC CCATGGCTTA GGAGCACAGC ACTGACGGCT GCAGTGCTC GAAAGGCTGA 420
AATTCCACAT TGCTCTCTAG CGATCCCGCA CTGCTGCGAC GCCCTCGCTT CCCGGCTTCC 480
GAGAGGTCCC GCAGGGAGCT GCTGAGGGCG CTGCGCTTGA GGCCCTCACC GCTGGCATAG 540
CTGTCGTCCA GGCAGGCCCG GCTCAGTGT TCCGTTGCC GACTCCTTTT TGAGGCTAGA 600
GCACTGGGAC ATGCTGGGCC GCACGACGCC TTTCTGCTTC TCGAG 645

```

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

```

GCGATTGAAT TCTAGACCTG CCTCGCACCA CCCCAAATCC CACATCCTGC ACCCCTGCCT 60
CAGGCTTCCT GCCCTCAACC CCAATATCT GAGCCTTCTC TTTTITTTTG TTGTTTTTTT 120
GAGACAGAGT CTTGCTCTGT CTGTGCACA GGCTGGAGAG CAGTGGCGCG ATCTCAACTC 180
ACTGCAACCT TCACCTCCA GGTTCAGCA ATTCTCCTGT CTCAAGTGCC TAGATACCTT 240
GGTAATGATT CCATTGGCCC CACCATGCC TGTCTGCCT TCCTGGCTGT GCCCAAGCTT 300
GGTCCCTGCC TGCCTGCCTC ACTCTCTGGG TCTCGAG 337

```

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

```

GAATTCGGCC TTCATGGCCT AGGTTT TAGA ATTTATATG AAGTATCTTA TTTGATTTC      60
ATAATAACCA TAGAAGATAG ATACTATTAT TATCCTTGGA TTATAGATGA AATTGAAGAT      120
TGCTTCGCAG GTAGAGTTAA GATCCAGAAT GGTGACAAGA AGTATAATGT CTGCTTTTAT      180
GCCATAATAT ATCAGACTAT TCTGACTCAT TTAGATTACT TCAGGGCTAT CACTGAAGCT      240
TACAGTATTA TCACTACTGT GATACCCCTG CTCACACAAT TTGGTAAGTG TTTTGTATC      300
TTTTAGAACT TATACATTAG GCAGCAGCTA TCTGTTTGGT CAGCTGAAAG ACGGCCACAG      360
GATTTGCTTC TGGGTGGCCA TTAGCACCTT TCACCCATGC ACCAGAGAGA TACTTCCAGC      420
ACGAACTCGA G                                     431

```

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

```

GAATTCGGCC TTCATGGCCT ACCAAAATTG TGCATACCCT TGGGATGAAA ATCATTGTAA      60
AGAAAAGAAA AAAGCAGGAN TATTTGAACA AATCACTAAA ACTCATGGAA CAATTTTTGG      120
CATTACTTCA GGGATTGTCT TGGTCCTTCT CATTATTTCT ATTTTAGTAC AAGTGAAACA      180
GCCTCGAAAA AAGGTCATGG CTGCAAAAC CGCTTTTAAT AAAACCGGGT TCCAAGAAGT      240
GTTTGATCCT CTCATTATG AACTGTTTTC ACTAAGGGAC AAAGAGATTT CTGCAGACCT      300
GGCAGACTTG TCGGAAGAAT TGGACAATA CCAGAAGATG CGGCGCTCCT CCACCGCCTC      360
CCGCTGCATC CAGGACCACC ACTGTGGGTC GCAGGCCTCC AGCGTCAAAC AAAGCAGGAC      420
CAACCTCAGT TCCATGGAAC TTCCTTTCCG AAATGACTTT GCACAACCAC AGCCAATGCT      480
CGAG                                     484

```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

```

GAATTCGGCC TTCATGGCCT AGCGTTCCTG GTTCCGTCCT TGTACATAAT ATTGTACAGC      60
-ATTEAACCAC TTTTGTGAT CAGCAAAGTA GTCTCCAATG GCATTGTTGG CTTGTTCCAG      120
GAGACTGTCA TCTGCATCAC CAGATCCAGT TTTCAGGAGC TGGAGTACTC TAAACCAATC      180
CCCCAATTTT AGCCGGAGGC CAATAGCAAG ATCCCTTCTG TCCATCTCGA G               231

```

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

GAATTCGGCC	TTCATGGCCT	ANAATGCTTC	ATGAACTNGC	NGACAGGACT	GACACAGCTN	60
AGCTTTCCTG	ACTGATTCCG	GGCCATGCAG	TCTACCAAAG	GGCTAGCTGT	TGAGACAATG	120
AGGATCAGGG	ACATTTGCCC	TCGTTCTGAA	TGTCCCAGC	CACAGTACNT	ACATNGTTCT	180
TACATGTACC	TTCCCCCTCG	GTGACATTTT	ATATTTTCCA	AGNTGGCCAC	ANCNGTTCCC	240
TTCCCTTTCT	NNTNGNGNNG	NACACTCACA	CCCGTCTCTG	NGAGGTGAGG	CCACATATTC	300
TCTTTTCTGG	AATTTGGGTG	GGCCTGTGAC	AATGGCAGGA	CAATGCTGAG	TGGCTATGTC	360
ATAAAGGCAA	TACCCCTTCC	ATCCAATTCT	CTTGGGATGC	TCATGTTTAG	AATCCAGCCA	420
CCATGTTGTG	AGGAAGCCCA	CGTCACCTAT	GAAGACCTAC	ACAGAAAAGA	CTCAAGGCCC	480
CAGGCACTTG	AGCTGAAGGA	TGAAAAAGAG	TTAGTCAGCA	GGGGAATG	GGGAAAGGGT	540
ATCTGGTAGA	AAGAAGGAAC	AGCTTGTGCA	GAGGTNCAGA	GGCAAGAGAG	AATTTGGCAT	600
ATTTGGGAAG	CTGCAAAGA	TCTCGAG				627

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

GAATTCGGCC	TTCATGGCCT	ACGACTTCAA	AAATATGGGA	ACACAGTTAG	TTATTTTTAC	60
ACAGTTCTTT	TTGTTTTTGT	GTGTGTGTGC	TGTCGCTTGT	CGACAACAGC	TTTTTGTTTT	120
CCTCAATGAG						130

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

GAATTCGGCC	TTCATGGCCT	ACTGGGGGAG	GGGAAGGATG	TGGTTGNAG	AGNGGAAGCA	60
GAGTTTGAA	ACGCATGAGA	GCAGAGCTTC	GTGTGTTCCC	ACCCTCANTG	AGGANGTGTG	120
AGTGGGTGAG	CATGTGAGAG	TTGGGTGTTT	CTACCCTCAG	TGAGGAGGTG	TGAGTGGGGG	180
TGCATATAGA	GGCAGTGCCT	GCTGTGGGGT	CACAACTGGT	GCATGCCAGC	GCCAAAGGGA	240
CCTGTCTTTA	GGGGTCATTT	CAGCCAGCTC	CTCCATCAC	AGATGACAGC	TCCAAGCCTA	300
GAAGGGGCTC	AGTGACAGGG	CCAGGACAAG	CCCTCAGGAC	TGTGGCCTCC	TGGCCCTTGG	360
TTCCCTGACC	CCACAACATG	GTCTCCACAT	GGCTGGCTGG	CTGGCTGTCC	CTGTGTGTGT	420
GTGACACAGC	GTGTGAGTGC	AGGGCTGTGC	CCGGGTGGG	AGGGTGTCTA	TGTGGCACTG	480
ACTATCGAGC	TCGAG					495

(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:620:

```
GAATTCGGCC TTCATGGCCT AGCTGATGAT TCCAAACATT TNGTAAATTA ATTTTCTCT      60
CTTTACCTTT CAGCTTGGAA GGAAGACAGA AGCCTTAACC TCCAGGGTAA CATGTTGCAA      120
TTTGTTCACT TATTAATCTA ACAAGAATGC ACTGAGGTGC TCATTAAATG TCAGACCTTG      180
TGTGAGGTG AGGAAATCCA AAAGCAAAGG AGGCATGAAC CTCCATGCCC ATTCAGAAGG      240
GCACCAGGCC TTTTAAGAAG GGTGGATATG CACAATTGA AAATAACTGA TAGTCTGAC      300
TTATCTTGC AATTAATAAG GCAATTCAT ACACATTTA TACTCGAG      348
```

(2) INFORMATION FOR SEQ ID NO:621:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 294 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:

```
GAATTCGGCC TTCATGGCCT AGCAGGATGG CACCGGACCC CTGTTCTCC ACATACGATT      60
CTACTGTGCA AATTGCCCAA GAAATTGCTG AGAAAATTCA ACAACGAAAT CAATATGAAC      120
GAAAAGGTGA AAAGGCACCA AAGCTTACCG TGACAATCAG AGCTTTGTTG CAGAACCTGA      180
AGGAAAAGAT CGCCCTTTTG AAGGACTTAT TGCTAAGAGC TGTGTCAACA CATCAGATAA      240
CACAGCTTGA AGGGGACCGA AGACAGAACC TCTTGATGA TCTTGTAAC CGAG      294
```

(2) INFORMATION FOR SEQ ID NO:622:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:

```
GAATTCGGCC TTCATGGCCT AGGTCAAGGG ACAATGAAAA TGTGACCCTT ACCAACGACA      60
GAAACTCCCA GGAAGCCACA ATTAAC TCA GACCACCAGG ATATTGGGG AAGTTTATCC      120
TTCTGGAAAC CAGAATTTCT GATTGTGGA AAATTCTATA GATATTCTCT GCCAGACTCC      180
AGCCTATTTG TGTGAGACAT CTGGGGAGGC TCCCCTTTT TCCACCATTT GAGGACTGAA      240
AGTAAATTTA GCTTCCTCAG CAGAAAGAAA AGAAGCTGTT TTGGAGGTTA GGAAGAAGCT      300
CGAG      304
```

(2) INFORMATION FOR SEQ ID NO:623:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 497 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:

GAATTCGGCC	NTCATGGCCN	ACTCTATTGG	TGCAAAGTAA	GATTTACATC	TGTGTTTCAGA	60
ATCTTTGAGA	TAATACCCCT	TTTCTACATT	TCTGCATTTT	TTTTCTGTGA	NCCCCACTAG	120
TATTNCNCCA	TTTNACCTT	TTCATTTAAC	TTATCCTCAC	ATTATAAGAG	ATGGATGACC	180
TATACAGACT	TGGCCTTTGG	GCTTTGGCTT	CATTCAATAT	CATCTTGGGT	ACCACTGAAT	240
ACCGTTCAAT	CTAGAGCTGG	GTGGTAGGTT	GAGATGTATA	TTTCCTAGCC	CAGATCCCAG	300
AATCTAGAAG	AAGTTAAATC	TGATATGACT	TTGATAAATA	AGACAGTATG	TTCTTCTAAC	360
CCCATCTCCC	GTTCTCTGAC	ACTGAACATA	TATATGAAGT	ATATATAACA	TATACCGAGT	420
ATTTAAATTT	TTAGAATAAA	AATGTGCATT	ACTGCACATC	TTCTGTCTT	TCATTCTCTG	480
GTTGAGTTTC	CCTCGAG					497

(2) INFORMATION FOR SEQ ID NO:624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:

GAATTCGGCC	TTCATGGCCT	AGAGCAAGCA	GAGGTGGCCT	GCGTGTGTAT	GTGCTCATGT	60
GTATGTGTGC	ACATGCATGT	CTGTGTGTGG	ATGCCCATGC	GTGTAACATC	TGATGTGGCA	120
CATGATACAA	CATAATTTAT	TTATTATAGA	AACCTGCAAG	TAAAGATTCA	AGAGGAATCG	180
CAGATCCCAA	TCAAAGTGCC	AAGTGGTAGG	TTACCCTGAC	AGATAGTACC	TCCCTTTTTT	240
ATTTTCAAA	TGCTGGCATA	GTTTTGTGTT	CTTTACCAAC	TCATTGATT	ACTGGGGACA	300
TCCTCTGTAC	TTATCACAAC	AGGTTCTCGA	G			331

(2) INFORMATION FOR SEQ ID NO:625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

GAAGTTGCAT	TACACCTTCT	CTTCTGAAGT	AAACACTAAA	AATATCAGGT	AACTTCTGCA	60
TTAAATTTTC	TGCCATCTGA	AGTGCTCCCA	CTTACTATCT	TCAGGTCTTG	GCTTGACAGC	120
ATGGAAGCAA	TGTGACTTGA	AACAGCATGA	TTTTTCAGAA	CATCCTTCAG	AAGTTCAGCA	180
TCCGCAAAAT	AAATTATCCT	AAGAATTGCT	CTAAGGCACT	TATGTCTGAC	CGCAGGTCCT	240
GCTGAGGAAC	TATACACTTC	ATAAAGAACA	CCAAATAATG	TCTTAATAAA	AGACTTAGCC	300
AGTTCCGGAT	CCTCTTTCAT	AAGCTGTGCT	CGAG			334

(2) INFORMATION FOR SEQ ID NO:626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:

GAATTCGGCC TTCATGGCCT AGTCGGATTC CCAGTGGAAC TTTAGTAGTA CTCAGATCCT	60
CCTTTGTTTG GTGCGTAGTA TATTAACAAG TAAACCTGCC TGTATGCTCA CCAGAAAGGA	120
AACAGAGCAT GTCAGTGCTT TGATCCTGAG AGCCTTTTTC CTTACAATTC CAGAAAAATGC	180
TGAAGGCCAC ATCATTTTAG GAAAGAGTTT AATTGTACCT TTAAAAGGTC AAAGAGTTAT	240
AGATTCCACT GTATTACCTG GGATACTCAT TGAAATGTCA GAAGTTCAAT TAATGAGGCT	300
ATTACCTATC AAAAAATCAA CTGCCCTCAA GGTGGCACTC TTTGTACAA CTTTATCCGG	360
AGACTCTCGA G	371

(2) INFORMATION FOR SEQ ID NO:627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:

GAATTCGCCT TCATGGCCTA GATGTTTCAA TTTCGAAGTA CTTTGAAGT TTAGTAATGT	60
CAGAGTTGAA CATTTTCTGT AGCATGACTA TCGACTTGTC TTTCAAGGC AGCCTGCAAA	120
GCCATTGAAC AAGCAAAGAC TCAAAACATC AATAAACTGG TTCTGTATAC AGACAGTATG	180
TTTACGATAA ATGGTAAGCT TTCACATTG ATTTCTTCTG TTTTCCAGT AACTGTGAAG	240
GGAAATTGGT AGGAGGTGTT GTAACAGGGC AGGACCCAAA TGGGAACGGG GGGATGACAT	300
TGGTTTGTC GGTACCGAGC AAAGAGTGAG GATTTTGAG TCTCCCTTCT GCTGCTCTGA	360
TGTTTTCCAC ATGCTTATTT CTTTGCCAGG CACTGGAGAT GCAGTCAGAA GTGGAAGTGG	420
CTCTTACTTC TAGTCTGTGT GTGTATAAGT CACTTAAGAT GGCGTGTGA CTGCTTCTTT	480
GGGAAATGCC CTGAATAGGA GCATGTAGGG GATGTGCTCG AG	522

(2) INFORMATION FOR SEQ ID NO:628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:

GAATTCGGCC TTCATGGCCT ACAAATATC TGTGGGAAGG TGAGCTACTT AGCATTCAAC	60
AATGCAAAGT TTCAAAGCAT TTTGCAAATT TTAAATATAC GCTATAATTC TTCTGTAATT	120
GGTGTCTTTG GTACTTTTTG GGTAAATTGG AGTTATTCCA AAATAATTAT ATTTTATAGC	180
ACTTTTGACA CCATAACACT TAGCATCTCG AG	212

(2) INFORMATION FOR SEQ ID NO:629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:

GAATTCGGCC TTCATGGCCT ACTCCTTCCG CGCGAGTCTC TGGAGAAGCC GCAGCGCGAG	60
TTGCCGCGCG TGCTGCCCGG GGCCGGCTTG CCTTGCGCCA TGGACTGGCA GCCAGACGAG	120
CAGGGCCTGC AGCAGGTCTT GCAGCTGCTC AAAGACTCAC AGTCGCCCAA CACAGCCACT	180
CAGCGCATCG TGCAGGATTA ACTCAAACAA CTCAATCAGT TTCCTGACTT CAACAACACTAC	240
CTGATTTTCG TCCTGACCAG ACTCAAGTCA GAAGATGAGC CAACGCGCTC TCTCAGTGGC	300
CTCATCTCA AGAACAACGT GAAGGCACAC TATCAGAGCT TCCCACCCCC CGCTCGAG	358

(2) INFORMATION FOR SEQ ID NO:630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:

AAGAGAACAA TAAATAGGC AGTCTCTAC CTCTTGCTT ACTCTAATAT AAATCCATG	60
AAGATAAGTA TTGTATCCAT ACTGTTTCATG CTGCACAGCA GTTGCCCTTA TCTGACGGG	120
GACGCATCCC AAGACCCCCA GTGGATGCTT GAAACTGCAG AACTCGAG	168

(2) INFORMATION FOR SEQ ID NO:631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:

GAATTCGGCC TTCATGGCCT ACATAACTGC ATTCTGACCT CCTTCTTGCA GTGCCAAGAG	60
AAATGATGGT GAACTAAGTG CGGGGTGTGG GGTGTTCTC AAAATGCGGT CATTGCTACA	120
GAACTAGGGT TTTTGGTTAG TTACATNCTT TGTGGAAGGA CAGGGTGGTG GGTACAGGTC	180
CCTGAGAAGC AGACATGTGG AATTGTTTGA GACAATCCTA CTCCCTGTGG TACTCTCTCT	240
ATGTATATAT TCCAATGAAG GTAATTACC TCATGCTTTC CTAAATACAT AAATCTTTAC	300
ATTTCAAATG CCTTGTTAGA CTGTACTCAA GATTCCAGAG ACATTTTAAA ATAATTCATT	360
TTCAAATCAT AAATTGGGA AANGGGGCC TGGGATAAGC AAGTTGACTG GGCCACTGCT	420
TATGCCATTG CCTGCACAAT TCTGGGCATG GAGCAGCTCT CCCAGAGCCC ACTCGAG	477

(2) INFORMATION FOR SEQ ID NO:632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:

GAATTCGGCC TTCATGGCCT ACTGCCTCCT GATGAAGTCC CTACTGTTCA CCCTTGNAGT	60
TTTTATGCTC CTGGCCCAAT TGGTCTCAGG TAATTGGTAT GTGAAAAAGT GTCTAAACGA	120
CGTTGGAATT TGCAAGAAGA AGTGCAAACC TGAAGAGATG CATACAAAGA CTACAAGAAT	180

```

TTCAACAGTA ACAGCAACAA CAGTCAACAA CAACTTTGAT GATGACTACT GCTTCGATGT      240
CTTCGATGGC TCCTACCCGT TTCTCCCACT GGTGGAACAT TCCCAGCCTC NGTCTCCTGC      300
TCTAGGATCC CCGACCCATT AAGACTCGAG                                     330

```

(2) INFORMATION FOR SEQ ID NO:633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:

```

GAATTCGGCC TTCATGGCCT AGGAGAAGGC CCTGCAGGCC GCATATGGCG CCAGCGCCCC      60
CAGTGTGACC TCGGCTGCCC TCCGGTGGAT GTACCACCAC TCACAGCTGC AGGTAACCAG      120
CGACCCTGGG TGCTCAGCTT CTTCCTTCC AGGGGGACCA GCGTCACCTT TAGGTGAAGC      180
CCAAAGCATT TGATTTCTGA ATTCTCTGA AATTTTCTT TCTTCCAATT CTCATAAGCA      240
CTCTTCCCAC TGGTCTTTGA TGGTATCTGA GTGGAGGCTT TGTAGTGAGG GATTTTCATT      300
ACAGGGATT TCTTATTCCT TAGGCTTTCT GAAGTATGAT TATCCAGTG TTATTGATGA      360
GGAAACCGAG GTTCACCCAG CTATTCTCGA G                                     391

```

(2) INFORMATION FOR SEQ ID NO:634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:

```

GAATTCGGCC TTCATGGCCT AAGTACAAAT ACCTATTATG TTGGTTGGGA ATAAGAAAGA      60
CCTGCATATG GAAAGGGTGA TCAGTTATGA AGAAGGGAAA GCTTTGGCAG AATCTTGGAA      120
TGCAGCTTTT TNGGAATCTT CTGCTAAAGA AAATCAGACT GCTGTGGATG TTTTTCGAAG      180
GATAATTTTG GAGGCAGAAA AAATGGACGG GGCAGCTTCA CAAGGCAAGT CTTCATGCTC      240
GGTGTATGTA TTCTGCTGCA AAGCCTGAGG AACTGGGAA TATATTCWAC CTGAAGAAGC      300
AAACTGCCCC TTCTCCTTGA AGATAAACTA TGCTTCTTTT TTCTTCTGTT AACCTGAAAG      360
ATATCATTTG GGTGAGAGCT CCCCTCCCTT CAGATTATGT TAACTCTGAG TCTGTCCAAA      420
TGAGTTCACT TCCATTTTCA AATTTTAAGC AATCATATTT TCAATTTATA TATTGTATTT      480
CTTAATATTA TGACCAAGAC TCGAG                                     505

```

(2) INFORMATION FOR SEQ ID NO:635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:

```

GAATTCGGCC TTCATGCCTA CAAATATGTC CTCTGTCAAG ACCCTGAAA CAGTTGTCCC      60

```

CACAGCCCCT	GAGCTCCAGA	TTTCCACCTC	CACAGACCAA	CCTGTCACCC	CTAAGCCCAC	120
ATCTCGGACC	ACTAGGAGCA	GGACAAATAT	GTCTCTGTG	AAGAACCCTG	AATCAACTGT	180
CCCTATAGCC	CCTGAGCTCC	CACCTTCCAC	CTCCACAGAG	CAGCCTGTCA	CCCCTGAGCC	240
CACATCTCGG	GCTACTAGGG	GAAGAAAAAA	TAGATCCTCT	GGCAAGACCC	CTGAAACACT	300
TGTCCCCACA	GCCCCTAAGC	TCGAG				325

(2) INFORMATION FOR SEQ ID NO:636:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:

GAATTGGCCT	TCATGGCCTA	GCTTCCTCTT	CAAAAATGTG	TCTACCTAAG	ATACTATTAT	60
TTAAGCCTCT	GTGTACTTTT	AACCGTAGAA	CTGATTTTAT	AGGAAGACGA	AACCTGTCGG	120
CTTCAAGAC	ATGGAGTGTG	TGCCTTGTGG	AGACCCTCCT	CCTCCTTACG	AACCGCACTC	180
TCATCCACAA	AGAACCTCGA	G				201

(2) INFORMATION FOR SEQ ID NO:637:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 417 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:

GAATTGGGCC	TTCATGGCCT	AGGCAAAGCC	TGAAAGTCCT	TGGACTTCTC	TGACCAGAAA	60
GGGAATTGTT	CGAGTTGTAT	TTTTCCCTT	TTTCTCCGG	TGGTGGTTAC	AAGTAACATC	120
AAAGGTCATC	TTTTTCTGGC	TTCTTGTCT	TTATCTTCTT	CAAGTTGCTG	CAATAGTATT	180
ATTCTGCTCC	ACTTCTAGCC	CACACAGCAT	ACCTCTGACA	GAGGTGATTG	GGCCGATATG	240
GCTGATGCTG	CTCCTGGGAA	CTGTGCATTG	CCAGATTGTT	TCCACAAGAA	CACCCAAACC	300
TCCTCTAAGT	ACAGGGGGTA	AAAGAAGAAG	GAAATTAAGA	AAAGCAGCCC	ATTTGGAAGT	360
ACATAGGGAA	GGAGATGGTT	CTAGTACCAC	AGATAACACA	CAAGAGGAAT	GCTCGAG	417

(2) INFORMATION FOR SEQ ID NO:638:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:

GAATTGGGCC	TTCATGGCCT	ACCCTCTCC	AATGAGTCCC	GCCAATGCCC	CAATGCCCCG	60
TGCCAGTTCC	CTTTCTACGG	TGGTGAGTCG	GGCTACCACC	GGGCCCTGCT	GGGCCGTGCAG	120
ATCTTCAATG	CCTTCATGTT	CTTCTGGTTG	GCCAACCTCG	TGCTGGCGCT	GGGCCAGGTC	180
ACGCTGGCCG	GGGCCTTTCG	CTCCTACTAC	TGGGCCCTGC	GCAAGCCGGA	CGACCTGCCG	240

GCCTTCCCGC TCTTCTCTGC CTTTGGCCGG GCGCTCAGGT ACCACACAGG CTCCTTGGCC 300
TTTGGCGCGC TCATCCTGGC CATTGTGCAG ATCATCCGTG TGATACTCGA G 351

(2) INFORMATION FOR SEQ ID NO:639:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 567 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:

GAATTCGGCC TTCATGGCCT AATTTTTTTG AGACAGAGTC TTA CTCTGTT GGCAGGCTG 60
GAGTGTGGTG GTGCGATCTC GGCTCACTGC AACCTCTGCC GCCTGGGTTC AAGCTATTCC 120
CTGCCTCGGC CTCCCAAAT ACTGGGATTA CAGGCGTGTG CCGCTGTGCC CAGCCGCTGT 180
CTAGTCTTTT AAAACTTGGT GTTTGAGCAT GCACATTCTC CTTCTGGAAT ACCTGATCAC 240
CCAGCACAAAC TCACGTTNTC TTCTGCTGG CTACCTTGC CTTGCTGTGA CTGTGTCATG 300
GTTCTCAGCT AGACTCGGTG GCGTGTGTA TGGCCCAAGC ATCGTCTGCC CAGTGGGTGT 360
CCTGTTACCC ATGTATGACA GACTGTACCC AAGATATCAG TCTTACGAAT AAGGCCACGA 420
TGAACACTTT GAGCTTTTTC TGTATCTAGC ATATCCCAG GGTAGATGCT CAGGCAGGAA 480
ACTGGTGGGA GATGAGGGAT ACACAGATGG CTCCCNACAG GTGCTGTGAG GTGCTCAGGA 540
GTTTATCATC ACTTAACTGA GCTCGAG 567

(2) INFORMATION FOR SEQ ID NO:640:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:

GAATTCGGCC TTCATGGCCT AGCTCCGCAN AGGTAGGGAG GGAAGGGCCC CTCAAATANA 60
TGGAGGGAGC AACATCCCTC CAAGGGAAAG GGCTTCCAAN ACNAAATCCT GGACAGAAGC 120
GGAGCANGGG ATGGGCCTCC TTACAGAGCA GGAGGAAGAC AGCGCTCTTC NAANANGAAA 180
GGAGAGGGGC ATCRAAGTCC CTCACAATGG TGGAGGGGGC GGGGCTTCTC ACCGAAGGCA 240
GAGGAGGGGG CCTTAACTGA GGGGCAGGGC GCCTCCAGG GATGAAAGGA GGAGGCCTGC 300
GCGAGAGCAG GGA AAAAGTT CAGTCCTTTC CTGCATTTCT TGGCTGAAGG GGTCTTAAGA 360
TGAAGGGTTC AGTGTCAGA AGGAAAAAAC CCTGAGATGG GCCTAGACCA ACATGAACTC 420
AGCTAGCAAG TTCATACATG ACATGGGACT GATAGACTTG TGTGGCATCT CGAG 474

(2) INFORMATION FOR SEQ ID NO:641:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:

GAATTCGGCC TTCATCCTTG AGAATATCAG AATTAGAAAG CCAGGTTGTT GAAATGCATA	60
CTAGTTTGAT TTTAGAAAAA GAACNAGTAG AAATTGCAGA AAAAAATGTT TTAGAAAAAG	120
AAAAGAAGCT GCTAGAACTA CAGAAGCTAT TGGAGGGCNA TGAGAAAAAA CAGAGAGAGA	180
AAGAAAAGAA AAGAAGCCCT CAAGATGTTG AAGTTCTCNA GACAACTACT GAGCTATTTT	240
ATAGCAATGA AGAAAGTGA TTTTAAATG AACTCGAG	278

(2) INFORMATION FOR SEQ ID NO:642:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 413 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:

AGGGAGAGGA GGCTGGGAAC AACGTGACCC ACTAAGGATT CTGCTCCAAG GACAGTGGGT	60
TTCCCGCTGG GCACCCACTC TTAAGTGCAG ATCGGGGAGAC TAAGACAGGA ACACCCGCG	120
TGGGCAGGCC AGGCTGGAAG GATAGAGGAC TGTGGTCGAA CCAAGAGGAG GTTCAACTGT	180
GACTTATGCC AGTGTGGTCA CGAAGGCAGA TGGGTTGAAC TGAAAAGGGG GCACCGGTTT	240
CTGGCATGGA GGCACCCAAG GTCTTAGGAG GTGGATGGAC TGTCACATGG GCAAAGAAAT	300
GTCCAGGGC AGGACTGCAA AGGCCACAGA AGAATAATTT GGGAGAGAGA CAACCCATGA	360
GAAGTCACTC AGACCAGGGT CAGAAACAGA ACAGGAACAA CAATGGACTC GAG	413

(2) INFORMATION FOR SEQ ID NO:643:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 658 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:

TTTCNTCCCT TNGAATGTTT GTCCCTTTTT CTGTTTTTT TTTGACACAA AATTNCAAGT	60
TNTACCAAGC AAACATTAAA TCCAAGTTGG AATTTTAATT AAGGAATTCG GCCTTCATGG	120
CCTACTGGTG CCTTCCCGGA AGGGCTCAGA GCGGGCTCG GGCAAGCACT TTAACCTTTT	180
AAGCCCAACC AGATGAGTTG CCTGCAGTTT TGGAGGCCTT CAGAGCATT CACTAGACCT	240
CTGTCTGTGT CGGTCCAATG TCTTTAGCCA AGCTTTGATT AAAGATGACT TCCTTGTTTG	300
CTCAAGAAAT TCGCCTTTCT AAAAGACATG AAGAAATAGT ATCACAAAGA TTAATGTTAC	360
TTCAACAAAT GGAGAATAAA TTGGGTGATC AACACACAGA AAAGGCATCT CAACTCCAAA	420
CTGTTGAGAC TGCTTTTAAA AGGAACCTTA GTCTTTTAAA GGATATAGAA GCAGCAGAAA	480
AGTCACTACA GACCAGGATT CACCCACTTC CACGGCCTGA GGTGGTTTCT CTTGAGACTC	540
GTTACTGGGC ATCAGTAGAA GAATATATTC CCAATGGGA ACAGTTTCTT TTAGGAAGAG	600
CACCATATCC TTTTGCTGTT GAAAATCAAA ATGAAGCAGA AAATACCATT CCCTCGAG	658

(2) INFORMATION FOR SEQ ID NO:644:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:

GAATTCGGCC TCATGGCCTA CCAAAGAGTG TTATACATGC TCAGCAAACA ATATCTACAG	60
GAACTAGCCC TCAGGAAAGT AAAAAAAAAA AAAAAAAAAAG GCAGCAGAGG GCCAGCCCAT	120
TCTTCTCATA GCTCACTGAT ACACTTGGTC ACATTCTGCC ACTACCTGCA AGGGAGGCTG	180
CGGAAAGGTA TCCCTACAGA GGCAGACGTG CCCAGCAAAA ACTTTGGCCG GTGGGGGGAC	240
ACTCCATGAC AAAAAATACA AAGGAGAGAA TGGGAGCTCG AG	282

(2) INFORMATION FOR SEQ ID NO:645:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 172 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:

GAATTCGGCC TTCATGGCCT ACCTTTCTCT GACCTGTGCC CTCGGCCTCT TGGCCTCCAT	60
CGCCATGACC TTTGCCACCC AGGGCAAGGC ACTGCTGGCT GCCTGCACTT TTGGGAGCTC	120
TGAATCTAGT GCCCTCGCAC CTGACTGTCC CTTCGACCCC ACACCACTCG AG	172

(2) INFORMATION FOR SEQ ID NO:646:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:

GAATTCGGCC TTCATGGCCT ACCAGAAACC GGCCAGGCAA GGAAAGAGGC CGGTCACCAG	60
AAGCCAGCAG GCGTGGGGTG TGATACTCTC TATAGCCACT ACAGGGCGCG CGCAGGTCCG	120
GGATCTCCCC AGTTGCTAAT CCCGGCTCTG CCACTCAATC CTATCCCTAG TTCCCGAGCG	180
CGGGTCCCCC GCCTTGCACT CTCCAGCCGT GCGGGGCCGG GAGCAGGCCT CCGGCCTCCC	240
AGACTTCTAG AGCCCGCCGG GCCCATCTTT GTACTCATCC ACCCCGGCTC GAG	293

(2) INFORMATION FOR SEQ ID NO:647:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:

GAATTCGGCC TTCANGCCT ACAGAAACAG AAATGCTAAC TGAAATGTAT TCTTCTAACA	60
AAGCATTTCT AACTTTCTAG AATGTAGTCT TTCATTTTTC TTTATCTTTT TTCAGCTTAT	120
TCCCAAATAT ATACTTTGGC CATTTAAATA AATGGCCAAA GAAATGGCCA AAAAATGCTT	180
TATTAGTTT TTGTTTATT ATGAAGGATG ATTACTCTT AATGCTGCTA AATCTTTTTC	240

TAGCTCTGTA TTTCACCTCA AGAAAACTCG AG

272

(2) INFORMATION FOR SEQ ID NO:648:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:

GCGAGCTGTT GGGATTACAA AGTTGCGCGT TTCATCGGTA CAAACTGGTC TTGAAACCTC	60
CTTTGTGAGA GCAATTGTAG TGTCCAAATT GTTAGGGAAA ACAAAAAAAA AAAATCCCAA	120
GGAGGAGGGT TTTCCCCCT TCCCTGTTG GTTTATCACA GCATTTTGCT TTTTTTTTGG	180
CACAGCTTTT TACGTTCTT TCCATTCAGC CATCACAGAG CCTGTTCCGG GTGGAACCA	240
ATCCACACGC CTCGAG	256

(2) INFORMATION FOR SEQ ID NO:649:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 266 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:

GAATTCGGCC TTCATGGCCT ACCCACCTTG GCCTCCACACA GTGCTGGGAT TCCAGGCGAG	60
AGTCCCTGCG CCCAGCCCA CTGTCTATT CTGTGTTTTG CTGCCTGTTT TTGGTGCTT	120
ATCTGCACAT GAATATTTAT AGCAGCTTTA TTCATAATTG CCAAACTTG GAAGAAACCA	180
CAATGACAAT GTCCTTCTAT AGGTACACCC ATACAATGGA ACATTCAGTG ATAAATGAG	240
CCATCAAGCC ACCCAAAGG CTCGAG	266

(2) INFORMATION FOR SEQ ID NO:650:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 490 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:

GATTTCTCAG CTTTGAACA GAGTGGACTT GTCAATATCA GAGCAGAGCA CCAACTGAA	60
GATGTCTCAC AGAGACAGTA ACCACCAGCT TCAGCTTTTG GACACTAAAT TTAAGGTAC	120
AGTTGAGGAA CTCAGTAACC AGATATTATC TGCACGGAGT TGGTTGCAAC AGGAACAAGA	180
ACGGATAGAA AAAGAGCTTT TACAGAAAAT TGATCAGCTT TCCTTGATTG TTAAGGAAAA	240
CAGTGGAGCC AGTGAAAGGG ATATGGAGAA GAAGCTCAGC CAGATGTCAG CCAGGCTTGA	300
CAAAATAGAA GAGGGTCAAA AGAAGACTTT TGATGGTCAG AGAACAAGGC AAGAAGAGGA	360
GAAGATGCAC GGGCGAATCA CCAAGCTGGA GTTACAGATG AACCAGAACA TCAAGGAAAT	420
GAAAGCAGAA GTTAATGCTG GGTTTACAGC CGTCTATGAA AGCATAGGAT CCCTCAGGCA	480
AGTTCTCGAG	490

(2) INFORMATION FOR SEQ ID NO:651:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:651:

```

GAGATAGAGG GGACCCTGGC TATGGACATT TTGAATTATG TCGGGAGAGC TGATGGANAA      60
AGAGGCTCCN GGAGGACTGG TTAAACTGAA GCCNGGAATG AGATGAAATG TATAAAATTC      120
TCTTGAATGA TTATGAATAT CGTCAGAAAC AAATCNTAAT GGAAAATGCA GAACTTAAGA      180
AGGTTCTTCA ACAAATGAAA AAGGAAATGA TTTNTCTTCT TTCTCCCAA AAGAGAGAAC      240
CTCGAGAAAG AGTAGATGAT AGTACAGGAA CTGTTATTTT CGATGTTGAA GAAGATGCCN      300
GGGAAGTAAG CAGAGAGAGT ATGTGGGACC TTTCCTGTGA AACTGTGAGA GAGCAGCTTA      360
CAAACAGCAT CAGAAAACAG TGGAGAATTT TGAAAAGTCA TGAGAAAAG CTTGATAACC      420
AAGTTTCAAA GGTACACCTG GAAGTTTTA ATGATGAAGA TGTAATCTCA CGACAAGACC      480
ATGAACAAGA AACTGAAA

```

(2) INFORMATION FOR SEQ ID NO:652:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 203 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

```

GAATTCTTCT TTCTCTATAA ATTTGCCTAC TATTGAAGAT TCTTCAGAGG AAGAAGAATT      60
GAGAGAGGAA GAAGAATTAT TAAAGGAGCA AGAAAAGCAG AGGGAAATAG AACAGCAACA      120
AAGAAAGAGT TCTAGTAAAA AATCAAAGAA AGACAAAGAT GAACTTCGAG CTCAGAGAAG      180
AAGGGAAAGG CCAAAGACTC GAG

```

(2) INFORMATION FOR SEQ ID NO:653:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:

```

GGAAAGAAAN GGACAAACCT ATAAATTAAC TCAACCTATA TCTCCCTTGA AAATACTTTC      60
AGGCTCCACC AAAACGTAGA ACTGAAAGCA TGTATTTTGG AAGAAAGAGA TACATTTTGT      120
ATGCTTTCTT TTCCTTTTGT AGATTCCCAG TTTATTTTCT AAGACTGCAA AGATCACTTT      180
GTCACCAGCC CTGGGACCTG AGACCAAGGG GGTGTCTTGT GGGCAGTGAT GGGGNCCTCG      240
AG

```

(2) INFORMATION FOR SEQ ID NO:654:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:

GATTCGGCCT TCATGGCCTA GGGAGGAGAA GAAGGGGGAG AAATCACAAA GAGATTGGGG	60
AGGAGATGAA GTAGCAGGGC TCAGCGATT CTTCAATTCC AGTGACACACC CAATAGTGTG	120
TTGGAAGAAT GCACACTGTT CGGGATTTGT GGGAGAATTG TCCCATGACA AAGGAGGCAG	180
GGTTATGCTT GTTATAGTCC AATAAGCCGT GCCAGTCAAA CAAGAACCCA CACTCCTCGA	240
G	241

(2) INFORMATION FOR SEQ ID NO:655:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:

GAATTCGCCC TTCATGGCCT AGTGGTGAGA CTGAGCAGAT TTAATTAATG TCTGTTATGT	60
TCAGGGCACA AGGGTGAGCT CTTGCGAGGG GCTGATGCAC TGGGTGTGGA GCTGAGCAGA	120
GAGGCCTAAC CAGGATCAGG CAGGAGGGCA GGGATGGTGG CAGCCATAGG AGGGCAGGGT	180
AGGGTAGGGC CTCTGAGGAG GAGGGAAAAA GTGAAGGAGA GGCTTTGGAC CTGGTGACAG	240
AGTGATCAGA TGACAGAGGG GTTTTGGGA GACTCGAG	278

(2) INFORMATION FOR SEQ ID NO:656:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:

GGAAGGAGAA GTGGAGAAGA AATCAGTCAG CCGCAGTGAA GAGCTCAGAA AAGAAGCAAG	60
ACAATTAAAA CGGGAAGTCT TAGCAGCAAA AAAAAAAAAA GTAGAAAATG CAGCAAAACA	120
AGCAGAAAAA AAGAAGTGAA GAGGAAGAAG CCCCTCCAGA TGGTGCTGTT GCCGAATACA	180
GAAGAGAAAA GCAAAAGTAT GAAGCTTTGA GGAAGCAACT CGAG	224

(2) INFORMATION FOR SEQ ID NO:657:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:

ATACAGTAAT CAAAGTAAGT AATATTTCAA TCCAATATTT TAAAAATCA GAATTAATGC	60
AAAAAAAACC ATGATGAACA AAATATTAAA ATTTAAAATA AAGACAGGAT TAGTATTACT	120
GAGTTTTTCT TTTGTCCCAG GCTCTAATAT GGCTTGGCAT GGGGCAGAAC ATTACAACAT	180
ACCAGTCGTG TCATGGTGCC CAAGGCTCCA CAGACCTCAG TGGCTCCCTG CTGCTCGCCA	240
CAGCAATCTC GAG	253

(2) INFORMATION FOR SEQ ID NO:658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:

GAATTCGGCC TTCATGCACT TTTGAGCATC AGTTTCTTTT CACTCCTTCT TCATGTGCTA	60
TTCTTCCAA ATCTTTCCCA CTTTCTTCT TCTCTCTCT GTCTTTTCT CTCCCTCTTC	120
TGTTGTCTC TGGTTTCCAT CTGTTTCTCC TTCTCCTTCC CCATTCTCA CTATCCTCTC	180
TTCTGTCTCC TCACCTACTT CTCCATCCCT CCTCTCTCCA GCCCTCTCTC CCCCTGTCT	240
CGAG	244

(2) INFORMATION FOR SEQ ID NO:659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:

GAATTCGGCC TTCAGCCTAG TCTCAAACCT CAAGCAAACC TCCTGCAATC CCAGCGCTTT	60
AGGAGGCCGC TCGAG	75

(2) INFORMATION FOR SEQ ID NO:660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:

GCNTTCATGG CCTAAGTTCA CCTTTAANTC TTTGATGACC ATTTCCAGAN GCCCTTACCG	60
TGGGCTATCT TAGCTTGATG TGCTAATCAA GTTCCCCCTA ATTTGACATA CTAGAATCTA	120
ATACTAGAGG CAGCATGACA TTATTAAGGG GGAGGAGGTT GAGAAGCACT AACCTOGAAG	180

TTAGAATTTT	TGGTTTGTCA	TCCCAGTCTG	CTAATTAGCT	TTCTGATTTA	AGACAAAATA	240
CTTTTCTGT	GCCTTCTGGG	GGTCAAATTC	GATTTTAAAG	ATTCTCTCAG	TTGGAAGAAA	300
TCTAACTAAA	AATATACTTA	AAATAATTCT	TTGGTAGTAT	ATTATTTTGA	AATTTGGTCC	360
AGAATCCTAT	TTGTTTATTC	CTGTAGTATA	CATACATCTG	TAGTTACCCA	GCAAGCGCGC	420
TCCCTATAGT	GAGTCGTATT	AATTCAGAG				450

(2) INFORMATION FOR SEQ ID NO:661:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:

GAATTCGGCC	TTCATGGCCT	AGAGAAAAAA	AATTAGAGTG	ATTCAGGAC	TCAAAGGAAG	60
AGCCTTGCAA	AGAGTTGGGA	GGATTAAACT	CTATGGATT	AAGCTCTGCC	TGCAAAATAA	120
CATCGCTGGG	AATTTAGACA	CAAATTAGGA	ATATTCTGGA	ATTCATTAG	CAGCAAATCT	180
CCTGACTAGT	TGTCAAATGG	AGCTGTCTTA	ATTGGCCTGT	TCTAAATGGG	CCTGTCTCTAA	240
TTGCAGAAAT	ATTGCAGAAT	ATGTTTTTAG	TAAGCTCTCT	ATAGAAAGTC	ACCTCTGAGT	300
TGCTCAGCAT	TTAGATTCAA	ATATTCAAAT	GTTTTTTAAA	AATGCCAGCA	TATCAATTAT	360
ATTGAAGAA	CAGTATAGAG	GCTTGAAACA	TGCCAAACAG	CAGGGAACAG	GAATAACCTT	420
TAATGAGTGC	CTACTCTGGT	GCAGGGTCCT	TTACACACAT	TACATTATGT	GATCTTCACA	480
ACAAACCGAC	TCGAG					495

(2) INFORMATION FOR SEQ ID NO:662:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 474 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:

GAATTCGGCC	TTCATGGCCT	ATAGGCCATG	AAGGCCGGCC	TTCATGGCCT	ACGAGGAAAG	60
GTCAGAGAGA	TGCGAAGTTT	CTGGCTTTGA	AGATGGGGAA	AGGTCTCCAG	CCAAGTGTGA	120
GCAGCCTCTA	AGAGTCAGAG	AAGCCAAGGA	ACAGCTTCTA	CTCTAGAGCC	TCCAGAAGGA	180
TGGCAGCTCT	GCTGATGTCT	GGCCTTATCT	CAGGGAGCCC	TGTTGGATT	TGAGCTGGTG	240
GAAGTGTGAG	ATAATGACTG	TGGTGTTTAA	GCCAGTAAGT	TGGTGTAAAT	TGTTAATGTG	300
ACTGCAGAAA	CCCAATAGAC	CGAGTGCGTG	TTGGGCTCTC	CCTGTACAAA	GGCAGAGGGA	360
CAGCAAGTGT	GAGCAGGCC	TGCTGTGAGG	TAGAGGGCAT	CCTCTGAAGT	GTGTGGGGAA	420
GGGGGAGCCT	CACATGAGCC	CAGGGCTGCC	ACATGTTTCA	TCTGAGCGCT	CGAG	474

(2) INFORMATION FOR SEQ ID NO:663:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:

GAATTCGGCC	TTCATGGCCT	ACTCTACTCG	TGCGGTGCTT	CTTCTCCTTG	GCATACAGCT	60
CACAGCTCTT	TGGCCTATAG	CAGCTGTGGA	AATTTATACC	TCCCGGGTGC	TGGAGGCTGT	120
TAATGGGACA	GATGCTCGGT	TAAATGAC	TTTCTCCAGC	TTTGCCCTG	TGGGTGATGC	180
TCTAACAGTG	ACCTGGAATT	TTCTCTCT	AGACGGGGGA	CCTGAGCAGT	TTGTATTCTA	240
CTACCACATA	GATCCCTTCC	AACCCATGAG	TGGGCGGTTT	AAGGACCGGG	TGTCTTGGGA	300
TGGGAATCCT	GAGCGGTACG	ATGCCTCCAT	CCTTCTCTGG	AAACTGCAGT	CAACCTCGAG	360

(2) INFORMATION FOR SEQ ID NO:664:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:

GAATTCGGCC	TTCATGGCCT	ACCCTGTGAA	AGTGGTGCCT	GA CTGTCTGA	GGAGGGACGT	60
GGGCTAGAGA	GTTCTCCCTG	GGCTCAGGAA	GGATAGCTTG	GTTGGTAAGG	GAATGCAGTG	120
TGGATGACAC	TGAGGCTGCC	AGAGGTCTTG	GGTTGGCTGC	TCCTAGGTGG	CTTGATGAAA	180
ATGGGAGGAC	CAGAAGAATT	GGAA GTTGCA	GCCAACTGAT	GGCTGCTACT	GAAGATTCCT	240
GACAGGAAAT	AGAAAATAGG	ATGTAAGACC	CTCCTCTCCT	CCTTC TGGCT	CCCAATATTT	300
TCTGGTGATT	CCCAT TGGTG	GATGCTAACA	GGA ACTCACC	TGGCAAGGGA	GCTTGAGACA	360
TGTAGTTTGA	GAGCTCGAG					379

(2) INFORMATION FOR SEQ ID NO:665:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:

GAATTCGGCC	TTCATGGCCT	AATCACACAC	CAACAAAACA	CATTATTTT	GTAATTTATT	60
TTCTCCTGAT	ATTTATGCTA	GAAAAGTCCA	TTTGATTTTC	TTTACTATG	GCATGTTTTT	120
ATAGGTTCTG	TCITTATTTT	ATTAA GTTCA	TGTTTTTACT	CTTCATTATC	AGGAGTTCCT	180
ACCATATTTT	ATTNGCAAGC	CTCGAG				206

(2) INFORMATION FOR SEQ ID NO:666:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 469 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:

GCCGATGAGG	ACCAAGATNA	AAACAGTGCT	CAAAAGTCGT	GGCCGCCCAC	CTACAGANCC	60
GCTGCCCGAC	GGGTGGATCA	TGACATTCCA	TAACTCTGGA	GTCCCGGTGT	ACCTACACAG	120

AGAGTCTCGG	GTGGTCACCT	GGTCCAGGCC	ATACTTCTTG	GGAACGGGAA	GCATACGGAA	180
ACACGACCCT	CCTCTGAGTA	GCATCCCTTG	TCTGCATTAT	AAGAAAATGA	AGGACAACGA	240
GGAACGGGAG	CAAAGCAGTG	ACCTCACCCC	TAGTGGGGAT	GTGTCCCCCG	TCAAGCCCCT	300
GAGCCGATCT	GCAGAGCTGG	AGTTTCCCCT	GGATGAGCCT	GACTCTATGG	GTGCTGACCC	360
GGGGCCCCCG	GACGAGAAAG	ACCCACTAGG	GGCTGAGGCA	CCCCCTGGGG	CCCTGGGGCA	420
GGTGAAGGCC	AAAGTCGAGG	TGTGCAAAGA	TGAATCCGTT	GATCTCGAG		469

(2) INFORMATION FOR SEQ ID NO:667:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 331 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:

GAATTCGGCC	TTCATGGCCT	ACACATACAA	CAAACCGAAG	CTTCCGAAC	CCGAAGAGGA	60
ACTTCTCCAG	CAATTTAAAC	GGGAGGAGGT	GTCCCAACA	GGGAGTTTCA	GTGCCCCTA	120
CTTGTGATG	TTTCTCTTAA	CTGCTGCCTG	CTTATTTTTC	CTAATACTGG	GACTGACTTA	180
CCTAGGAATG	AGAGGGACAG	GAGTATCTGA	GGATGGAGAA	CTCAGCATAG	AAAACCCCTT	240
TGGTGAACA	TTTGGAAAAA	TACAAGAAAG	TGAAAAAACT	CTTATGATGA	ACACATTATA	300
TAGCTTCAT	GATCGATTAA	CACAGCTCGA	G			331

(2) INFORMATION FOR SEQ ID NO:668:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:668:

GAATTCGGCC	TTCATGGCCT	AGGACCCAAA	GTCCGCGTGG	AACCGCGATA	GGGATCTGTC	60
AGGGCCCCCG	GCCGGGTCCA	GCTTGGTGGT	TGCGGTAGTG	AGAGGCCTCC	GCTGGTTGCC	120
AGGCTTGCTG	TAGAGGTGGA	GCACAGTGAA	AGAATTCAAG	ATGCCACCTA	ATATAAACTG	180
GAAAGAAATA	ATGAAAGTTG	ACCCAGATGA	CCTGCCCCGT	CAAGAAGAAC	TGGCAGATAA	240
TTTATTGATT	TCCTTATCCA	AGGTGGAAGT	AAATGAGCTA	AAAAGTGAAA	AGCAAGAAAA	300
TGTGATACAC	CTTTTCAGAA	TTACTCAGTC	ACTAATGAAG	ATGAAAGCTC	AAGAAGTGGA	360
GCTGGCTTTG	GAAGAAGTAG	AAAAGCTGG	AGAAGAACAA	GCAAAATTTG	AAAATCAATT	420
AAAAACTAAA	GTAATGAAAC	TGGAAATGA	ACTGGAGATG	GCGCACTCGA	G	471

(2) INFORMATION FOR SEQ ID NO:669:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:669:

```

GAATTCGGCC TTCATGGCCT AGAGAGGTTG CTCATTTCGTC AGAGCGTGCT GCCCACCTC      60
CACCCCTGCA TGGCAGAAAC TGTGCAGGGG ACGAGGCCAA GGAATCAGGA GACCCAGAGG      120
CAGGGGTGGC CCGGAGACGG TGAAGAAACC AAGACGCAGA GAGGCCAAGC CCCTTGCCTT      180
GGGTACACA GCCAAAGGAG GCAGAGCCAG AACTCACAA CAGATCCAGA GGCAACAGGG      240
ACATGGCCAC CTGGGACGAA AAGGCAGTCA CCCGCAGGGC CAAGGTGGCT CCGCTGAGA      300
GGATGAGCAA GTTCTTAAGG CACTTCACGG TCGTGGGAGA CGACTACCAT GCCTGGAACA      360
TCAACTACAA GAAACGGGAG TATCTCGAG                                     389

```

(2) INFORMATION FOR SEQ ID NO:670:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:

```

GAATTCGGCC TTCATGGCCT AGTGTACAAA AATATAGAAA GAAAAGAACA AACAAAAAAA      60
GAGACAAAGG TGGAATACCT TTTTGAAATA AAAGAGAGCT AGCAATGCAG TACATGGTCC      120
TTGCCCTATT ACTATCCATC CTCATCCTAG CAATAATCCC CATCCTCCAT ATATCCATAC      180
AACAAAGCAT AATATTTTCG CCACTCGAG                                     209

```

(2) INFORMATION FOR SEQ ID NO:671:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 271 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:

```

GAGTTCATTC AAGATATTTT TCACTTGCTG TTCAGGAGCT TTGATGTGCG TCACCATTC      60
TGGCATGTTT ACGCTGTTCC TGTGCAGGTA TTTGAGGAAG ACGTCTGCAT TCCTCCGAGC      120
AAGGGTGCAA GCCTTCAGGA ATGCCTCCTT CTGTCCAGG TGCTTGCTGA TCATGGGCGT      180
CACGTGGTCC GTCTCAGAGT TTGGGCCCCAG CTTATCCGCC CCGCCACACC AGTCTTCTTC      240
TCTCTGTGAC TCCCTGTTCC AGGCTCTCGA G                                     271

```

(2) INFORMATION FOR SEQ ID NO:672:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:

```

GAATTCGGCC TTCATGGCCT AAGATAAATT TGACAAAGTT AACTGAAATT TATCTGGTCC      60
ATTTTATTCA TGCTACTAAG ATGGGAATCT TTAACACAA GGGTCAGCAA GCTTTGGCCC      120
ATGGATTGTC CACCTGTTAC GTAAATAAAG TTTCTTTGAA ACAAGCCTAC ACTCATTCAT      180
TTATGTTTTG TCTGTGGTTG CTTTCCACAA CTGCAGAGTT GTATGGCTTG CAAGTCTAAA      240

```

AACATTTACT ATTTGGCCCT CTAAGAAAAA GTTAAGACAC CTAGTCTAAT GGCCTTTTGG 300
 GAAAAAACAA ATCACTAACT CATAATCATT TATATCCATT ATTTTCTGCA TAAATGTAAT 360
 GCTATTGTAC AGGGTACTCG AG 382

(2) INFORMATION FOR SEQ ID NO:673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:

GAATTCGGCC TTCATGCCTA CCAAATTGT CTAAGCACTG GCCAGTCTGT TGTGGGCATT 60
 GTTTTCTACA ACCAATCTG GGTTCCTTTC TTCTTTCTTT AAACATAGAG GTACCACCAC 120
 AAGGGATGCC CTACTCTCTC GCAGCTCTTG AAAGCATCTG TTTGAGGGAA AGGTCTCTGG 180
 GCAAGCAAGT GGTATTATGG ATTGCTTGCT TCCCTTTTTC CACCTGGGAC ATTGCAATCA 240
 TAAAATAACA GTAAATCCA AACCTCAAAA ACTATTATGG CCTGAGCACA GCTGAAATCT 300
 AGCAGAGTTT AACTCTTCTG CCTCCATGTC TGTCACCTAT AATTCAGGTT CTGCTGTTGG 360
 CTTCAGAACCA TGAGCAGAAG AATCGTTTTA TGCTAGTTAT TGCATTCATG GTTGAACTC 420
 AACTTAGGGA AAGGGTTCCA ATGTATTAAG CAATGGGCTG CTTCTCCCA ATCCTCCTA 480
 ACAATTTGTT GTGTGGACTT CTCATCTAAA AGGTTAGTGA CTCGAG 526

(2) INFORMATION FOR SEQ ID NO:674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:

GAATTGCTTC TCAATTACC CGAGATTCA TTCGAGATTC AGGTGTTGTC TCACTTATTG 60
 AAACCTTGCT TAATTATCCA TCCTCTAGAG TTAGGACAAG TTTTGTGGAA AATATGATTG 120
 ACTGGCTCGA G 131

(2) INFORMATION FOR SEQ ID NO:675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:

GAATTCGGCC TTCATGGCCT ACCTAATCTT CCTTTTCTTT TTAGCATTTT TGGGCTTTTC 60
 AAAGCAATCT CCCCCAAAAA AGAATCATTT GGTTCCTGAA AAGAAAACAG AATCAGCAAC 120
 TTTTCGGGTG TGTGGTGAAA ATGTCACGTG TGTGGAATAC GCTATCTCCT GGCTACAAGA 180
 CCTGATTGAA AAAGAACAGT GTCCTTACAC CAGTGAAGAT GAGTGCATCA AAGACTTTGA 240
 TGAAAAGGAG TATCAGGAGT TGAATGAGCT GCAGAAGAAG TTAAATATTA ACATTTCCCT 300

GGACCATAAG AGACCTTTGA TTAAGGTTTT GGGAATTAAC AGAGGACTCG AG

352

(2) INFORMATION FOR SEQ ID NO:676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:

GAATTCGGCC TTCATGGCCT AAACCCATAA AACAGGAATT CCTTATAATC CTAGAGGACA	60
AGGCATTATA GAATGGGCAC ATCAAACATT ACAACGAATG TTGAAAAGAC AAAAAGGGGG	120
TATAGGAGGC CAACTACCAC CTCAATCAAA ACTACATTGA GCCTTATTGA CTTTAAAATT	180
TTTGACTCCT GGTACGGATG GTAAGACTCC AGCAGAAAAGA CATTGGCAAG TGTTAGAGGA	240
AAAGACTCGA G	251

(2) INFORMATION FOR SEQ ID NO:677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:

GGGCATTGTC AGTTTTCTTC CCTGCTGCAT GTAATGTCTC AGAATCAACA TTCTTTTAAA	60
ATCTAGACTA TATTTTGAGG CAATGAATTA CTTATATTCA ACTTAGGCTT GTTTTGACAT	120
TCAGTAGAAC TTAAAGTCA ATCTAAAGGC TTCAGTCCAC ATTTTTTTAT ACGTTGTATT	180
TTAAAAACGT TTGAAAGGAG TCTTACACCT GTATCATGAA AACTGAATCC TTTTGAAATA	240
CCACTATATG AAGAGAGAGA TGAATTTAG TGAACAGAAT TGAAGAGGTG CTCATAATTT	300
CACTATGCAA ACTTACCCA GTCAACTCGA G	331

(2) INFORMATION FOR SEQ ID NO:678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:

GAATTGAACA ATGCTGACAG GCTGGTANTC CTGCCCTGAA GCAACTCACA GACTCATAGT	60
TATAGAACAT CTTTATCTTT AGTTAATCCA TNGCACAGCA TTGGCCAAGG GTCAATACCT	120
TGTAATAAGC ATGTGTGTAT TGGTCAGGGT TCTACAGAGA GACAGATCAA TAGGAGCTAT	180
CGATAGATAT AGACATATGA GAGGGGGTTT GTTAGGGGAA TTAGCTCACT TGATTACAGA	240
GGTTGAGAAG TCGTCCTCG AG	262

(2) INFORMATION FOR SEQ ID NO:679:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:

GAATTCGGCC	TTCATGGCCT	AGCAGCCCGA	GGCCTTGAGG	CCACTGCCTC	CCCAGGGCTC	60
CTGAAGCCAA	AGAATGGAAG	TGGTGAGCTG	AGCTACGGAG	AAGTGATGGG	TCCCTTGGAG	120
AAGCCTGGTG	GAAGGCACAA	ATGCCGCTTC	TGTGCCAAAG	TATTTGGCAG	TGACAGTGCC	180
CTGCAGATCC	ACCTTCGTTC	CCACACGGGT	GAGAGGCCCT	ATAAGTGCAA	TGTCTGTGGA	240
AACCGTTTTA	CCACCCGTGG	CAACCTCAAA	GTGCATTTC	ACCGGCATCG	TGAGAAGTAC	300
CCACATGTGC	AGATGAACCC	ACACCCAGTA	CTCGAG			336

(2) INFORMATION FOR SEQ ID NO:680:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:

GAATTCGGCC	TTCATGGCCT	AAATTAAAGA	TGATTTTTTT	AATGTGAATA	AAGTTATGTT	60
CTGATAGTTT	GTACAGAAAA	AATAAAATGG	ATGCCCATGT	TTTATTGCTA	TTACTAAATG	120
TCAAGATTGT	ATGCTATTAT	GTCTTGTAAG	TTCTTTTGT	TGGTGTAAT	ATGGAAATGC	180
CACATTGGTT	AAGTGCCATC	ATTGTAAATG	CAATGTGTCA	CTTGAAAAGA	GATTTGAAGA	240
AAC TGACAAC	TTCAAAAACA	AATGAGAAGC	CCAAGGAACT	GTGAGCAATT	AAAAGCAAAC	300
CGCGACACCC	TTTGTCTCCA	CCACACATAG	TGTACTTTGG	AAGCACAACG	TCCAGGCTGG	360
TACCGCAGCG	CCATGCCCAT	TCCTCGCCG				389

(2) INFORMATION FOR SEQ ID NO:681:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:

GATTTCTCTG	TTGACTTCTG	CAGTGAACCA	CCTCAAAGCC	AATGTTAAGT	CAGCTGCAGA	60
CTTGATTAGC	CTGCCCTACCA	CTGTAGAGGG	ACTTCAGAAG	AGTGTAGCTT	CCATTGGCAA	120
TACTTTAAAC	AGCGTCCATC	TTGCTGTGGA	AGCACTACAG	AAAACGTGTG	ATGAACACAA	180
GAAAACGATG	GAATTACTGC	AGAGTGATAT	GAATCAGCAC	TTCTTGAAGG	AGACTCCTGG	240
AAGCAACCAG	ATCATTCCGT	CACCTTCAGC	CACATCAGAA	CTTGACAATA	AAACCCACAG	300
TGAGAATTTG	AAACAGGATA	TCCTGTACCT	TCACAACTCT	TTAGAGGAGG	TAAACAGTGC	360
CCTAGTGGGG	TACCAGAGAC	AGAATGATCT	TAAACTCGAG			400

(2) INFORMATION FOR SEQ ID NO:682:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:

```

GGAGATCGAA AATTGAAACT CTCAAAGAGA CAACAAATAG CATGGTAGAA TCAATTAAAC      60
ACTGCATTGT GTTGCTGCAG ATTGCCAAAA GTACTATTAA TCCCGTAGAT GCAATATATC      120
AACCTAGTCC TTTGGAACCT GTGATCAGCA CAATGCCTTC CCAGACTGTG TTACCTCCAG      180
AACCTGTTCA GTTGTGTAAG TCAGAGCAGC GTCCATCTTC CCTACCAATT GGACCTGTGT      240
TGGCTACCTT GGGACATCAT CAGACTCCTA CACCAAATAG TACAGGCAGT GGCCATTACG      300
CACAACTCGA G                                     - - - - -      311

```

(2) INFORMATION FOR SEQ ID NO:683:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:

```

GTGAGGGGTT CCGTGACTGA GGTTCAGAGC TGCTGTTGAT GTGCTATACC TCCTTCAATT      60
CTCAGCTCTC AAAGGGGAAA ACAACTGCAG AGGATGGGAA ATGCTATACT GCCATGCCTG      120
GAAACACCCA CAGGAAAATT ACCAGTTTTC AGCTTGCTCA ACTGCAAGAA AACTGAAGG      180
AGACAGAAGC AGCCATGGAA AAATTAATCA ACAGAGTGGG ACCTAATGGT GAGAGAGCAC      240
AGACTGTGAC TTCTGACCAA GAGAAACGGT TGCTACATCA GCTCCGAGAA ATCACCAGAG      300
GTCTCGAG                                     - - - - -      308

```

(2) INFORMATION FOR SEQ ID NO:684:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 448 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:

```

GCTCCGGACA ATGAAACATA ACCAATACTA CCAATCAATA CTCATCATTATAATCATATA      60
TGGCTATAGC AATAAACTA GGAATGGCCC CCTTTCACCT CTGAGTCCCA GAGGTTACCC      120
AAGGCACCCC TCTGACATCC GGCCTGCTTC TTCTCATATG AAAAAACTA GCCCCCATCT      180
CAATCATATA CCAAATCTCT CCTCACTAA ACGTAAGCCT TCTCCTCACT CTCTCAATCT      240
TATCCATCAT AGCAGGCAGT TGAGGTGGAT TAAACCAAAC CCAGCTACGC AAAATCTTAG      300
CATACTCTC AATTACCCAC ATAGGATGAA TAATAGCAGT TCTACCGTAC AACCTTGACA      360
TAACCATCT TAATTTAACT ATTTATATTA TCCTAACTAC TACCGCATTC CTACTACTCA      420
ACTTAACTC CAGCACCACG GGCTCGAG                                     - - -      448

```

(2) INFORMATION FOR SEQ ID NO:685:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:

GTTGACAAAC AAGCTCAAGC TCGGATAAA ATGAAGGAGC AGGAAGACCT GGCCAAGGTG	60
GTATCTAAAG AAGAATCAAT TGTTTCATCA TTACGATTAG CCTATAAGGA TCTTGAAATT	120
CAAATGAAGA AAGACGAAAA GATGAACATT AGTGGCAAAA AAAATGTTGA CTCAGACAGA	180
CTCGGCATGG GATTTGAAA TTGCAGAAGT GTTATTTAC ATTCAGTGAC TTCAGATATG	240
CAGACCATAG AGCAGGAATC ACCCATTATG GCAAAACCAA GAAAAAGTA TAATGATGAC	300
AGTGAACCTG AG	312

(2) INFORMATION FOR SEQ ID NO:686:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:

GTAATGGCAC AATGGATTCA AATGGGACAT TTGTTAATGT AACAATGAGC ACATTTAACT	60
GGAAGGATTA CATGGAGAT GACAGTCACT TTTATGTTTT GGATGGGCAA AAAGACCCTT	120
TACTCTGTGG AAATGGCTCA GATGCAGGCC AGTGTCCAGA AGGATACATC TGTGTGAAGG	180
CTGGTCGAAA CCCCAACTAT GGCTACACAA GCTTTGACAC CTTAGCTGG GCTTTCCTGT	240
CTCTATTTG ACTCATTCTT CGAG	264

(2) INFORMATION FOR SEQ ID NO:687:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 277 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:

GGGAACAGCA GTTCCTATGG CTTTTTTTTT TTTTTTCTG TGTATGAGCA ATTCGACTCA	60
GTGGGATGAT ATTTTCTTTT ATAATCATT AATGTTTGGC ATACCGTGTA CTCAAATATT	120
CAATGTCAGC TGTAGCTAC CATTGGGATC CATCCACAG ACCATCAAAA TGTACTTTTG	180
GGCTGAATTA GTCCTATGCC AAGACTTGTG GGTGGATCCA GCAGCAGTTG GGAACCACGT	240
GCCAGGCCTG GTGTATGTGC TCACGAACAC ACTCGAG	277

(2) INFORMATION FOR SEQ ID NO:688:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:

GAATTCGGCC	TTCATGGCCT	AAATAGTTTA	GTTCTCTGGT	GCAATTTGAA	GTATATCTTA	60
TAGTCACTTT	TAGTAATGTG	TGTTACTTCC	CTGTAAGGAA	TAGCAATGTT	ATACTTCTCC	120
TTTTGCAGTG	AAGAAATTGA	GATGTAGAAA	GGAAGAGACC	TGCCCAAGGT	CAAAGAGCAA	180
GGCAGTGGA	AGCCTGAGAT	TAGACTTGTG	GTCTTTTAGA	TTTTTCATCT	GTTGTTCCACC	240
ACTGAGGAGC	CAGCTTCTG	TTTGCTGGAG	ACAGTTCAGC	CTAATGGAAT	TTTCTCTGCC	300
AGATGTCCAC	ATTGTGTTAG	GTGATGATTC	TAACCATCCT	CTAATACCCA	TTCTCTCCA	360
AAGTGGCCCT	TTAGTTCCCC	ACCAGAACTC	GAG			393

(2) INFORMATION FOR SEQ ID NO:689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:

GAATTCGGCC	TTCATGGCCT	ACTGTTCTGC	TCCTCCAGA	CAGAGCCTTT	CCCTCAGCCC	60
AGGGGGTCAG	GGGGTGAGGG	AAAGGCTCTG	TCTGGGAGGA	GCAGAACAGC	AGAAGAGAGG	120
AGGAGGCAGG	GAGTTACAGG	AACCTGGGGT	ACCAGGCTGC	TGGGAAGATG	CAGATTATGA	180
CAGAGCTTGC	ACGATGCTGG	CACCCCATGC	CAACCACTCT	ACGTGGCTTT	CCTCTTCGGA	240
GAGGTGGTGG	GCTCCCTTCT	TCACTGTGCC	CTCCCTCCTC	TGGCCACTAG	GGGTGGGAAA	300
TACGAGTGAG	AATCCTTCCA	GATTTACTTC	CGCCAATCCA	GAGGTACAGG	CTTTTAGGCA	360
AGGGGCAGAG	AACTGCCCAA	TTTGCTGCTT	CATGGCCTAG	GGGTGGGGTT	CCTTAGGAGC	420
TGAAAAGTTG	AACAAGGTGT	GTGAGCAGGT	GGCTTGTTCC	TTGGTTTCAA	GCTCGAG	477

(2) INFORMATION FOR SEQ ID NO:690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GAATTCGGCC	ATCATGGGCT	AAGACGTGGT	ANTGACATGC	CTGTAGACCC	AAGTATTTGG	60
GAGGCTGAGG	TGAGAGGTTT	GCTTGAGCCC	TGGAAGTCGA	GGCTTCAGTG	AGGCAAGATC	120
ACACCACTGC	ACTCCAGCCT	GGGAGAGCAA	GACCCTGTCT	CCAAAACCAA	AAAAAAAGGG	180
AAAAAAGTAA	ATGTTATAGA	TACTTGCTAA	GGGCTTTGTA	TATACTTATT	ATTGTTATTT	240
CTCAGCACGT	ATGTAGCAGA	TGAGGAAATG	AAGGCTAAAG	GTATATATATN	TACAAAGTGG	300
GGAGGTCAGA	CTTTGAACCC	ACAACCTGAC	TGTGGAGCCA	CTTCAGTATA	CTCTCTCCCC	360
ATAAGAAAGT	TCCAATAGAA	AAAAAATGCT	ACTTAAAGTAG	GGAAATCACA	AAATAAGTGC	420
CAATGAACAA	TAAATGTTCA	ACCTCACTAC	AGTTAAATG	TATATTAAAG	CAAGAGTTGA	480
GATGACACTT	TTCTTTATAA	AACAGACAGG	GATTCAGGGA	CATTGGGACT	CTAATGCTGC	540
TGGTAAGACA	TGAATAAATA	CATACCATCT	CTGGCAATCA	ATACCAGAAG	ATCTCGAG	598

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691:

```

GAATTCGGCC TTCATGGCCT AGTTCCTCCCT TCCATTCTGC CCTTGTATCT TTGCAGTCAT      60
TGTATACAGC AGATTCTAGA AAGTGTTAAT CATTGTCACC TAAATGGCAT AGTTCACAGG      120
GACCTGAAGG TCAGTATATG GAGTCCATAA ATCTGAATCA AAGCAGTTT ATTTTTTTTT      180
CTGGGGAAAG GGCAGAGGGT GGGTATTTAA AATGGTTCCC TTGCCTTTCC CAACTTGTTT      240
CTAAAATGAG TAAATGATGA AATGATAATG CATGATGCCT CTTCCAGTTT GCTCATCTAC      300
AGGCTAAATA TACATCATAG CAAAAGGGA AGAATACTAA AGAATACAAC CTGCTAAGTT      360
TCCAAGCAGT AACTACCTA CAAAAGGGA TTGAGGATCC CTCGAG      406

```

(2) INFORMATION FOR SEQ ID NO:692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:

```

GTCCTGGAAG AATGTGTCCA GCAACCCAAA AACTAATAGA AGAGTCACAG AGAAAAATGA      60
ACGCTTTATT TGAAGGTAGA CGCATCGAAT TTGCAGAAC AATAAATAAA ATGGAGGCTA      120
GGCCTAGAAG ACAATCAATG AAGGAAAAAG AGCATCAGGT GGTGCGTAAT GAAGAACAGA      180
AGGCGGAACA AGAAGAGGGT AAGGTGGCTC AGCGAGAGGA AGAGTTGGAG GAGACAGGTA      240
ATCAGCACAA TGATAGACTC GAG      263

```

(2) INFORMATION FOR SEQ ID NO:693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:

```

GCCGCCGAAG AAGCATCGTT AAAGTCTCTC TTCACCCTGC CGTCATGTCT AAGTCAGAGT      60
CTCCTAAAGA GCCCGAACAG CTGAGGAAGC TCTTCATTGG AGGGTTGAGC TTTGAAACAA      120
CTGATGAGAG CTTGAGGAGC CATTTTGAGC AATGGGGAAC GCTCACGGAC TGTGTGGTAA      180
TGAGAGATCC AAACACCAAG CGCTCCAGGG GCTTTGGGTT TGTCACATAT GCCACTGTGG      240
AGGAGGTGGA TGCAGCTATG AATGCAAGGC CACACAAGGT GGATGGAAGA GTTGTGGAAC      300
CAAAGAGAGC TGTCTCCAGA GAAGATTCTC AAAGACCAGG TGCCCACTTA ACTGTGAAAA      360
AGATATTTGT TGGTGGCATT AAAGAAGACA CTGAAGTCCT CGAG      404

```

(2) INFORMATION FOR SEQ ID NO:694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

GAATTCGGCC TTTCATGGCC TACTGGATGG CTTTTTATCT TTTGCTTTTC TTTTATGGCA	60
GATGCGCTTTC CATCGGCATC CCAGCTGTGG CTGGGGACGT TTTGGGAAGT GTGTTTGGCT	120
CACTCCGAGA GAACGAGGTC TCAAGAGGAA GTGTGTCTGG CTGCAAAGA TGTCCCTGGG	180
CCTGGACAGG ACCCGCTGT GTTCTGCAGC CCTCGACGCA GTGGGTGAGT GAGGCCTTCC	240
TCTCCTGCTG GCTGCCCTGG AGGATTTCAG CATGTCCAG GATTTGCTCC ACCCTCGAG	299

(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:

GAATTCGGCC TTCATGGCCT ACCTGTTGAA AACTCTCCAA TGACTTCCCA CTCCATCATC	60
CTGTGGGATG GGTCCACCAT GCTGGACCAC AAGGCTCTGC ACAATGCGGC TCCCACCAGC	120
CTCTCCCCTT GGCCCAGATT GCTTCCTCCT ACCCCTTCT CTAGCTGCCA GGCCCCCAA	180
CCCCCGCATG GAGCCCTTCA GCAGCTCTGT GAGCTCCCTG CCTGTTGGCA GCCATCAG	240
CAACGGGCTC TGGTGTGCCC CTGTTATCC CTGTATTGAG GCCATTATCT GTAATGACAG	300
CCTGGCATAA TTTTATTTTC ACAATTGTA TAATTATATT CTATTGAGCT AAATGATCAT	360
TATAATCATT ATTAAATATT TATTAAGCAC TTCTAGCTGT GCAAACATAA TAAGATGTGG	420
CCTCAGCTCT TAAAATCTTT CTCCTAATT CCAACCCAA TACTCGAG	468

(2) INFORMATION FOR SEQ ID NO:696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

GAATTCGGCC TTCATGGCCT ACAAGGGAAC ATGTAAACTA ACATAACCAA TTGTCAGTTC	60
TCCATGTATT CCTCAAAGA ATGTCAGAGT AAATGTATTA GAAATACAGT ATCCAGACTG	120
CTAGTCCTTG CCAGAGACAT TCTTACCTCT GCCCTGTGAT AATATTTTAT GCTTGACAGT	180
GAAAACAAGT GTGGCCCTT GCACCGGTTA GCTAGAAGTA CAGCCAGATT TCAAGCTAGT	240
GCAGTCACCT CTTCGTCAT TCTTCACAAA TCTTGTC AAC CTGGATCTTA GACTTCATCT	300
GAACCTCGAG	309

(2) INFORMATION FOR SEQ ID NO:697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:

GAATTCGGCC TTCATGGCCT ACACGGATCC GTGTGAAGAC CTACACAGAT GAGCTGACGC	60
CCATTGAGTC TGCTGTCTCT GTGTTCAAGG CAGCCAACTG GTATGAAAGG GAGATCTGGG	120
ACATGTTTGG AGTCTTCTTT GCTAACCACC CTGATCTAAG AAGGATCCTG ACAGATTATG	180
GCTTCGAGGG ACATCCTTTC CGGAAAGACT TTCCTCTATC TGGCTATGTT GAGTTACGTT	240
ATGATGATGA AGTGAAGCGG GTGGTGGCAG AGCCGGTGGG GTTGGCCCAA GAGTTCCGCA	300
AATTTGACCT GAACAGCCCC TGGGAGGCTT TCCAGTCTA TCGCCAACCC CCGGAGAGTC	360
TCAAGCTTGA AGCCGGAGAC AAGAAGCCTG ATGCCAAGTA GCTCCAGGGA ACGCATGTGG	420
ATCTAGACA GCGCCTTATC TATGATTGAG TGCCCATCTCT CGAG	464

(2) INFORMATION FOR SEQ ID NO:698:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:

GAATTCGGCC TTCATGGCCT ACGGTGGTGA ACGAGTCTCC AGCACCATGT CTGTTTGTG	60
TGGCCCAACCA GCGCGGCGCG GCCCTTTTCC GTTAGCGTTG CTGCTTTTGT TCCTGCTCGG	120
CCCCAGATTG GTCCTTGCCA TCTCCTTCCA TCTGCCATT AACTCTCGCA AGTGCTCCG	180
TGAGGAGATT CACAAGGACC TGCTAGTGAC TGGCGGTAC GAGATCTCCG ACCAGTCTG	240
GGGCGCTGGC GGCCTGCGCA GCCACCTCAA GATCACAGAT TCTGCTGGCC ATATTCTCTA	300
CTCCAAAGAG GATGCAACCA AGGGGAAATT TGCCTTTACC ACTGAAGATT ATGACATGTT	360
TGAAGTGTGT TTTGAGAGCA AGGGAACAGG GCGGATACCT GACCAACTCG AG	412

(2) INFORMATION FOR SEQ ID NO:699:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:

CAGCTCCTGT GACATTGAA GTTTCTTTTA AAGGGGTTT TCTTAATCAA AGTTTACAT	60
TTGGTAGCAT AAGTAGTTCT TTATGCTTCA CAGGACATTG TCTTCAGAGT AATCTCTCTG	120
CTAAAATGGT ACATGTGGG	139

(2) INFORMATION FOR SEQ ID NO:700:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 406 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:

GAATTCGGCC	TTCATGGCCT	ATGAAATGAT	ACCTATGGAG	TGTGATTCAT	TTTGCAGTGA	60
CCAAAATGAA	TCTGAAGTTG	AACCATCTGT	AAATGCTGAT	CTTAAACAAA	TGAATGAAAA	120
TTCTGTGACA	CACTGTTCCTG	AAAATAATAT	GCCGTCTTCT	GATCTTGGCG	ATGAAAAGGT	180
TGAAACTGTT	TCTCAACCAT	CTGAAAGCCC	AAAAGATACC	ATAGATAAAA	CCAAAAAGCC	240
TCGTACTCGA	AGATCTAGAT	TTCATTCTCC	ATCTACAACT	TGGTCACCCA	ACAAAGACAC	300
TCCACAAGAA	AAGAAGCGGC	CCCAGTCTCC	ATCTCCGAGA	AGAGAAACTG	GGAAAGAAAG	360
CAGGAAGTCT	CAATCACCAT	CTCCTAAGAA	TGAGTCAAAC	CTCGAG		406

(2) INFORMATION FOR SEQ ID NO:701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:

GGCAAGATGG	TGTTGCAGAC	CCAGGTCTTC	ATTTCTCTGT	TGCTCTGGAT	CTCTGGTGCC	60
TACGGGGACA	TCGTGATGAC	CCAGTCTCCA	NACTCCCTGG	CTGTGTCTCT	GGGCGAGAGG	120
GCCACCATCA	ACTGCAAGTC	CAGCCAGAGT	GTTTGTGACA	GCTCCAACAA	TAAGAACTAC	180
TTAGCTTGGT	ACCAGCAGAA	ACCAGGACAG	CCTCCTAAAC	TGCTCATTTA	CTGGGCATCT	240
ACCOGGGAGT	CCGGGGTCCC	TGACCGATTG	AGTGGCAGCG	GGTCTGGGAC	AGATTTCACT	300
CTTCACCATC	AGCAGCCTGC	AGGCTGAAGA	TGTGGCAGTT	TATTACTGTC	AGCAGTATTA	360
TAGTAGTTGG	ACGTTCCGGC	AAGGGACCAA	GGTGGAAATC	AAACGAACTG	TGGCTGCACC	420
ATCTGTCTTC	ATCTTCCGCG	CATCTGATGA	GCAGTTGAAA	TCTGGAACTG	CCTCTGTTGT	480
GTGCTGCTG	AATAACTCCT	ATCCGCTCGA	G			511

(2) INFORMATION FOR SEQ ID NO:702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:

GAATTCGGCC	TTCATGGCCT	AGGGATGGTC	TTAACAGGGA	ANAGAGAGGG	TGGGGGAGAA	60
AATGTTTTTT	TCTAAGATTT	TCCACAGATG	CTATAGTACT	ATTGACAAAC	TGGGTTAGAG	120
AAGGAGTGTA	CCGCTGTGCT	GTTGGCACGA	ACACCTTCAG	GGACTGGAGC	TGCTTTTATC	180
CTTGAAGAG	TATTCCAGT	TGAAGCTGAA	AAGTACAGCA	CAGTGCAGCT	TTGGTTCATA	240
TTCAGTCATC	TCAGGAGAAC	TTCAGAAGAG	CTTGAGTAGG	CCAAATGTTG	AAGTTAAGTT	300
TTCCAATAAT	GTGACTTCTT	AAAAGTTTTA	TTAAAGGGGA	GGGGCAAATA	TTGGCAATTA	360
GTTGGCAGTG	GCCTGTTACG	GTTGGGATTG	GTGGGGTGGG	TTTAGGTAAT	TGTTTAGTTT	420
ATGATTGCAG	ATAAACTCAT	GCCAGATATT	CTCGAG			456

(2) INFORMATION FOR SEQ ID NO:703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:

```

GAATTCGGCC TTCATGGCCT AGTCCTTTGC TCTACTGTTG AATGGAGGAG GATTTTTTTT    60
TTTTCCCTC  NACACAGGGG TTTTCTGGA  GCTCAAGTTT GGATGACCCC AGACAGTAAG    120
ATAATCTCAT CATGGTAAAG TTAATATGAA ATATGTGGTC TCCAAACAGC CTCTCCGAGA    180
GGCCAGGATC AGCAGGTTTG AGTGGATAAT TGGCTTGTGG TCATTTTCTC ATAGGATTTT    240
TCTTTTAGTA GTGGAAACTG TTTTCAAAT  CAAATTGGA  TGCCAACTAT GTGGAACAGA    300
AGTGTGGCTG CTCTGGTGA  AGTGGCAATG GTAGTCCTAG AGTCTCCCTG TCAGCCACAC    360
CCTTTGTCTC CCCCTACCCA AGGGACCCTG TGGCCTGGAA CCGCAGTGTG AAATGCTATA    420
TAGTGCAATG AAGCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:

```

GAATTCGGCC TTCATGGCCA ACAGCTGAGA TAAOGAGGAA ATATTCTGAA ATGGATCCCA    60
AATATTTTCT CTTAATTTTG TTTTGTGGAC ACCTGAACAA TACATTTTTT TCAAAGACAG    120
AGACAATTAC AACAGAGAAG CAGTCACAGC CTACCTTATT CACATCATCA ATGTCACAGG    180
TATTGGCTAA TTCTCAAAAC ACAACAGGGA ATCCTTTGGG TCAACCAACA CAATTCAGCG    240
ACACTTTTTC TGGACAATCA ATATCACCTG CCAAAGTCAC TGCTGGACAA CCAACACCAG    300
CTGTCTATAC CTCTTCTGAA AAACCAGAAG CACATACTTC TGCTGGACAA CCACTTGCCT    360
ACAACACCAA ACAACCAACA CCAATAGCCA ACACCTCCTC CCAGCAAGCC GTGTTACCT    420
CTGCCAGACT ACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:

```

GAATTCGGCC TTCATGGCCT ACATTCACAT GTTCCCAATC ACTTCCCTCA CACACATATG    60
CTCACTGATT TACACAGCCA TTGCACTTA TACATACTCG NTCACATTCA CACAGGGTCA    120
CCCATTCACA CACACTCGAC ACATTTACCC TCACATTCAC CCACTCACCA TTCCCACTCA    180
CCAGTTCACA TGCACCTACC CAAGCTCACA CTTGACCACG GACACACCCT CAAACATAGG    240
TGCTTACACA CAAGCCNACA CACACTCACC TAGCCATTCA TACTACGTG CACCTATACC    300
TTCACACACA TCCTCACATA CCCACACAGC TCTACACATA CCCACTTTCT TACACATTCA    360
CACACATACC TATAGACACA TTCAAACACA CCCNACGCTC GAG

```

(2) INFORMATION FOR SEQ ID NO:706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:

```

GAATTCGGCC TTCATGGCCT ACTCAGAATC ATAATGAAGT CCAGTCTACC ACACCACCCT    60
TCACTACTGT TGATTCACAG AAAGACTGTA GAAAATTTC AGTTCCACAG AAGGATGGTA    120
GTGCTTTGGA GGATTCTAGC ACTTCAGGGG CATCCTGTTC CAAGTCAAGA CCACATTTAG    180
CTGGGACACA TACTTCTCTT AGACTTCCGC AGGAAGGAAA AGGAACCTGT ATTCTTGTAG    240
GTGGTCATGA AATCACTTCT GGATTAGAAG TAATTTCTTC CCTAAGAGCA ATTCATGGGT    300
TGCAAGTAGA AGTTTGTCTT CTTAATGGCT GTGATTACAT CGTGAGTAAT CGCATGGTGG    360
TGGAAAAGGAG GTCTCAATCT GAGATGTTAA ATAGTGTC AAAGAACAAG TTCATTGAGC    420
AGATCCAGCA CCTGCAGAGT ATGTTTGAAA GAATATGTGT GATTGTGGAA AAGGACAGAG    480
AAAAACAGG CGAAACTCGA G                                     501

```

(2) INFORMATION FOR SEQ ID NO:707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:

```

GAATTCGGCC TTCATGGCCT AGGACAACCTG TGATATTTC GTTCCTGATT GTAAATACCT    60
CCTAAGCCTG AAGCTTCTGT TACTAGCCAT TGTGAGCTTC AGTTTCTTCA TCTGCAAAAT    120
GGGCATAATA CAATCTATTC TTGCCACATC AAGGGATTGT TATTCCTTTA AAAAAAACC    180
AATACCAAAG AAGCCTACAA TGTGGCCTT AGCCAAAATT CTGTTGATT CAACGTTGTT    240
TTATTCACTT CTATCGGGA GCCATGGAAA AGAAAATCAA GACATACACA CAACACAGAA    300
CATTGCAGAA GTTTTAAANA CAATGGAAAA TAAACCTATT TCTTTGGAAA GTGAAGCAAA    360
CTTAACTCA GATAAAGNAA ATATAACCAC CTCAAATCTC GAG                                     403

```

(2) INFORMATION FOR SEQ ID NO:708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:

```

GAATTCGGCC TTCATGGCCT AGGTGGGGGG CCTTCTGCAC AAAAAGGGAG TAAGTCCAG    60
CTATACCTGT GCTCAAATAA CAGCGCCATT GATGTCTTGG CANACTGGG ANGACATTCC    120
TTCTGCAAGA CTTGNTGAGC ATATTTCTGA GCTCTCTTTA CATGGTCAGG GTCCACATAA    180
TGCATTTTTT TCATGTCACA TTCTTCAGTA GTATAATTTA ACTTGAGGAT ATAAAGGATC    240
CACTCTCAA ACACAAGCAA GTACATTG AGGATGTCTT TTAATNACAA GCTGGGCCTT    300

```

CTCATCTTGC TTTGAGCTCG GGTGTACCAT TGCAGGGAGG GCCTCGAG

348

(2) INFORMATION FOR SEQ ID NO:709:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:

GAATTCGGCC TTCATGGCCT ACAGAATTGG CAGCACAAAG AAAACGCCCT CTCCTGACTT	60
GTATTGTGGC AGTCTGAACG CCCCCAGAAA ATTGTGCCAA AGAGTTTAGA AAAATAAATA	120
TACAATAAAA GTAAACACAT ACACACAAAA CAGCAAACCT CAGGTAACCTA TTTTGGATTG	180
CAAACAGGAT AATTAAATGT TCAAACAATC TGATAAAATA ACCATTGGA AACTGCTTGG	240
CCTTCTGTTC TTTTATTGA TTGACTACAA TGCGGTATTG GTCTCTTGCT GCACTTCAAA	300
AGCAACCAAC AAAACCTCG AG	322

(2) INFORMATION FOR SEQ ID NO:710:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:

GAATTCGGCC TTCATGGCCT AGCCATAGAA ACTGCCTCTT TTCATGTGGG ATGAAGACAT	60
CTGTGCCAAG AGTGGCATGA AGACATTTGC AAGTTCTTGT ATCCTGAAGA GAGTAAAGTT	120
CAGTTTGGAT GGCAGCAAGA TGAAATCAGC TATTACACCT GCTGTACACA CACTTCCTCA	180
TCACTGCAGC CATTGTGAAA TTGACAACAT GGCGTAATT TAAGTGTGA AGTCCCTAAC	240
CCNTAACCC TCTAAAAGGT GGATTCCTCT AGTTGGTTTG TAATTGTTCT TTGAAGGCTG	300
TTTATGACTA GAATTTTATA TTTGTTATCT TTGTTAAGGA AAATAGAGGA ANNCAAAGGG	360
ACTCGAG	367

(2) INFORMATION FOR SEQ ID NO:711:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:

GAATTCGGCC TTCATGGCCT AGACTTCCAC AGAGACCTAT CTGGAACCTC TGGTTCCTTA	60
CCTCTGCTTC TGTCAGAGCA GCTCTGGGTT TTGGTTTGT ACTATTGTAC ATATTAGGCT	120
TCTATACAAG AAGAACTGGT CCCATTGGTT TAAAAATAAG TTTGAAAATC CTAGAAACAG	180
TGAGAGTCAG AAAAAAATC TGTTTTATA TACATATTCT CTCCTCCACC CCCTTTCTCT	240
CCAGTTGAAA TATGTTGCAG AGCTCTAAAT TTAGGGATGC TTTTGGCGTA TTTCTTATAC	300
ACTCCAGAGG CACTCGAG	318

(2) INFORMATION FOR SEQ ID NO:712:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 468 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:

GAATTCGGCC AAAGANGCCT AGGTTTGAAA ACTCTGCTTC CTTTGTGAAT TTGGTGTTAG	60
GAGTTCTTAT TGTTATTCTG CAGCCTTTAC TATTGTCCTT TATTTACTGA ACACAGTGAA	120
TACCAAGCAC TGTTTATTAG AGGTTAGGAG TAGGGGCAGG TGATTAAAAA AACBAAAAAG	180
CTAATAATCT CCTCAAGCAA TTTCTGGCCT AATAGAATTA TAGTAGACAG TGAAGTATCT	240
AAACCCAGGG AATCAGATTG AGGCACCATG TCCATCGCCT TGAGAATTAA TAGGCTGCAT	300
TTCTGGGTTT TCCNTTTTTT TTTTTTTTTT GCCCAACTGA GTCTTTCTGT GGACTTACAT	360
GGAAGTTCTT ATTCTCTTAA ATCATTAACT TACTTGACAA TATTCTTGGA TTGAGAGAAA	420
CTGGATGTAG GGCCGTATGA AAAATCATT CGAAATCAGA ATCTCGAG	468

(2) INFORMATION FOR SEQ ID NO:713:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:

GAATTCGGCC AAAGAGGCCT ATTTTATTGC CAAACTTCTG AATAAACTGA AACAGCAGCA	60
ACAGCAGCAA CAACAGCATT CTGAAAATAA GAGAGAAAAC TCTGAAGATC CCGAGGAATC	120
TTGGGAAAAT TTAGTTTCGG ATGAGGATTT TTCTGCACTG TCCTTGGAAT CAGCAAATGT	180
GGAAGATTGG GAACCTGTGA GAAACCTCTT TAGAAAGTTG CAAAGCACAC CTAAGTATCA	240
GAAACTTCTA AAGGAAAGAC AACAGCTACC TGTATTTAAA CATCGGGTCC TCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:714:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:714:

GAATTCGGCC AAAGAGGCCT AGAAATACTG GGAAAAAGGA CACTTACTGT GTGACTTAAA	60
TTGATTAAAG GGTATTTCAG TTCAACTCTC TTGAATCTAA TTAGTATTTT TGTGTCAATT	120
ATTATTATAG GGCACACATT TTTTACATTT GATTTAACTT GACCRAAATT AAATGAGCAA	180
ATGTTTATTT CTATGTCCAT TGTTCCTTCT TCTCTGTAC TGTTAAAAAG AGGAGCCATG	240
GCTTCTGCTT CTTCTGTGTA TTCTCCATTA GACCTTCTTC ATCCACCCTC TTCCCCATCC	300
CTTTCAGCTC TGAAGGGTCC TCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:715:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:

```
GAATTCGGCC AAAGAGGCCT ACTTCTCCAA GCATTCATGT ACATCCTTGG GATCTGCCTC      60
ATCATGGAGC TCATTGGTGG CGTGGTGGCC TTGACCTTCC GGAACCAGAC CATTGACTTC      120
CTGAACGACA ACATTCGAAG AGGAATTGAG AACTACTATG ATGATCTGGA CTTCAAAAAC      180
ATCATGGACT TTGTTTCAAG AAAGTTCAAG TGCTGTGGCG GGGAGGACTA CCGAGATTGG      240
AGCAAGAATC AGTACCACGA CTGCAGTGCC CCTGGACCCC TGGCCTGTGG GGTGCCCTAC      300
ACCTGCTGCA TCAGGAATCT CGAG                                     324
```

(2) INFORMATION FOR SEQ ID NO:716:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 495 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:

```
GAATTCGGCC AAAGAGGCCT AAAGGGATTT AAAACCTCTG TAGAGGCTGG GCGCGGTGGC      60
TCACACCTGT AATCCCAGCA CTTTGGGAGG CCAGGGCGGG CAGATCACCT GAGGTGCGGA      120
GTTGAGAGCC AGCCTGACCA ACGTGGAGAA ACCATGTNTC TCTACTAAAA ATACAAAATT      180
AGCCAGGCGT GGTGGCACAT GCCTGTAATC CCAGCTACTC GGGAGGCTGA GGCAGGAGAA      240
TCACTTGAAC CTGGGANGTG GAGGTTTGGG TGAGCTGAGA TCGTGCCATT GCACTCCAGC      300
CTGGGCAACA AGAGTGANAC TCCATCTCNA AAAAAAAAAA AGAAGAGTTT ACACGAAGTC      360
ACCTCTATTT CAGAAGATAA TCTAGACTCT ATTCCCTCAG AGTCTTTTTT CTCCCCAAAG      420
ATAACACTGT CCTAGGTATT TCCTCATACC CCCAGGCCCA CAGTTCATGG CCCACATGTC      480
CCCTGTAAGC TCGAG                                     495
```

(2) INFORMATION FOR SEQ ID NO:717:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:

```
GAATTCGGCC AAAGAGGCCT ATTTTITAGA TCATCAGCTA TTGTTAGTGT TTGTGTATGT      60
TATGTGTGGC TCAAGACAAC TTTGCTTCTT TTAATATAGG CAGGGAAGTC AAAAGATTGG      120
ATATCCCTGC TTTATACCAA GAAAGACAAC ACCCCACATT TGCAGTGCCT GAAAAACATA      180
CCAGCCATCT GAAAAACATG TGACTTCTAA CTTCTGTTCT TTTTGTAGC AGTGGAAATCC      240
CACGGTGATA TCTGAGGGAT GTGGTTACCT TTTGGAGGAG GTTGACGGTT TCTAAGGATG      300
ATTCTTTCTG AGTGAAATAT TGTCAGTGTC ATTGACCTTT TCATTATTTT AACTATTATT      360
ATTCCAGGTT ATCAATACTC TGGCTGACCA TCATCATCGG GGGACTGACT CGAG                                     414
```

(2) INFORMATION FOR SEQ ID NO:718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:

```

GAATTCGGCC AAAGAGGCCT AGGATGAGAA TGA CTGTGCC TCATTGCATC TTCCTGGCTG      60
CCTGATGGGC AGAAAACCTG GGTCTCCTCC CCATTTTAGG AATGGGAAGG CTGAGTCTCT      120
GCGATGAGCC TTCCTCAGGG ATGGTGAGGG GCCGGCCCGG CACTAAGCCC CATTCTCTGA      180
GTTAGGACCT GTAGGAGGGT GGCAGGGGCA AGCGGGGCAG GTGGGTGGCC CAGGCAACTT      240
TGCAACATC TTCCCTTTT CCGGGAGAAG CAAACGCGCT GTGTGGAAG GCACATTCCG      300
AAGATGGAGT TTCACATCAG CAAGTCAGC TGGCTCGTGG ATGTTGCAGG GTGGGGTGGG      360
GCAGTGCCAG CTTGCTGGGC CTCAGCTAGG TTAGCAGGAG CTGGGGAGGT GCCCTCGAAG      420
CAGGGATCAG GGCCTCTGGG TATGGTGCAG GCTCGAG                                457

```

(2) INFORMATION FOR SEQ ID NO:719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:

```

GAATTCGGCC AAAGAGGCCT AACTTGCAGA AGCTGTTTTA TGCAGAGATA AATTGGAAGA      60
ATGGTCAGCC TCTTAAGCTA GCTTATTCGA AGAGGTACTG GAAAAAATAT GGCAAAGACT      120
TCAACGACAT ATGCCAAAAC TTTTCCCTT GGAAATCATT GACTAGCATC ACTGAATGTT      180
ATTTCTTGTG GAGAACTACT GACAGATATG TGCAACAGAA ATGGTTAAAA GCAGCAGAAA      240
CTGAGAGTAA GCTGAAACAA GTATATATCC CAATTTACAG GAAACCAAAT CCAACCAA      300
TATCTACCAG CAATGGCAAG CCTGGTGCTA TGAGTGAAC CATGAGGTG ACATTCCTGC      360
CTCAGAATCC CTTGTAGTGT CAAGCCTGGG AGGGCTGCTG TGCTACACAG TCTAACCAGT      420
AGTATTCTTG GGGCCACCT AATATGCAGT GCAATTTGTT GGCTTTATG AGAAAAATAT      480
GGAGACCTGA AAATGCCAC CCGCTCGAG                                509

```

(2) INFORMATION FOR SEQ ID NO:720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:

```

GAATTCGGCC AAAGAGGCCT AATGTGTAGT CATCTGGGAT ATGCTAGCAT CACAGTTACC      60
TGGAGTCATC TTGAATATGG AGATGACAGG GACTGATTTT GCAGATTTCGT TGAGTTGGTG      120
GGATATGTAA ATATGTTTTT CACCAACAAA TCAGATATTT CTGTTGGGCA GCCAAGTGTA      180
ATAACCATTG CTGTAAATGA TCTCTGCTCT CTCAAATCA CATGATTAAT TAAATTATGT      240

```

GAATGCCTAG TTGACTGCTA GGAATGCTT GTACTTTGGA AATATTTTAA CCAAGGACAC 300
TCTAGAAATT CTCTTGCTCT CCCACCTCAA CAGTGCAACT CGAG 344

(2) INFORMATION FOR SEQ ID NO:721:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:

CGGTAGAGAG GCAGAAGCAA GAGAGCTACG GTTCAGGTG GGCACCAGTG ATGCCACTGG 60
 TTCTCTGCAA GCGATTCCA TGACAGAAAC CGTAGCAGAA AACATCGTTA CCAGTATCCT 120
 GAAGCAGTTC ACTCAGTCTC CAGAGACAGA AGGCATCTGC TGATTCTTTT CCAGACACAA 180
 AAGTCACTTA CGTGGACAGG AAAGAGCTTC CTGGGGAAAG GAAAACAAAG ACTGAAATAG 240
 TTGTGGAGTC TAAACTGACT GAGGATGTTG ATGTTTCCGA TGAAGCTGGC CTGGACTACC 300
 TTTTAAGCAA GGATAATAAG GAAGTTGGAC TCGAG 335

(2) INFORMATION FOR SEQ ID NO:722:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:722:

GGAACACACC TGTGGTGCTA GTGTTGGGAT CGGGGGCGTT TAACGCTGGT GGGCAGCAAT 60
 AAGGGGCAGA TGTGCCCAGA TGCTGCATC CCCAGGGTGC CGAGGGCAGC AGGAAAAAGT 120
 GGGGACCTCG GTGCATTTGC CCCACCCCTC CCCTCCCTGG GCTAAAGCAC AATGTTCTCC 180
 CCGCAGATTA ATGACCCCTGC ACCCTCCAGG CCCCTACTCA CATCCTCCCC CAACCGGCTT 240
 CGGGTCCTCC CACCACACTC TGGTTTTCTA TGCTGTTTG GTGCAAGTAC AACTGTCGTA 300
 TGCATGGCTT TGGGATGGGT TCTGTTTATT AAAATCCTAT TACTCGAG 348

(2) INFORMATION FOR SEQ ID NO:723:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:

GAATTCGGCC TTCATGGCCT AGTAGTTGTT CCATGCTGTT GTTTTTTGTT TTATCTTTCA 60
 TTGCCTTTCC CTCTGCAGTC AACATTATGA CCTGGGGACT CCAGCATCCT TCAAGCAAGC 120
 CATTTCCGAA GAAGGTGAAA AGAAGCCAGG ATGATTGGCA CCTCCTCCTC CTCCTCCTCT 180
 TCTTCCTCTT CCCTTGCCCA GCCCCCTCCT GTGCGTGTGT TTCAGACAAC ACAGGAGCCA 240
 GCACAGGAGT GGAAAATCCT GTAGCGCAAC TCGAG 275

(2) INFORMATION FOR SEQ ID NO:724:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:

```
GAATTGGCAT CTTTTCATG CTTTGGCCCT TTGAGAGTTG TTTAGTTTTT TAAAAGTCAG      60
ATAATTTTGG ATTATATTCT AGACCTTTTG AATATTATGT TATAGGACTC TGGAGTCTGT      120
TAAAATCTTT AGGAAGACAT TAATTTTTTG AATTTTAACA GACAGAAGTC CTTGTTATAT      180
TGATCCATTG GTTTGTTCTA CACTTGTGCA CCTTGGAGAT GAGTCTGACT TCATATGTCAG      240
AATTTAGTAT CCCTTTCTTG AGCTCCCTCC CCTCTGTGAT CCTCCCCATT CTTCTTTTCT      300
CCCAAGAACT TCTCGAG                                     317
```

(2) INFORMATION FOR SEQ ID NO:725:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:

```
GAATTCGGCC TTCATGGCCT AGGGTCAGTG AATCTGCATT ATTACATAAA AAATAAGGCA      60
GAGGAAGCAA TCAAATATGC GTTTGTCTCT GGTGAGCCTC AGCAGGGATG ACTTTGAGTT      120
CTGTCTGTCC TTTGTCCACA AGGAATTTCC TTGTGGAAAA TTGTGAAGGA GGTATGTCGC      180
TTCTTAACTC TGTACCTATC TTATTTAGGA ATAAATGGG AGGCAGGTCT GTCTGACATA      240
GTTCCAGATT TGACTTTTCC CCTGACTTAG TGATTTTGAG GTCTCGAG                                     288
```

(2) INFORMATION FOR SEQ ID NO:726:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:

```
GAATTCGGCC TTCATGGCCT ACACACTAAT AGGATTGGAT TTATGTATGT CCAGCTTGGG      60
AATTATTACA GGAATTAAAA ACAACTTTTT AGAGTGCTTT CCTGAGCTCT CTTTCTATTT      120
GTTCCCCCTT CTACTTTTTG CTTCCCTGTG GCTGCTGTTT CTATCCTCCA GCCAGAGAGC      180
TAGTGTTTAT TTTCTCCATT GTGTTACACA CTTGTGCAGC TGCAACCACC ATATCCAGGG      240
GCTCGAG                                     247
```

(2) INFORMATION FOR SEQ ID NO:727:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 256 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:

```
GAATTCGGCC TTCATGGCCT AGAATTCTAG ACCTGCCCCG GTCTTCCTCC TCGTCCTGCC      60
GCAGGGCCAG AACCCCTGAC GGTATTCAGC TGC CGCTAAG TCTGGCCGGT GCCATCTGTC      120
TCCGCAATGC CCCCCAAGAA ACAGGCTCAG GCCGGGGGCA GCAAAAAGGC GGAGCAAAAA      180
AAGAAGGAGA AGATTATCGA AGACAAACT TTCGGTTTGA AGAATAAGAA AGGAGCAAAG      240
CAACAGTTAT CTCGAG                                         256
```

(2) INFORMATION FOR SEQ ID NO:728:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 279 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:

```
GAATTCGGCC TTCATGGCCT AAGTGCTTGC GCTCTAATAA CCATGTTTAT CTCATGCCTT      60
TGGGCCTTTG CATATGTGTT TCCTCTGCTG ACACCAACCT CCTCCTCCTC CTCCTCCTCC      120
TCTGCTTGGC TGGCTTCTCT CAGTCTCAGT TGGGATACCT TCTCTTCTAG GAAAGCTCCC      180
CTGACCACTC TTCTTTGGG CTTCATAAC CCCCTGTCT GCCCCCATCA GGGCACCTCC      240
CAAATTCAG TGTTCCTTT CCTCCTCCC AATCTCGAG                                         279
```

(2) INFORMATION FOR SEQ ID NO:729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:

```
GAATTCGGCC TTCATGGCCT AGAGAAACCT ATTTTTCAT TTAACCTGTT CTTAAATCC      60
AGTATGTTCC AGAACATACA AAAATGTTTA AATGTTCCAT TTGTAAGAGG ATATCATGTA      120
TTTTATATCA ATTAAATGC AGTTATCCTA ATCATTTTTC TTTCATTTT ACCCTTTATT      180
AACTCTTCAT TTGTTTACAA AACAAATCCA CTCTATAAAC GCAATCTCGA G      231
```

(2) INFORMATION FOR SEQ ID NO:730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:

GAATTCGGCC	TTCATGGCCT	ACACACATAA	TTAGTTATTT	TACCATTCTT	TCATAGTTTT	60
AAGAGCAAGT	TTTCAACAAG	GCGATTTGAA	TTAGAGGGTA	GAATAATATT	TTAAAAATCG	120
TTTTCTATTA	TTCAAATATA	GAATGTTATT	AAATTTTTTG	GTATCGCTGG	TTAAGTGCCT	180
AGAACTTGAT	CATCTTCTAT	TTCTTTTCC	TTTTTGCTAT	GAGAAAAATA	ATGCTCAGAG	240
AAGTATACTC	GAG					253

(2) INFORMATION FOR SEQ ID NO:731:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 239 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:731:

GAATTCGGCC	TTCATGGCCT	AAGAGACTTA	ATTATTAACA	AAGTATTAGA	AGCTAGAAGT	60
AGGTAAAAATA	AGTGATTATT	TTAATAAAAA	TTATCCTTAC	TTACAAAAT	CCATATTAAC	120
CTCACTTGAA	ATTTATGAG	CTTTTCCTAT	AAGTTTAAAG	AGATAGAAAT	CAGTGAAAGA	180
CCTCAGTAAT	TCCTGCAATG	ATCTTAATAG	AAAATATTTT	ATACCTTCTC	TCCCTCGAG	239

(2) INFORMATION FOR SEQ ID NO:732:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 262 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:

GAATTCGGCC	TTCATGGCCT	AAATAAATAT	CTCATTTTAA	TGTTACTTT	GTTGGACTTG	60
ATTACTGCAA	ACCTATCACT	AATTCITTCT	GAGTTCACCG	AAAGAAGTGC	AAAACCC TTC	120
AATATATTAC	CATCATGTGC	TTCTTCTGTC	CCACTCTTTT	CCTTAGAGAC	ATTTTGTTTT	180
TGTTGTTTTT	AATTGGTATT	GTATTGTTTT	TCAAATCTTT	GTCCCCCAGC	GCTCGACCTA	240
TAGTGAGTCG	TATTAATTTC	AG				262

(2) INFORMATION FOR SEQ ID NO:733:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:

GAATTCGGCC	TTCATGGCCT	ACACACATAA	TTAGTTATTT	TACCATTCTT	TCATAGTTTT	60
AAGAGCAAGT	TTTCAACAAG	GCGATTTGAA	TTAGAGGGTA	GAATAATATT	TTAAAAATCG	120
TTTTCTATTA	TTCAAATATA	GAATGTTATT	AAATTTTTTG	GTATCGCTGG	TTAAGTGCCT	180

AGAACTTGAT CATCTTCTAT TTCTTTTCC TTTTGTCTAT GAGAAAAATA ATGCTCAGAG 240
AAGTATACTC GAG 253

(2) INFORMATION FOR SEQ ID NO:734:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:734:

GAATTCGGCC TTCATGGCCT AGTATCACAG GCTTCTTCA AATAACCAGT TCCCTAAGA 60
 CATTGAAAAT ATAATTCGGT GTTTAAAATA AATTCATACC CGTTTGTGT GCTGTGCATA 120
 AATAGCAAGT ATATGTGTAC CTTACCAAAC TTATGGTCCC CAGTCCCCAA ATTCCAAAAT 180
 TATGCAGGAG GGAAGGTTAG CCATTGCAGT AAACAATTTC TCCCTATTGA CCCATGCTCT 240
 CCAGCTGATT ATGATGTGGG CAGTACTCAT CCAAGGCTAT ACAGACCAGC CGGGTCTCGA 300
 G 301

(2) INFORMATION FOR SEQ ID NO:735:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

GAATTCGGCC TTCATGGCCT AGAGACACAA TGGGCTCCAA GAATTGAAA TCCCTCATCT 60
 GTGAAGGCAG AAATACTAGG AGAATGGGTA ATGTTTATAC CATCAATGAA GAAACTCTTG 120
 TAACCTAGGG TTTTCAAATT ACAGAAGAGG AAGAACAATG GAGGCTGATC TCCAGTTTGT 180
 GACAGTCTAG ATAGGTGGCC TCAGTCTTGC TCTTATAAAT TCTAATTCCC AGAAGCTCGA 240
 G 241

(2) INFORMATION FOR SEQ ID NO:736:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:

GAATTCGGCC TTCATGGCCT AGTGTCTTCTA TCTTCCAATT TTCTTCTAAG TTTGTACATT 60
 TTGCCCTTAG CTTTTGTGT CCTAGCTTGT CTTTTTCTT CTGCTTCCTA CTTTTCAGGT 120
 TTAAATTTAT CTTTTTCTT CTAAAAGTAT GTTTTATCT TCTAATTCC CTATCTTCTC 180
 TATTCTTTTC TTGCCTTCC CGTACTTCTG TCTTCCAGTT TTACACTTCA AACTTCTATC 240
 TTCTCCAAAT T 251

(2) INFORMATION FOR SEQ ID NO:737:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:

GAATTCGGCC	TTCATGGCCT	ACAGGGTTGC	TGGGATGATC	AGTGATTTTG	CTAATATCAA	60
AAGTGCCCG	CACAGTGCTT	GGGTTGTTGG	AGGCATTGAA	CACACGGCAT	TGTTATTATT	120
TATATGCCTT	GTAACCTGAA	GAGCCTGTGG	GCAAACAGTG	GATGCTAAAA	TTCAGTTTGT	180
GGAAGAACCA	GGTGACAAA	CTCCTGTTCT	ACCTGTGGTT	GAGTCTACAC	TCCCCACCA	240
CACCCAGCT	GCTCTGATCT	ACCTCCTGTT	CCTTGAGCAG	GCCATTTTCT	TTCTTGCTTC	300
AGGGCAACTC	GAG					313

(2) INFORMATION FOR SEQ ID NO:738:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:

GAATTCGGCC	TTCATGGCCT	AGTGTGTTG	TTCCATCTGG	TTTTCTTCTT	TCAAATTCGC	60
ACTGACTGTT	CACAAGCGCG	CTGGTCAGCT	TTCTCCAGA	TTCTTCACG	ATGCGGTCAA	120
GCTGCTCCTG	CTCTCTCTCT	AAATTATTGC	TTTTAAACTT	ATCTTCAAGC	ATATCTTTGT	180
CTTTCTTTT	ATTTTCTTTG	CTGGGACTCT	TGAAGGCGTG	TGCTTCGGCA	TCTCCAGAGT	240
CCTCTCTCTC	TCTCTGCCAG	CAGCCTCCGT	CCTCCCCACT	CTGTGAGGTG	TCTGTTCTCG	300
AG						302

(2) INFORMATION FOR SEQ ID NO:739:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:

GAATTCGGCC	TTCATGGCCT	AGGACTGTAC	CAGCGCTATA	CTGTAGTTAT	TTTTTTAAAT	60
GAACTTCACA	TATTTTGTGA	TTCTTTCAAA	TTGTTTGCTA	TATATAAAAG	AAGCTCACTG	120
CAAAATGCTT	GAAGGAAAAA	AGGAAACAAA	AGAAATTCAG	AACTTCCCAG	AAATGTACAG	180
CTTTTCGGCC	TTCATG					196

(2) INFORMATION FOR SEQ ID NO:740:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:740:

ATGGCCTATG	CCTCCCCACT	CCACCCACCT	CTGCCTTCCT	TACTGCTGTA	TCTGCTGCTT	60
GAACTGGCAG	GAGTCACACA	TGTGTTCCAT	GTGCAACAAA	CGGAGATGTC	ACAGACTGTA	120
TCAACTGGGG	AGTCAATCAT	CTTGAGTTGC	AGCGTACCCG	ATACCTTACC	AAATGGACCT	180
GTCTTGTGGT	TCAAGGGAAC	AGGGCCAAAC	CGGAAATTAA	TCTACAATTT	CAAACAAGGT	240
AACTTTCCCA	GAGTAAAAGA	GATTGGAGAC	ACCACCAAGC	CTGGCAACAC	AGACTTTTCC	300
ACACTCGAG						309

(2) INFORMATION FOR SEQ ID NO:741:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:

GAATTCGGCC	TTCATGGCCT	ACTGAAGGTA	GGTGAGTTCA	TCCTCTTCAT	AGTAATGCTG	60
TTTTACCAAG	ACTTTATAGC	AGATGGACCC	AGAAAGAATT	TCTGCTATT	GTGTTCACTA	120
CAACAGGATA	GGGACATCAG	ACAGCCCCAG	AAACCCCTTC	CAGATCTGAT	ATGGGACTAT	180
TAATTTTAT	GCTGTTAATT	GGTATTCATT	CACAATGCAG	TTGAAGGGGG	AAGGCTCCAC	240
TGCATTCTTT	GGCTAAGGCC	TGAATGCTTG	CTCATCTGTA	AGATCTATAC	TCGAG	295

(2) INFORMATION FOR SEQ ID NO:742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:

GAATTCGGCC	TTCATGGCCT	ATAAAAAGTG	GGCCAGTTTA	AAGAAAAATT	TTATCTAAGC	60
AGTAGTACAG	CTGGCTTTCC	AATATGGCAA	AATAAGTCTT	TCTGTAGGAG	ATATCAACCA	120
TTTGGCAGGA	TTGAAAAGCC	TCTTGTTTTG	TGCCATATAA	TCAAACATA	TCTGTGATTT	180
GAAAAATGAC	AAAGGGTATA	ATAATTCCTA	GAATTGGTTT	TAAAATGAAG	GAAAATAGTA	240
TCCTAGTTCA	AAAGTTATGG	CTCATTGTAA	GTGCTGGTCT	GGTATAACCA	TACAGATTGT	300
TTAAAATCTT	TAAATAAATA	CTTGGCCCAA	TCCCTTTTGT	TCCCCCTTTC	TCGCTGCCCT	360
GTAAACTCGA	G					371

(2) INFORMATION FOR SEQ ID NO:743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:

GAAATGACTC TAGCCTGTGG AAAGAGAATC ATAATTCTAC GGACCTTTTA AATCCGCCAG	60
GAACCCTGAA TATCTATCTT TTTTGCTTGA CATGTCTCAT GACTTTTGCA GCCTTGGTGG	120
GCAGCATTTA TTTCACTAATT TCCCTGCTGA AAATGCAGAA CAGAACTGTT GTGTCCATGC	180
TTGTGGCTTC CTGGTCTGTG GATGATCTCA TGAGCGTCCT GTCGGTGACC ATCTTCATGT	240
TTTTGCAGTG GCCAAACGAG GTCCCCGGTT ACTTCCAATT TCTGTGCAAC ACCTCTCGAG	300

(2) INFORMATION FOR SEQ ID NO:744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:

GAATTCGGCC TTCATGGCCT ACCCTAAGAG AAATTCCTG GTGATAATCA CAGGGTCCAA	60
AAGTAAAGGA AACCTGGCAG TCTCTGGTGT CCATCATGTG CTTATTCCAC TTGGTAAAAT	120
AATTTGAGAT GCCTTCTAGT AAGGAATGGA CCTTAGTGGT GATGGTTAGT TGCATTATGA	180
TGACAGCCAC TGGGTTGGAG TACTTAGAAA GCTTCCGAGT ACTAGACAGC TCCACAACCT	240
CTTCAAAAGT ATCCATGGGA TACAAAGGCT TAGGATCATT GAGACACTGA ATCAAGGGCT	300
CAATCTGGTA AAAATCTGCT TCTTCCGAA GCAGATCAAA TTCCTTAAAA TCCNACGGTA	360
AGGTCAATTC TGAAGTTCTT AAGAAGTTGA GGACATATCG GAAAAGAGGT CCATCTCGAT	420
CAATAAAGTA ATTGCCTTGA GGGTCTCGAG	450

(2) INFORMATION FOR SEQ ID NO:745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745:

GAATTCGGCC TTCATGGCCT ACTTATTAAC CCCAATCAAT AGAGTTGAGA GACTATGGCT	60
TTAAAAAATT AATGCAAACC TGGCTTTAGC TGTAATAACA CCCACCGTAA GCACTTGGAC	120
TTAGTTATTA TAGACAAATG TAAAGAAAAT TTAATGAAAA ATAACACCCT CTCTCTTAAA	180
AAAAAGAAGT CTCAGGCAAT AGATGCCTGG TACTATGAGG AAGAATGTGA GAAATAGAAG	240
TGAAATCCCA GAGAAGCCCN AAACCCCCCA ATCTCGAG	278

(2) INFORMATION FOR SEQ ID NO:746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:

```

GCAATATCAA ATAGCTAACT TCACCCCCAA CCACAGTCCT TGCTGTTGGC ATTTACTCAA      60
CTAGTCTTTA ATTCTGTTT GACAACTTT ATAAGGTGCT ACAAGACAGA TGATTTTCA      120
CCATCTACCA TAATGTGGAA CAGATATTTT GTCTTCTATC TCCTGCTTTT GTCAGCGTTT      180
ACGAGTCAAA CAGTATCCGG ACAAGAAAG AAAGGACCAA AATCAAATT GCTTGCAAGG      240
AAAAGTGATG TCCAGGGGCA CCTCGAG                                          267

```

(2) INFORMATION FOR SEQ ID NO:747:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:

```

GTTCTACCTG GAATATGGTC CTTCTACCTG GAATATTTT TCCTCAGGCC TTCTCTGGCT      60
TCTTCTTCCT TTATTCCTTG GATCTCAGCT TAATCATCTC TTTGGCAAGT ATCCATGATC      120
CAAACTGGGT TAGTGCCGCT CCCAAGACCC CCTTTATTAA CCCTGTACTG GCACTTAAAA      180
CATACTCTAT TGTATTTGCC AGCTCCTTGG CCTGTCTGCA AGTTCCTTCA GGCATGCTGC      240
CATCATTCTC ATTTATCACT GTATCTCCTG TGCCAGCAG TCTOGAG                      287

```

(2) INFORMATION FOR SEQ ID NO:748:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:

```

GAATTCGGCC TTCATGGCCT ACTTATCTG CCTCTACACT CTCTTCTGGT TATTCAGGAT      60
ACCTTTGAAG GAATATTCCT TCGAAAAAGT CAGAGAAGAG AGCAGTTTCA GTGACATTCC      120
AGATGTCAAA AACGATTTTG CGTTCCTTCT TCATATGGTA GACCAAGTATG ACCAGCTATA      180
TTCCAAGCGT TTTGGTGTGT TCTGTGTCAG AGTTAGTGAA AATAAACTTA GGGAAATTAG      240
TTTGAACCAT GAGTGGACAC AAGAAAAACT CGAG                                          274

```

(2) INFORMATION FOR SEQ ID NO:749:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:

```

GAATTCGGCC TTCATGCCTA GGCAGTTTTT GTGCCTGCC ATTTTTTTT TTTTTTTTNG      60
CACATCTCAT TATATATTC TTGTGATCTT TGGAAAGTGA ACATTTTACA GAATACATTA      120

```

TAGCAACTCT GAGTAACCTT CTCCCAGGTT TATTTGTATT TGCTCATGTC TTATTTATTT	180
ATTACTAGCT GGGTTTTTTT AGTGGCACCT ACTCCTCTCC CCACTTAACC CTCTGATGTT	240
ATGCTTGTTA TGCCTGATCA GGGCAGTTAC GGATTGAATT GTGTCCACTC AAAATGTATA	300
TGCTCATGCA CTGACCTCCA GTGCCTCAGA ATGTGACACC TCGAG	345

(2) INFORMATION FOR SEQ ID NO:750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:

GAATTCGGCC TTCATGGCCT ATAGAGTAGT GATTTTGGTC AGCGTGTGTG CTATTTCCGGT	60
GTTTCAGTTT TTCAGCTGGT GGAATAGCTA CAATAAGGCA ATCAGCTACC TAGCCACAGT	120
GCCCCAAGTAC CGTATCCAAG CTACAGAGAT TGCCAAGCAG CAGGGACTGC TCAAAAAAGC	180
CAAAGAAAAA GGCAAAAAA AAAAGTCCAA AGAAGAAATT CGTGACGAGG AGGAGAACAT	240
CATAAAGAAC ATTATAAAAA GTAAATAGA TATAAAGGGT GAACTCGAG	289

(2) INFORMATION FOR SEQ ID NO:751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:

GAATTCGGCC TTCATGGCCT ACGTAGGCAG ATGGAGCTTG TTATAATTAT GCCCCATAGG	60
GATAGTACAA GGAAGGGGTA GGCTATGTGT TTTGTCAGGG GGTGAGAAT GAGTGTGAGG	120
CGTATTATAA CAAGCTCCAT CTGCCTACGA CAAACAGACC TAAATCGCT CATTGCATAC	180
TCTTCAATCA GCCACATAGC CCTCGTAGTA ACAGCCATTG TCATCCAAAC CCCCTGAAGC	240
TTCACCGGCG CAGTCATTCT CATAATCGCC CACGGGCTTA CATCCTCATT ACTATTCTGC	300
CTAGCAAACCT CAACTACGA ACGCACCTT CTCGAG	336

(2) INFORMATION FOR SEQ ID NO:752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:

GAATTCGGCC TTCATGGCCT AAGGAAAGAA GAGCAACTTT GTCAGCTTGA GAAGGAACAG	60
AAAGCCGCCC TTCCAGCTA TTTCCAAAAT AGAGTCTGCC TTAACTGTG GATGTCCGAG	120
GTTGCGCTGA TTTTCAGGGC TATTCTCAA GAGAAAGGCA GAGTCAGTCT TCCTGCCTTT	180
CTACTCTCAG GCCTCTTCC TGAGTGCTAG AAGGAGCTCT TTTAGTTGGT TTATACCTCG	240
GGACCCTTAT TTCCCTCTCA CCCTCGGCCC CAATCTCGAG	280

(2) INFORMATION FOR SEQ ID NO:753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:

```

GAATTCGGCC TTCATGGCCT AAGAAGAAGT AAAGTGCCTT GCCTGGACTA TTTCCAATGA      60
TGCCAAACAA TAATTGTTGC CCCTTGCTTT TCTTAAAAGG AGACTGCATC CATTTAACCA      120
AACTAAGAAA TTTTCAATTA GTCCTCTGCT GAAGTCATAC TATACACATC TACTTAATTA      180
AAGATACATT TATTGAAGAG AACAGGTCTC CTCGGGTTT ATCTGCTATA GCCTTGCTTA      240
GGAAAGGAAT AATAGTCTGT CTTTAAATTA GGTGTGGCTA TTGATTGGAG CAAATGTTGT      300
CAGGTGGCCC AAGCATGAAT CAATGAGTGA CCATGAGGTC ACCCATCAGT GAGGGCACCC      360
CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:754:

```

GAATTCGGCC TTCATGGCCT AACCTATTTG CCTCAGTCCT ATCTGATTCA TGAGCACATG      60
GTTATTACTG ATCGCATTGA AAACATTGAT CACCTGGGTT TCTTTATTTA TCGACTGTGT      120
CATGACAAGG AAACCTACAA ACTGCAACGC AGAGAAACTA TTAAAGGTAT TCAGAAACGT      180
GAAGCCAGCA ATTGTTTCGC AATTCGGCAT TTTGAAAACA AATTGCGCGT GGAAACTTTA      240
ATTTGTTCTT GAACAGTCAA GAAAAACATT ATTGAGGAAA ATTAATATCA CAGCATAACC      300
CCACCCITTA CATTGTTGTC AGTGATTATT TTTTAAAGTC TTCTTTCATG TAAGTAGCAA      360
CGGGCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:

```

GAATTCGGCC TTCATGGCCT ATGGAAAAC ACTCATTCTT TCTTCAGAAC TGTTTTTCAGG      60
ACTTCAAGGA GGCCTTCCCT AACCACCTTA TTTAACATTC CAGTTCTTGC ACCATCCCCA      120
CCCCTACTCT GCCCTCACTT TTTTCTCCAT GGCCTGGGC ACCAGCTGGC TAACTCTGTCT      180
TTCAAAAAGT ACTTTTCTTT GGGGGAGGTT TTTCTTTTGT TTTTGTTTTC TTTCTTTCAG      240
TCCTGTATCT TCAGCACTTA GAAGAGTTCA TGGCACACAT CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:756:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:756:

GCGCGAGTG	GGACAGCGCT	GGTGGGAGA	CTGCTCCGG	ACTCCAGGTA	CCGCGCTTGG	60
CGGCAGCTGG	CCCCAGACTT	CTGTCTTTTC	AGCTGCAGTG	AAGGCTCGGG	GCTGCAGAAT	120
TGCAACCTTG	CCAATGGACC	TGATCGGTTT	TGGTTATGCA	GCCCTCGTGA	CATTTGGAAG	180
CATTTTGGGA	TATAAGCGGA	GAGGTGGTGT	TCCGTCTTTG	ATTGCTGGTC	TTTTTGTG	240
ATGTTTGGCC	GGCTATGGAG	CTTACCGTGT	CTCCAATGAC	AAACGAGATG	TAAAAGTGTC	300
ACTGTTTACA	GCTTTCTTCC	TGGCTACCAT	AATGGGTGTG	TTCTCGAG		348

(2) INFORMATION FOR SEQ ID NO:757:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:

GCGAGGTCAG	GAGCTATGGG	ATGGTATTAA	TACATTGGCA	GAGCAACCCA	AGGGGGCAGC	60
ACATGCAGTG	AACTGCCATG	CAGAACTCCC	GACGGGCCTC	TTCCCATCC	CAGAGTGGGG	120
AACAACACGC	CGTCACAGAC	AAGGAAGTGG	GTGCCCCCGT	CCCCTCCCG	ACCCCGAGAC	180
CCAGGAGTGC	TGGGCTCCGA	GCAAGTCTAT	TGCATGCTTT	CCTGGCCAAA	GCTATATGGA	240
AAGCGGGAAC	AGCAGGCTGG	GGAGATGATG	CTGGGGGGTG	GGGAAGGAAA	GCGTCTCGAG	300

(2) INFORMATION FOR SEQ ID NO:758:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:758:

GAATTCGGCC	TCATGGCCT	AGAATATTTT	ATTATAAATA	TAATATATGA	TTTTTTAACC	60
TGTTTTGTG	CCTCATATGC	TGTCAGGTTA	ATTGTTTTC	CTTCGTGCCA	GAGGTGGGGA	120
GGAAGGCACT	CTGTCTGCTG	GGTAAATGCC	TAAATTCATC	CACCTTCATG	GTTTGGGGGC	180
AGCATGGTCA	TGTGGATAT	TGGTTTGTG	GAGTTGAGGG	AACTTAGGAT	ATAAGTTCAC	240
TCCCTCTATT	TTTCTTTGTG	ATTCACTTTT	TCAAAAATCT	TTTTTCTTC	CCTTCTCCC	300
CATTGTGGAA	ATTACAAATC	AAAGGCCTTT	TTCTTTAATG	TAAAGTGAT	TTATTTAAAA	360
AAAATACAAA	ATAAACTACA	AGTCTATCTC	GAG			393

(2) INFORMATION FOR SEQ ID NO:759:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:

GAATTCGGCC TTCATGGCCT AAGCACATTC AAGATGCCCA CNAGAACCAT CGTGTGGGC	60
TCATGTTTAT TACTTAAGCA AGAGAGCTCT TACCCAAATT CCTTGTTTC CCCACTGTCA	120
GAAACAACAT AGTCTGGAAC TGGAGGCCTA GAACTCTGGT TGTATTCCT GTAGTGGGTA	180
AAAGTCNACA AAGATAATGA ATGAGGCAGT GTCTCCTCAT GCCTTCATAT TTCTTTTGTG	240
TATTTTAATT TTTTATTATT TTTTATTTT GTGGGTGATA GTAGGTATAC GTATTTGTGG	300
GGTACGACTC GAG	313

(2) INFORMATION FOR SEQ ID NO:760:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:760:

GGAAAAAAA GGTAAAGATGG ATGAAAAGGA GGAGAAGGAA TTAAATACTA AGGAAACCAG	60
AATGGATCTT CAAATAGGAA CAGAGAAGGC TGAAAAGAAT GAAGGTAGGA TGGATGCAGA	120
AAAGGTGGAA AAGATGGCAG CAATGAAAGA AAAGCCTGCA GAAAACACTT TATTTCAAGG	180
CATACCCAAA TAAAGGAGTG GGTCAAGCTA ATAAGCCTGA TGAAACTAGT AAAACTAGTA	240
TTTCTGGCTG TATCAGATGT ATCTAGCAGT AAACCAAGGT CACTCGAG	288

(2) INFORMATION FOR SEQ ID NO:761:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

GCTCGAGGCA GGGGGAAATG GCGGCTTCAG GAGAGAGCGG GACTTCAGGC GCGGAGGCA	60
GCACCGAGGA AGCATTTATG ACCTTCTACA GTGAGGTGAA ACAAATAGAG AAGAGAGACT	120
CGTTTCTAAC TTCGAAAAAT CAGATTGAAA GACTGACCCG TCCTGGTTCC TCTTACTTCA	180
ATTTGAACCC ATTTGAGGTT CTTAGATAG ATCCTGAAGT TACAGATGAA GAAATAAAAA	240
AGAGGTTTCG GCAGTTATCC ATCTTGGTGC ATCCAGACAA AAATCAAGAT GATGCTGACA	300
GAGCACAAAA GGCTTTTGAA GCTGTGGACA AAGCTTACAA GTTGCTACTG GATCAGGAGC	360
AAAAGAAGAG GNCCCTGGAT GTAATTCANG CAGGAAAAGA ATACGTGGAA CACACTGTGA	420
AAGAGCGAAA AAAACAATTA AAGAAGGAAG GNNAACCTAC NATTGTAGAG GNGGNACTCG	480
AG	482

(2) INFORMATION FOR SEQ ID NO:762:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:

```
GGGGGATGCC AACATTTAAA GCAAGAGGCA GAAGGGCTCC TGCAGGAGAC AGGGAATCGG    60
GAAGGCAGCA GGTAAACTC GAG                                             83
```

(2) INFORMATION FOR SEQ ID NO:763:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:

```
GAATTCGGCC TTCATGGCCT AGGAATTGAA AAGAAAGGCA GAGGAGGAAA GGATTCGCCT    60
AGAAAGAGGA AGCCCGAAG CAGGAAGAAG AAAGGAAGCG GCAGGAAGAG GAAAAGAAAA    120
AACAGGAAGG GGAAGAGAAA AGAAAGGCAG GCGAGGAGGC CAAGCGGAAG GCTGAGGAGG    180
AGCTGTTGTT GAAAGAAAAA CAAGAACAAG AAAACAAGA GAAAGCCATG ATTGAAAAGC    240
AGAAAGAAGC AGCAGAAACA AAGGCCCGGG AGGTAGCTGA ACAGATGCGT CTCGAG      296
```

(2) INFORMATION FOR SEQ ID NO:764:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:

```
GAAAAGAAAC TAACCAGGAT TCCCTCAGTG TTATTTACTG GGATTGGCAT ACGTGTTTAC    60
AGGCAGAGTA GTTGATCTCA CGCAACGGGT GATCTCACA AACTGGTAAG TTTCTTATGC    120
TCATGAGCCC TCCCTTTTTT TTTTAAATT GGTGCTGCA ACTTTCTTAA CAATGATTCT    180
ACTTCCTGGG CTATCACATT ATAATGCTCT TGGCCTCTTT TTTGCTGCTG TTTTGCTATT    240
CTTAAACTTA GGCCAAGTAC CAATGTTGGC TGTTAGAAGG GATCTCGAG                289
```

(2) INFORMATION FOR SEQ ID NO:765:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:

GCACCAAGAG ATGTTTATTA GGGCAATCAA AAGATGATTT ATTATTTTTT AAAAAATCAA	60
TGTGGCCTTC CCTTCCTCTT TCTTTTGATT CCCCTCTTTG AGTTTTTATG TGTCTCTTTT	120
GCCTTCCCTT CCCAGAGTGG AGGAGTTAGA CCTGCATTGT GGGATGAGAG GAGTTGTGGC	180
TATGTGTCTG CTGGACCAA GAGGGCTGAG GGTGAGGTGT GGAAGGGACA GGGGGAGGAG	240
ATGGGCAGCA TTGTTAAGAG ATTGGTACCA CTGAGCAAAT ATGTTGAGAA TGATGATTGG	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:766:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:

GAACCTTGAC ACCTACACTT AAATTCTGAG TCATTAAACA GGCCTACATT TATCAACTGT	60
GGAAATATCA GCCAGTTTTT GCAAACCTCT TCTTAGGACA CTAAGTTGTT TGCAGAAATC	120
ACTAGCATTG ACTGACTCAG CAACAATGTG GTTATATTCT TTGATTAACT TAGTCCTTTT	180
TCTTGGTCAA GAGTCAGTAG ACAGGACTGA AGCTTATGCC CCTTGCCCCC CCACCACCAC	240
TCCATTACTA CCACCTTGGT TTAGCCATCC TTTTCTTGAT CTGTTCTCCC CACTTCTACT	300
GTGCTACTCT ACAGACTTGC CCTGAATGTA AGAGCAACAA TTACCTTGTA AAGTCCAAGT	360
TGGGGCAGGT CACTCCCAA CTCCACAACC TCGAG	395

(2) INFORMATION FOR SEQ ID NO:767:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:

GAATTGGGCC TTCATGGCCT GCCTGCTGCT TTTCTTTTCT CCAAGACGGG CTGAGGATTG	60
TACAGCTCTA GCGGAGTTG GGGCTCTTCG GATCGCTTAG ATTCTCCTCT TTGCTGCATT	120
TCCCCCACG TCCTCGTTCT CCCGCGTCTG CCTGCGGACC CGGAGAAGGG AGAATGGAGA	180
GGGGGCTGCC GCTCCTCTGC GCGTGCTCG CCCTCGTCCT CGCCCCGGCC GCGCTTTTC	240
GCAACGATAA ATGTGGCGAA TCTCGAG	267

(2) INFORMATION FOR SEQ ID NO:768:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:

GAATTGGGCC TTCATGGCCT AGCATGTCTT CTGCCTCGGC CTCCCGGGTA GCTGGGATGG	60
CAGGTGTGCA CCACCACGCC TGATTTTGT ATTTTATGTA GAGATGGGGT TCCATCCATC	120

CATTCTAGG	CCATGAAGGC	CGATCTTGT	TTCCTGAAAG	TATGGCATCA	AAAATACTTG	180
TAGAAAAACC	TTGTCACAAC	TGATTGAAT	GTTCTTATT	TCTTTTCCTT	TGACTTTGAT	240
ATTGGCTTGT	AATGTCTCTT	TTCATCATAT	GTAATATCAG	TGGAACAGGC	AGCGCTACTC	300
AAGTCCTAAG	GATTCCTCAG	TGATCAGTGA	TCCAGGGCCG	TTTATGAACC	ACTGGGCTGG	360
ATTTGACTGT	TGAGTGTGGC	AGTTAATGCC	CCTCAAGAAA	TCAAAGGATG	TCTTATAAGT	420
GTCTTCCAAA	AAAAAAGCAA	ATGCTGAAAT	CCTATTGGCA	AAGTAACTG	AAATTGGCTG	480
CTACCACTCG	AG					492

(2) INFORMATION FOR SEQ ID NO:769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:

GAATTCGGCC	TTTATGGCCT	AACGTGAGCT	GCAGGAGCTG	GCCCCGAAGC	TGCAGGAGCT	60
GGCCGATGCC	TCAGAAAACC	TCCTTACCGA	GAACACGTGG	CTCAAGATCC	TGGTGGCGAC	120
CATGGAGAGG	AAACTGGAGG	GCAGGGATGG	AGCTGAAAGC	CTGGCGGCCC	AGAGAGAGGT	180
CCACCCCAAG	CAGCCTGAGC	CCTCAGCCAC	CCCCCAGCTC	CCTGGCAGCT	CCCCTCCACC	240
TGCCAATGTC	AGCGCCACAC	TGGTGTCTGA	AAGGAATAAG	GAGAACAGGA	CAGACTAACT	300
TTTAAATGA	TATGAAGTAA	ACTCGAG				327

(2) INFORMATION FOR SEQ ID NO:770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:

GAATTCGGCC	TTTATGGCCT	AGTGGANTCT	TGGAGATAAG	CTGAGCTTGA	TGCATTGCTA	60
CCACACACTC	CAAACCATGA	AGAAGGTACC	GTGGGGCTTT	TGTTGTGTGT	GACAAAATCG	120
TAGGAAATGG	CGCCTGTATT	TCTTAATCTG	TTCTCTAATC	TTCTCATTAA	AAAGAACTTC	180
AGTTAGAACA	AGAGGGCCCA	TGGCTTTTAC	ATCCAGTCTT	TCTGCTTCAG	CAACGATTTT	240
TTTGTGAGAT	GAATCAATAA	CACCTCTTTC	TTCTTTTTC	TTAACAAAAT	CAAAGAGGAT	300
ATTGACCCTC	TCCTCAATTG	TTCTTTCCAA	ATCATCACTG	AGTGTGAGAA	CTTTTGCATG	360
GTCAGTGATT	TCATCCATTC	GAGGCCTTTG	AGCTTCCTCA	GTTGTATCTT	CTCCCCAGTC	420
ATCATCCTCC	TCTTCTTCCA	TTGTATGTGG	AGGAGGATTA	ATTTCAATTG	GTGGTGGTGG	480
TGGTGGTGGT	GTCTCACTGC	TGGATACGGA	ATTGAATTCT	AGACCTGCCT	CGAG	534

(2) INFORMATION FOR SEQ ID NO:771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:

GAATTCGGCC	TTCATGGCCT	ACTAGAATGT	GTGACTCTGT	GGGGACTGCA	TAGGTTTGT	60
AATTGACCTA	TAGCTAAACC	TTAATGTGTT	TGTGTGTCTA	TACATTGCTT	TCCGCATTTC	120
AAGACATCCA	GACGCTATTA	CCAACATTTT	CCTGTGCATT	AACCTCTGCA	TGTGAAAAC	180
TTTAACAGTT	ACTGAACTAT	GTAAATATGT	GAATTTTTTT	ATTTAGGTGG	ATGCATTTTT	240
TGCTCTTTA	CTGCTCTTCT	CAGCTTTATT	CAATAAACTT	GCATTTTAAG	GGTTGTATTG	300
GCAATTTTAA	CTTAAATGT	GCATCATGAT	GGAAGGTGCA	GACTTTTTTG	GAAGTTTCCG	360
AGAGGAGGGT	CTATAGACCA	TTGTCAGAA	ATCAGATCAA	CCCTCGAG		408

(2) INFORMATION FOR SEQ ID NO:772:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 288 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:

GAATTCGGCC	TTCATGGTGT	CGTCTCCATT	CTGATGCATC	AGCTCAAACA	GCTCTGAGTC	60
CAGGATCTGG	ATGAGGGAGC	GCAATGTTGC	AAAGTGGGTG	TCCATGGCAC	CCCCGTTGGG	120
GAAGTTCTGG	CTCATCTTCT	TCATGAGGTG	GCTGAAGCAG	CTGTAGGCCA	GCTGATCATT	180
GTCGAGGGTG	ACCAGGAGAG	GCGCCAGCAG	ATCGCACATG	CCCTGCACAT	AGCCCACGTC	240
CAGGTGCTCC	CACACGTAGC	TGCACATGAC	GTCTCTGAGC	CTCTCGAG		288

(2) INFORMATION FOR SEQ ID NO:773:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 255 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:

GAATTCGGCC	TTCATGGCCT	AATCCAGTGA	CTGACAAAGC	AAAATGTCAT	GAAATTTACA	60
TTTTTTTCT	TCTTGTAATT	TAAAACCTGG	TTCTGTATA	CCTTCCTGGA	TCTTTATACT	120
TTGTATCTT	TTCTACCATT	TCTGTAAAAC	CTCAACTGCA	GGGTGCAATA	ATGGGCCTTA	180
TTTTCTATAT	TTCAGCAGGA	CAGTTGCTGA	AAATGGGTTT	AAACTCCACT	GGCATTATAT	240
CCCACACAAC	TCGAG					255

(2) INFORMATION FOR SEQ ID NO:774:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:

GCNTTCAGGC	CNAAGGTACT	TTAATCAGTC	TAAATACTTG	AACATTTTAA	TTTCAGTGGT	60
AAAAAATAGA	CTGAGGCAGA	GTGAAGTTAT	AAATTAGAAT	CTAAAAATTT	ACCCTTCAAC	120

ATTAATATTT TTTAGTGCCT CTAATATAAA ACACAGAAAA CCTATCTCAA ATATAAAAGA 180
TGAATATAAA ATTATTAATT AAACAACNGG CGCTCGAG 218

(2) INFORMATION FOR SEQ ID NO:775:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:

GCCTTCATGG CCTAGAAAGG AGCATCCCTG TTTTGGAGT CAGGACCATT CAGGGGGTGA 60
ACGAGGCCCA GGCCAGGTGC CTTTTGGAG CTGGAATAT TAAAACCAGG ATGCCAAAAT 120
TGTAGTGTGA TCTCAGTCTT TACATTTAAC AATTATATAC ATTTTAAACA TGGGAAGATTA 180
CAGTATAATT TATTTAGGCT AATCAGAAGC TAATTATAGG CTATTTAAAA ATGTTAATTT 240
GTAACACANT ACTCGAG 257

(2) INFORMATION FOR SEQ ID NO:776:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:

GAATTCGGCC TTCATGCCTT AAAGAAACAA AGAAACAAAC CGTATATATA TATCTTCAGA 60
GTTAAAAAAT GGTGAGAACA AGAGCATTTGT TTTATATATT TTTTCAACTC TCTTTAACTT 120
CTGGCTTAAT AGAAGACAGC TGCATTCTCA TTATTATTTA TTTATTTTTT TTTAGATGGT 180
GTCTCGCTCT GTCACCCATG CTGGAGTGCA GTGGCGTGAC CTTAGCTCAC TGCAACCACC 240
ACCTCCCCAG GCTCGAG 257

(2) INFORMATION FOR SEQ ID NO:777:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:

AGCTTCATGG CCTAGTCTCA GGTAAAGTTT TTTGCAGTAA TCTTCTTTC CCCTAGAAGT 60
GAGTAAAACT TTCTGTATCC CTTTTCTCC CCACCTATGT TCCCTAAATT AGTGATTCTC 120
TTACAAGGAA TTATTATCGC CCCTGCAGTT TTGGAAGGAT ACCTCCAAAA TATATCTTGG 180
GGACTTCGAT TTATAGAATT TGGTTTAAGC TTAGATTCTG AGTCCAGGG TACCTGCCTC 240
GAG 243

(2) INFORMATION FOR SEQ ID NO:778:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:

GCTGACAGGA GCATTATGAA GCAAATGGTC ATTGATACAG TTCTACTGAG GGAGTATAAC	60
ACTGGGATTT TGCAGCCTGT GGTGTTTCAGT CTCCTGACCT CTATGCCAGC ACACAGACAG	120
CAAGAAGCAG TGGGGAACCT TGAGCTTCAA GCTCTACATT GGTTCGACAA AATCAATTCA	180
TCACTGTCTC ATTCATTAAT GTGCTGTCTG ATACTGACAT TTGTCAATGG CTTGTTTCTG	240
GAAGCCCTG GTCCTCAAGG CTGGTCAGCT CTACAGTCAC AGCCCCAGG TGAACCCAG	300
CAACTCGAG	309

(2) INFORMATION FOR SEQ ID NO:779:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:

GAATTCTAGA CCTGCCTCGA GCCTGGGTGA CAGAGTGAGA CAATGTCTCA AAATAATAAT	60
AATAATTTCA ACATGATTTT TGGTGCGGAC AAACAAACCA TATCCAAACC ATTTACTCAT	120
CCTAGTTTCA GACAGTGTCC TGGGACTGAC ACAAGGGCTC ACAGCCAGCT AGCACTGTGG	180
GCTCTCACGG GTCCCTTCTG CTGTTTATT TTAGTAGTGA TTTATTTCCTC TTCCTCACTT	240
CCACTACCACT TCGAG	255

(2) INFORMATION FOR SEQ ID NO:780:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:

GAATTCTAGA CCTGCCTCGA GCTAATGGGT GCATGCTACC ACGCCCGGGT AACTTTTTTTT	60
TTTCTGTTT TGTTTGTGTT TGTTTGTGAG ATGGAGTCTC ACTCTGTTGC TGAGGCTGGA	120
GTGCAATGGC ACGATCTCGG TTCACTGCAA CTCGAG	156

(2) INFORMATION FOR SEQ ID NO:781:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:

GAATTCGGCC TTCATGGCCT ACTCCACACA TTCATCTCCC AAAGGACTCC TTGAATATTT	60
GCCCCAAAAC ATCAGCTCCC AGAAAACACC CCTCCCAGTC ACACACACAC CCAAATTCTC	120
CGATGTATTT TCAITTTTTT TCTCCTCTTC TCTTCTCTTT TTCCTTCCTT CCTTCTCTCT	180
TTTCTCTCTT NCCATCCCTC CCTTCCTTCC TCCCTCCCTT CCTTCCTCCC TCCCTTCCTT	240
CCTCCCTCCC TCCTTTCCTT CCTCCCCCA CCCACTCGAG	280

(2) INFORMATION FOR SEQ ID NO:782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:

GAATTCGGCC TTCATGGCCT AGCCGTGTTG TTAAGTGGTG AATGATAAGG CCTAGATCTG	60
GTAGTGCTTT TGTTCCTCTT AAGGTCTATT AATTTAATGT AGCAATCTTT CTTTCCCTT	120
TTTCTTTCTT AACTTCACAT CAACCTAACT GGCTACCTAA ATGTTTCATTG AATGACTGTT	180
TTTGCTTTGG GATAGAATCC TCCTTTTTTA TTTTGGGGT GTTAAATTGA TATAGTATTG	240
TTTAATAGCT AATAAGATAC ATTTTGGGCT AAGTTTCTTA GGCCATGAAG	290

(2) INFORMATION FOR SEQ ID NO:783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:

GAATTCTAGA CTGCCTCGA GAATGGCTTT GCAGATCTGG GATCTTGTGT TCCTTCTTTT	60
TGGGTGGTT TTATACGTTA ACTGTCAGAG GCATATGCCA CTTTATTCAG GTTCCTCGAG	120

(2) INFORMATION FOR SEQ ID NO:784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:

GAATTCGGCC TTCATGGCCT AGTTTAGGTC AGTAGCAAAT GGGCCCAGTG GGAGAGAGTA	60
TGCCCAGAGT TTGGAGAGGG TCAGGGTGTG GGTGCTGGG ATGAGGGCTT CATGTTTGA	120
AGACGCAAGG TAGAGAGCAA GAGAGGAGGA AAGGTAGAAC AGGATGGAGG GCAAGACCTG	180

TGTAAGAAGA AGTCTTAAAC TGTAACATG GGTGTAGTGA GGGTAGTGTG GCTAAGAGGA 240
AATGGATCCA GATGGGCTTG ATGGGTAGCA CTCGAG 276

(2) INFORMATION FOR SEQ ID NO:785:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:

GAATTCTAGA CTTGCTCTCA GGCAGTGAAG GACTGGCACA TTGTGTAATA AACAGAAATCA 60
 AAGGCAGAAA TTAGATTACA AGCCACCTGA TGATGATAAA ATCAATCACC CTCATCAAAG 120
 GGATTGCTT TGTGTGTGTT TTCTCTTTC ATTCTTGTGG ATGCAGACAG GATATTGAAC 180
 AGCAGCTGGG CTCCTTGATC TTGGCAACAG ACATCAACAG GCAGCGTCTC GAG 233

(2) INFORMATION FOR SEQ ID NO:786:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:

GAAGATTTTG CCACTCTAAG GAGAGGTGAT ATTTGTATTT TTCTTTTAC TGAAACCAGA 60
 TCGTGAGACA CGCTTTTCAT TCATACTGA AACTTGATAA AATGTTTGGC TTTATATTAA 120
 TTTTCTCAAT TATAAGTGTG GGAAATGAAT TCGTTGATAA CCCTTTTCAA GTAAATGAAC 180
 TGATTAGAAC CAGTAAGCTC GAG 203

(2) INFORMATION FOR SEQ ID NO:787:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 262 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:

GAATTCGGCC TTCATGGCCT ACGAGATTGT CCTGGGTCAC ATAATGCCAG CTGAGCGTAA 60
 AAAGCCAGCA AGTATGGAAG AAAAAGACTC TTTACCAAAC AACAAGGAAA AAGACTGCAG 120
 TGAAAGGCGG ACAGTGAGCA GCAAGGAGAG GCCAAAAGAC GATATCAAGC TCACTGCCAA 180
 GAAGGAGGTC AGCAAGGCCC CTGAAGACAA GAAGAAGAGA CTGGAAGATG ATAAGAGAAA 240
 AAAGGAAGAC AAGAACCTCG AG 262

(2) INFORMATION FOR SEQ ID NO:788:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:

GAATTCGGCC TTCATGGCCT ACAAACAGCT GGAATGTCT CCAAGCCAGA GTGGACTACT	60
AGTAGGTATT CGTACTTCA TTGAATCTG CAGTGCCCC TTTGGGGTG TAGTTGCAGA	120
CCGCTTTAAA AAAGGCAAAA TTGTCCTCT CTTTCTCTT TTGTGTTGGG TTTTATTCAA	180
CCTGGGCATT GGATTGTCA AACCTGCTAC CTTGAGATGT GTACCAAAGA TTCGCCAAC	240
AACTACCCC CAACTCGAG	259

(2) INFORMATION FOR SEQ ID NO:789:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:

ATACTTTAAG TTCTGGGATA CGTGTGCAGA GCATGCAGNT TTNTTACATA GGTATACAG	60
TGCCATGGTG GTTTGCTGCA CCCATCAACT CCTCATCTAC ATTAGGTATT TCTCCTAATG	120
CTATTCCTCC CTTAGTCCCC CGTCCCCTCG AG	152

(2) INFORMATION FOR SEQ ID NO:790:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 241 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:

GAATTCGGCC TTCATGGCCT AGGCAAATTT GGCAGTGAAT ATGTACTGGA CTGTGATTAT	60
TTTTATTGTT TTAAAGTCA GCTTCCTCC CTCCTTCCTC CTCCTCCTT CCCAAGCTGA	120
ATCTGAACCA AGGAAGTCTT CCTACAGAGC CACTGACTGG TCCCCACTAA GGCAGGGGTG	180
GAGGGAGGGG CAGGATGTTT TCCTCTCCAG CTTTGTCTT GCAGCAGATC CCCAACTCGA	240
G	241

(2) INFORMATION FOR SEQ ID NO:791:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 182 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:

GTATTTGACT CAAAGTATTT TTTGACTGAT AGCAGTATAG CTCCTCATT CCTGCTCTC 60
 TTTTGGTTAT CATTTGCATG AAATATAATT TTCTATCCCT TTACTTTTAC TGTGTCCATA 120
 AAAGTGAAT GAGTCTCTTA TGGGCAGGAT ATAGTTGGGC AATTTTATA CTAATTCTGC 180
 CG 182

(2) INFORMATION FOR SEQ ID NO:792:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 274 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:

GAATTCGGCC TTCATGGCCT ACAATCTTCT TGGCCTGGCA CTAAGGACCT ACTACAGACT 60
 GGCACGTAAA TATCTTCCCT ACCTTATCAT TCCTTGTGCT TCTCCACAAG CCCACTCTTC 120
 CCCTTCATCA TACATGTGCC GACCTTTCCT GTCTCTTTTA CTTTGCAGCA CCAAATGCTT 180
 TCTACTTTGT GGTCTAGGAG GAACACATGT CACTTTTGTG AGCTGCTCGA AAGCAGGGGC 240
 CACACCTTCA TCCTTGTTTT CCACACAACA CCAA 274

(2) INFORMATION FOR SEQ ID NO:793:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 416 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:793:

AATTCGCCTT TCANGCCTAG TGAGTAGTTA TCAACACCGG AGATGCATTA GATCAATCTC 60
 TGGGGGCTTC TTCCTGGACC TGCTTCCATA TACACTTATT CATTTTGTCT TCACCGGACA 120
 TGTTAAACTT CCAGAGTGAC TCTAATGTGC AGACATGGTG AACATCATTG GCTTAGCTGC 180
 ATGTCAGCGC TCACTCAATG TCTGTGAACA GTGAAAGCTA CTTATTCTAC TTATAAGTTC 240
 ATTAAGTCTG TGTATACTA TTGCAAAGCA GAATAGTTGT CCCAGCCACC TGTGTTGGG 300
 GAGATGAAGC TGGGAGGCCA TCAACCTTCT TTGCAATAAA TTCTCTCAG TTTTGTCAAG 360
 CAACCTGTTT TTTGTATTCT CAGCTAGAGG CTTTCATTCT CTATCCCCCA CTCGAG 416

(2) INFORMATION FOR SEQ ID NO:794:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:

GAGATGGATG TCTCTCTTTG CCCAGCCAAG TGTAAGTTTCT GCGGATTTT CTTGCTGGGA 60
 AGCGTCTGGC TGGACTATGT GGGCTCCGTG CTGGCTTGCC CTGCAAATTG TGTCTGCAGC 120
 AAGACTGAGA TCAATTGCCG GCGGCCGGAC GATGGGAACC TCTTCCCCCT CCTGGAAGGG 180

CAGGATTCAG GGAACAGCAA TGGGAACGCC AGTATCAACA TCACGGACAT CTCAGGAAT	240
ATCACTTCCA TACACATAGA GAACTGGCGC AGTCTTCACA CGCTCAACGC CGTGGACATG	300
GAGCTCTACA CCGAACTTCT CGAG	324

(2) INFORMATION FOR SEQ ID NO:795:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:

GATTCGGCCT TCATGGCCTA GCAAAAGGGA CAAGGGAGAG AACAGGAGTA GCAAAAATAA	60
AATAAGAAAT TATGATGCTG CTTTACCAG AGACAAGCTG CTGCCACCAC TAGGCTGGAA	120
CCTACAGGCT GCACCTGTCC CTAATTAGGG TATTGGATAC TATTCACACT GCTCCTGCAA	180
CAACTGCTAG CCTGTTCTAA TCAGTAACTT CTCTCTTCTT CCTGTCTTCT CACCCTCCAG	240
TTCTCTCTAA CAGGAACCCA GCTGGCAAAG ATGTCTGGGA AATGTCATT GCATTCTCAG	300
CCCCAGCAGT GCAGAAAGGT AGGAGTGGGG CTGCGAAACA ACAGAAAAAT AAGGACCATA	360
GGTGACAAAG GAAATGCATA TACACTTCAC AGATGGCCCA TAAACATATA ATACAAAGAG	420
GTGCCTCGAG	430

(2) INFORMATION FOR SEQ ID NO:796:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 275 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:796:

GAATTCGGCC TTCATGGCCT ACTCATGAAA TGTCCTCAAAG TCTTCTCATT CTGTTCTTCC	60
CTCTCCTTTT CTTTGGTCTT ACTTCTGTAG ACTCTAGCAG AGATGGCATC CTGGGATGGA	120
ATGGCAGAGA TCTGATGCAG TGGCATGCTC ATCCCAACCT CTTATCTGGT CGTCTTCTTC	180
ACAGAAGAGA GTCTCCACTG GTAGAGTCAT TTTGGGCCAT GGATTTCAG CTATGCTTTC	240
CTTCTGGCAC CCCGAATGTA CGCAGGTCTC TCGAG	275

(2) INFORMATION FOR SEQ ID NO:797:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:797:

GCACAATATT TCAAGCTATA CCAAGCATAC AATCAACTCC AAGCTCGGAA TTTTAATTAC	60
GAGGAGGTTA GTTGTGGCAA TAAAAATGAT TAAGGATACT AGTATAAGAG ATCAGGTTGC	120
TCCTTTAGTG TTGTGTATGG TTATCATTTG TTTCGAG	157

(2) INFORMATION FOR SEQ ID NO:798:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:798:

GAATTCGGCC	TTCATGCCAA	ATGACCAGCC	CCTACTGAAG	TCCCCAGCAC	CTCCTCTTCT	60
GCATGTAGCA	GCCCTGGGCC	AGAAGCAAGG	GATCCTGGGA	GCTCAGCCTC	AGTTGATCTT	120
CCAGCCTCAC	CGGATTCCCC	CACTCTTCC	TCAGAAGCCT	CTGAGTCTCT	TCCAAACATC	180
CCACACACTT	CACCTGAGCC	ACCTGAACAG	ATTTCCTGCC	CGGGGCCCTC	ATGACCGTT	240
GGGCTCGAG						249

(2) INFORMATION FOR SEQ ID NO:799:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:

GAATTCTAGA	CCTGCCTCCC	CCCCCCCCTT	TCAGAATAAT	TTACATAAAT	ACTCCTGAGT	60
TCAATTTTTT	TNAATTTTTT	TTCTGCTTTT	ACTTATTACC	CTTTAAGTGC	TGCTTACTT	120
TCTCTGATAA	TTTACTTTCT	TCTACTCTGT	GATTTCTTTT	ACAAATCAAT	GAAATGGTGT	180
TGTCTTGTTT	TCTCAAGTTT	TTTCTGTGTA	CCTTTCCTGT	GGTCACCTGG	ACATTCCAGT	240
CCGTTTTCCA	CACTCTCCCT	CTACCTTCTC	CCCCAGTTCT	TTAAAGAGAC	ACATAATCTC	300
GAG						303

(2) INFORMATION FOR SEQ ID NO:800:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:800:

GAATTCGGC	CTTCATGGC	TAGCCATGCA	ATATCTTTTG	CATTACAGTG	CAGTCTTTGA	60
GAAGAGCCAA	GTGGGTGAGA	GGTATATTTT	CGGTGGTAGT	TGAAGAGAAG	GACAAATTAG	120
CACAGGAACA	AGAACTTCAT	GTAAGTTGTG	TTGAAGGCAG	TAGAATTGCC	TTTTAAAAGT	180
CATATCTGGA	TGTTAAGCTC	TCTCTGGGAT	CCAGTTATTA	GGATGAAGAA	ATTCTGCCGT	240
TTAAGTGCCT	GCCATTTATA	GAGGTTGCTT	GTAAGTTGTG	TGGCTAGGTA	ATTGTGCTGT	300
GTGAATTTTC	TACTCAAGGT	TGGTTTGGCA	GAAAGTAGAA	TTCTGAGTCT	GGGTATAAAG	360
GGGTTTACTA	ACATGGGAGA	GATTTGTGTG	GAACCCAAAC	TCGAG		405

(2) INFORMATION FOR SEQ ID NO:801:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:801:

GAATTGGCCT AATTAGCATC CTCAAGGACA CCAAATCAC GTGTGAGGAG AAGATGGTGT	60
CAATGGCCCC AAACACGTAC GGGGAGTCCA AGGGCCGGTG AGGGAGGGTA TTGCCCTCCG	120
TGAGCACAGA GACTCTCCAT GGGAGGGGGA GCAGTATTCT CCTGGATCCT GGGGCCTGGG	180
TGGGCTGGGG GACAGCTGAG GATGGGCCTA GCAGATGAAG CTTGCCAGCA AGGCCAAAGC	240
AAACGGTTTC TCCTGTGGAT AGTGGACAGA GACCTTTGTA ACCAATGGAA TTATTCATTT	300
TTCTCTATCT TTTATTTTTT CAAAGATATT ATTTGACTCT ATCAAAAGTC TCTCCTTTT	360
AAACCTTTTC TTATGGCGGG CTATCTCGAG	390

(2) INFORMATION FOR SEQ ID NO:802:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 231 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:

GAATTCGGCC TTCNTGGCCT ACTTTTTGAC CTCTGAGTT TTAGTTGTC CACTGAGTTT	60
TAGGTNAAAA AGAAAAAAA AAAGGAAAA TTATCTGTAA CCTCAAGACT TTTATGAGG	120
ATTATGATTT TACTGTGTTT GATAATAAAT GCCTTTTGCA TGCACTGGTT TTCAGCATAC	180
AGTTATGAAC ATTCCTAGT GGATGAGCTT AAAAAAGGGG AAAAGCTCGA G	231

(2) INFORMATION FOR SEQ ID NO:803:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 492 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:803:

GGGACAAGGA CCTGTGCAGT GCGTGACAT GACAGACGGA CCTGNTCAGC GTCCTATTGT	60
CAGTGATGTT CGAGTTTAGC CACCGTACTG TGGACATGCA CCCAGACAGC GGATTAAACG	120
TTAGTGTGTA CCCTATTCCC AGAAGAAAGG GTCCAAGAAA CACCCACACA GATCCCAAAT	180
GCAGCACACC TGTGTGTGGG CCTTCATCTT TTGGAGCCCA CCAATGCCTG CCATCCCTAA	240
CAACTGCCTT CGCACCCACC AGGGATCAAG GCATTCTGTT TTTCGGAACG TGCTCCGACA	300
GTGGAGAAGT GCAGCATGGG AAGGTTGTAT CTAGGAACTT GAAGCAAATA AATTCCTTTT	360
AATTCATGCT TGTGATCCCT GTTATTCTGT CTCTGAACTG TGCCCTTTATG CTCCAGATTA	420
GCTTTGAATC TTATTGCTAG ATTCTCCAAT CTGTTTACAA AATAAATGCA CCTAATCTTC	480
GCCTGCCCTG AG	492

(2) INFORMATION FOR SEQ ID NO:804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:804:

```

GATACATAGT TCAATTCAGT TCAATCAAAA CCATTCAATA CATATTTACT GAGTCCCTTC      60
TGCGTGTGAG GCACTGTTTC AGGCACTTGT GATATATCAG TGAAAAAAAC AAAGGCCCTT      120
GCCCACATGG AGCTTACATT ATAGCCAGGG GAAACAACAG TATACAATAA ACACAAATAT      180
GTGAAGTATC TAGGGTGATA GGTGATATGA AAAACATAGA GCAGGTGAAA GGGGTATGGG      240
ATTTCTCGAT CTGGAAGGTA GACAGCTGCA GTATTAAATA GTATGGACAG GATAGGCTTC      300
AGTAAGAAGG CAACAATTGA GCAAAGATGA GTAGGTAAGG GTATAGGGCA TCTGCAACAG      360
CTAGTGAAAC GGGCCAAAGG TTAGAACAAG GCTGGAGTTC GGGAGAGGTC TGGGCTGGAG      420
ATGTAGNCCA TGAAGGCCGA ATTCTTC                                     444

```

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:

```

GAATTCGGCT TTCATGGCCT ACAAGAAGCT GGAGGAAAAA AATACGCTGG CTCAGGGCTT      60
TCAGAGAAGA GAGGAAAATG GTACAGGAAG ATGAAAAAAT TGGCTTTGAA ATTCTGAAA      120
ACCAGAAGAG GCAGGCTGCA ATGACTGTGA GAAAGTCCC TAAGCAAAA GGTGTCAACT      180
CTGCCCGTTT CAGNTCCTCC TTCTTACCCA CCACCGCAGG ACCCGTTAAA CCACGGCCAG      240
TACCTGGTCC CCGACGGCAT CGCTCAGTCG CAGGTTTTTG AGTTCACCGA ACCCAAGCGC      300
AGCCAGTCAC CATTTTGGCA AACTTCAGC ATGTTAACCC CCATCACTCG AG                                     352

```

(2) INFORMATION FOR SEQ ID NO:806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:806:

```

GCACCCCGGG AGCTGAGTGA TTGCAGAAAC TGGCCTTCCA TCTCTCTCAG ACACCAAGCT      60
GCAGATCCAG GCTTTTCTGG GAAAGTGAGG CCACCATGGC TCTGGAGAAG TCTCTTGTC      120
GGCTCCTTCT GCTTGTCTCT ATACTGCTGG TGCTGGGCTG GGTCCAGCCT TCCCTGGGCA      180
AGGAATCCCG GGCCAAGAAA TTCCAGCGGC AGCATATGGA CTCAGACAGT TCCCCAGCA      240
GCAGCTCCAC CTACTGTAAC CAAGGTCTCG AG                                     272

```

(2) INFORMATION FOR SEQ ID NO:807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:

```
GCCTTCATGG CCTAGGAGAA GAGCGGAGCG TGTGAGCAGT ACTGCGGCCT CCTCTCCTCT    60
CCTAACCTCG CTCTCGCGGC CTACCTTTAC CCGCCCCACC CTCAGGAACT TTTGTTAGGA    120
AAAAATTGAA AGAACTTAAG TCTCGAATGT AATTGGAATC TTCACCTCAG AGTGGAGTTG    180
AAACTGCTAT AGCCTAAGCG GCTGTTTACT GCTTTTCATT AGCAGTTGCT CACATGTCTT    240
TGGGTGGGGG GGAGAAGAAG AATTGGCCAA GCTCGAG                                277
```

(2) INFORMATION FOR SEQ ID NO:808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

```
GAATTCGGCC TTCATGGCCT AAACACAGAA AAACCAACTT TCTGATACCT TTCTCCCTGT    60
ATGTTTATCT TCTTTGTCTA GTTTTTCAGC AGAAATATGC CCGTTTCCCC CTGATAATTC    120
CCTTCCTTAG AGACAGCATA ATTGTAGACC TGGCCAGAGA AATGCTGAAA ACAAAAGGGAA    180
CCCCCTTGAG CCCAGCCCTT CACCTGCTCT TAGCACTTCT TCAGAGGTTT ACTCTGGAGT    240
GAATGAAGTA GTGTGACCAG AACTCCTGG CACCTCGAG                                279
```

(2) INFORMATION FOR SEQ ID NO:809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:809:

```
GAATTCGGCC TTCATGGCCT ACCTTCGCCT TCTGTCTTTC TCGTCCTAC TAGCAGGTGT    60
TACTTCCAAT TCCTATGGGC CAGAGTTTGC TCACTGCAGA GAAATACAGT GGAATTCGCT    120
GGGCAATGGT TTGGCTTATG AAGACTTTAG TTTCCCATC TTTCTTCTTG AAGATGAAAA    180
TGAAACCAAA GTCATCAAGC AGTGCTATCA AGATCACAAC CTGAGTCAGA ATGGCTCAGC    240
ACTCGAG                                247
```

(2) INFORMATION FOR SEQ ID NO:810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:810:

GAATTCGGCC	AAAGAGGCCT	ACCCGGGCTC	AGTGTGCCGA	CTTCTGACTG	CAAATGATCT	60
CATTTTCTAA	AATCTTTCTC	CCATTCTCCT	TTAAGAAAAA	ATCTTAGTTA	TTAAAAATCT	120
GCCTCACAAA	CTTAGAAATG	CTTCAGAGTA	AGTATCTGAG	AAGCAAGCCC	ACCCACATC	180
CACCATATAT	CATCGTTTCT	GTTAAGGGCC	ANCCCATTTT	TTAGACAAA	TTCTATCTTC	240
TTCTCCCAT	CCCACTTACT	TTTGACTTTG	AAGGTGGATT	ATCTCATCTC	AAATTTCTT	300
NCCAGAATAG	NACCACATT	CAGCAAAATA	TTGGGTGGCT	GGTCTTTTTC	TTCAAGACCC	360
ACCTGCATCT	GTGTTGGTCC	TCTATGTGAG	GAAGGTCCTC	TATGTGAGAA	GATCTGAGGG	420
GTAGGCAGGT	TTTAATGGAC	TAAGATTTT	TTTATATGTA	TAAGGGGGGT	GGGAGGAGGA	480
TTTTAGAAAA	CTAGATCCAT	TGGCTGCAG	TTAGAAGTCG	AACACTGAAC	TTGGGAAGGC	540
TTTCTGTGGC	CGAACCTCGA	G				561

(2) INFORMATION FOR SEQ ID NO:811:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:

GAATTCGGCC	AAAGAGGCCT	ATCAATNGT	TTTNTTACTT	GGTACTGTGA	TTTATTATNT	60
NTAATTATNG	TNAANTNNTA	AAGCTCAATT	TTACCAGCTT	CAGCAGTTT	AAGTGTATAG	120
TTGCACAACA	CNACATAACT	CATCTAAGGT	GAATTATACT	GTAATTTTCT	TTTNGTGCCT	180
AGCTTTTTC	NATTACCATA	GTATCCTGAA	GTTTTGTGAT	TGTNGTACCA	TGAGACAGGA	240
TGTTATAAGA	TTAATATTTC	AATGTATATA	TATGCCTAGC	ATATTTTCNT	TATGCATGCA	300
GCCACTCGAG						310

(2) INFORMATION FOR SEQ ID NO:812:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:

GAATTCGGCC	AAAGAGGCCT	AGGCGGCAGG	AGGCAGTGGC	GTTGGTGGGA	AGCGCAGCTC	60
GAAAAGCGAT	GCCGATTCTG	GTTTCCTGGG	GCTGCGGCCC	ACTTCGGTGG	ACCCAGCGCT	120
GAGGCGGCGG	CGGCGAGGCC	CAAGAAATAA	GAAGCGGGGC	TGGCGGCGGC	TTGCTCAGGA	180
GCCGCTGGGG	CTGGAGGTTG	ACCAGTTTCT	GGAAGACGTG	CGGCTACAGG	AGCGCACGAG	240
CGGTGGCTTG	TTGTCAGAGG	CCCCAAATGA	AAAACCTCTC	TTGCTGGACA	CTGGCTCCAA	300
GGAAAAAGGG	CTGACAAAGA	AGAGAACCAG	AGTCCAGAAG	AAGTCACTGC	TTCTCAAGAA	360
ACCCCTTCGG	GTTGACCTCA	TCCTCGAG				388

(2) INFORMATION FOR SEQ ID NO:813:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 460 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:

GAATTCGGCC AAAGAGGCCT AAGCAAGCTC TGCTTTAGTT TCCAAGAAGA TTACAAAGAA	60
TTTAGAGATG TATTTGTCAA GATTCCTGTC GATTCATGCC CTTTGGGTTA CGGTGTCCTC	120
AGTGATGCAG CCTACCCCTT TGGTTTGGGG ACATTATGAT TTGTGTAAGA CTCAGATTTA	180
CACGGAAGAA GGGAAAGTTT GGGATTACAT GGCCTGCCAG CCGGAATCCA CGGACATGAC	240
AAAATATCTG AAAGTGAAAC TCGATCCTCC GGATATTACC TGTGGAGACC CTCCTGAGAC	300
GTTCTGTGCA ATGGGCAATC CCTACATGTG CAATAATGAG TGTGATGCGA GTACCCCTGA	360
GCTGGCACAC CCCCCTGAGC TGATGTTTGA TTTTGAAGGA AGACATCCCT CCACATTTTG	420
GCAGTCTGCC ACTTGAAGG AGTATCCCAA GCTTCTCGAG	460

(2) INFORMATION FOR SEQ ID NO:814:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 225 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:

GAATTCGGCC AAAGAGGCCT AAAGTGCTTT AAAACAATTT TCACTGTGG ACAACCGAAG	60
ACCACAAAAC ATTTGAGAAC TACCATGACA GACAGAGAAC AAAATTACAA AACAGAAAAA	120
GTAAAAAAC AGGAGAACTG CACCACTGCA CTCCAGTCTG GATACCAGAG AGAGACTCCA	180
TCTCAACAA AACAAAACAA AACAAAAAAA CCCCAAAAAC TCGAG	225

(2) INFORMATION FOR SEQ ID NO:815:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 140 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:

GAATTCGGCC AAAGAGGCCT ATTTATCGTT TAAAAAGTC AGTAGAATA AACATGAAAG	60
TGATTCTTCT GATTTTGTGG GGGGTGGTTA TTTGCACATG GAAACAACAA CAAAAATGCT	120
TCAGATACAA TTTGCTCGAG	140

(2) INFORMATION FOR SEQ ID NO:816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 540 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:

GAATTCGGCC	AAAGAGTCCT	AAAACCAACA	AGCCAGGCTG	ATTTTCTAGA	GGGATCAGTG	60
ATGTGGGGTA	CAATGACACC	TCCCTGTGG	CTGTATTATG	CTCCGGTTTT	GTTTTTGAAT	120
CTTGGTTGCT	GGTGGGGTAT	TGCCCCCTCG	GCTCCTCTAT	GCTTTTCGCGT	GTGTGAAAAT	180
GCAGGAGTGG	ACCACTGTGC	ACAGCAGGAC	CATGGCTGTG	AGCAGCTGTG	TCTGAACACG	240
GAGGATTCCT	TGCTCTGCCA	GTGCTCAGAA	GGCTTCCTCA	TCAACGAGGA	CCTCAAGACC	300
TGCTCCCGGG	TGGATTACTG	CCTGCTGAGT	GACCATGGTT	GTGAATACTC	CTGTGTCAAC	360
ATGGACAGAT	CCTTTGCCTG	TCAGTGTCTT	GAGGGACACG	TGCTCCGCAG	CGATGGGAAG	420
ACGTGTGCAA	AATTGGACTC	TGTGTCTCTG	GGGGACCACG	GTTGTGAACA	TTCTGTGTGA	480
AGCAGTGAAG	ATTCGTTTGT	GTGCCAGTGC	TTTGAAGGTT	ATATACTCCG	TGATCTCGAG	540

(2) INFORMATION FOR SEQ ID NO:817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:

GAATTCGGCC	ANANAGGCCT	ACTNNNAGGC	CTGTGAGANAN	GCGTTGGGTN	CTGANGTGAC	60
AGCTTTCCCC	NTCCATGGGA	CNCNTTCCA	GACNNTCGNC	ACNTCTNCTG	AGGTGAATTN	120
NCTGTGGGTN	TTANGTCTGG	GGTGGANNTT	CTCTCTCCCC	NNNTCTNACT	TCNGTAGATG	180
TGGACCTNGN	CCNNCINTCC	ATTGGTCCNC	TGCCCTGTGT	CTCCAGGGTG	CTGCCTCTGC	240
CTCCTCATAT	CACCAGCGTC	CCCCTGCCA	CTAGTCTGTA	GGGGGATTCC	GGGCTAGGTG	300
CTCTTCCCAT	TGACTTCAA	CCAACCTATA	TAGCTCCATG	GTGGCCTGGG	CATCTTCCAC	360
AGAGGATGTC	CGCTCTTCCC	NACCTGGATA	TCCCGTTTGA	GCAGCTTCTT	GGTGAGATGC	420
TTGAGAGACA	TGGTGGCATT	CTCCGGGCAG	TCAGCCTTCC	GGTTGAGGGG	GGGGATATGG	480
GAGGTGTAC	GGGTGAGGGA	CTTGGGGTGA	AAGTACTGAA	GGGCTTTGAA	GTCGTTGTGG	540
ATGGCATGCC	CCACCACTAT	CTTNCCTGT	GAGTATCTTC	AAGATCTGCC	CCTCGAG	597

(2) INFORMATION FOR SEQ ID NO:818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:

GAATTCGGCC	AAAGAGGCCT	AGGAAATGAA	ACGAATGCAT	AAAGCTCTCC	AGAAAGATCT	60
GCCAAGACCA	TCAGAAGTAA	ATGAACTAT	TCTAAGACCC	TTAAATGTAG	AACCGCCTTT	120
AACAGATTTA	CAGAAAAGTG	AAGAACTAAT	CAAAAAAGAA	ATGATCACAA	TGCTTCATTA	180
TGACCTTCTA	CATCACCTTT	ATGAACCATC	TGGAAATAAA	AAAGGCAAAA	CTGTAGGGTT	240
TGGTACCAAT	AATTCAGAGC	ACATTACCTA	TCTGGAACAT	AATCCTTATG	AAAAGTTCTC	300
CAAAGAAGAG	CTGAAAAAGG	CCCAGGATGT	TTTGCTGCAG	GAGATGGAAG	TGGTTAAACA	360
AGGAATGAGC	CATGGAGAGC	TCTCAAGTGA	AGCTTATAAC	CAGGTGTGGG	AAGAATGCTA	420
CAGTCAAGTT	TTATATCTTC	CTGGGCAGAG	CCGCTACACA	CGGGCCAATC	TGGCTAGTAA	480
AAAGGACAGA	ATTGAATCAC	TTGAAAAGAG	GCTCGAG			517

(2) INFORMATION FOR SEQ ID NO:819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:

```

GAATTCGGCC AAAGAGGCCT ACTAAATTCT CATATATCTG TGTTCCTAGA ATACTTTGCC      60
TTTTTGGGCT TAGTTAATGG TAAGATTCTC ATGTCTGTCT ACATAGGAAT ACTCCACCGT      120
ACAGGACACT GCTTTCCTGGG TTTAGTTCAT TGATAATTTG TCCGAATGCT CATAAACATG      180
TCTATAGGAA TACTCCAATA TATCTAGGAC ACAGTTTCTC CCGCTCCTGA ATACAGGCAG      240
ATTTTGTTTC TTTCTGCCTC CCTGTGTTAA TGAGAAGGTA GTCCAGCAGG TTCTCTCTAC      300
CTCCTTGCTT TTTTTTCCCC TTAATGCTCG AG                                     332

```

(2) INFORMATION FOR SEQ ID NO:820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:

```

GAATTCGGCC AAAGAGGCCT AACCTGCTCC GTGGAGCGCC TGAACACCA GTCTTTGGGG      60
CCAGTGCCTC AGTTTCAATC CAGGTAACCT TTAAATGAAA CTTCCTTAAA ATCTTAGGTC      120
ATACACAGAA GAGACTCCAA TCGACAAGAA GCTGGAAAAG AATGATGTTG TCCTTAAACA      180
ACCTACAGAA TATCATCTAT AACCCGGTAA TCCCGTATGT TGGCACCATT CCGATCAGC      240
TGGATCCTGG AACTTTGATT GTGATATGTG GGCATGTTCC TAGTGACGCA GACAGATTCC      300
AGGTGGATCT GCAGATGGC AGCAGTATGA ATACCTCGAG                                     340

```

(2) INFORMATION FOR SEQ ID NO:821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:

```

GAATTCGGCC AAAGAGGCCT AGGAGCTATA ATCTTGTAAC AGAGTCTACG TGATTGTAGG      60
ACAATAGGCA CCACACAAAT ATGAGGAAGC AGGTCAGAGA GCGGGCTGAC TTAATGATTA      120
ATGCTGAATG TGCTACAAGC TTGTTTCATT TTCATTCTC CTCCTCCCTT TTTTCCTGAT      180
TAATTTAATA AAGTTCATAG GGGAGGCTTC AAACACATGA GAAATTAAAA CCTTTATTAC      240
CAGAGTCAGA GCCTGACTAT ATTGATTGAG TGAAGCTTTC CTTTATAAAA TGCAAAGCAT      300
GTAAACAATT CCAACACAGT AACATATTCA TGAGTTTTTA AATTCATGAG TTTTAGAGAA      360
AATATTTTAC TTAAAACAG CACTTGATGA TCTCTGACAA TGTTATGTAG CCTGAACCTG      420
GAGTTTGGC TGATGGGTTG TCTCAGCCTG TGACAGGTTT TAGCTGGCTT TGGTTCATCT      480
TGTATCACAC CCCCACTC ACATGCTCAC CACTCGAG                                     518

```

(2) INFORMATION FOR SEQ ID NO:822:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:

GAATTCGGCC AAAGAATTCT AGACCTGCCT CGTGCCTAAG GCAATTGAAT CGAGGGTTAA	60
GGGTTCATCT TGCTAATGTC AAAAGTGACA CTAACAAGAT TCTTAGCCTC ATCCGCCAGA	120
TGACGGGCCT CCGCTCGAG	139

(2) INFORMATION FOR SEQ ID NO:823:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:

GAATTCGGCC AAAGAGGCCT AAGATGAGAA AATCAAGGTT CTTAGATGTT CTGGAATTTG	60
TTCATTTTCA CATGATTGGA ACATTGTGOT CTGTCTTTC AAGTCCATGT CTACCATACT	120
CCACAGACCC TTTTCTGTCC ACTTTGTCCAC CTATAATTCT GAACTCCAAT ATAAAGACTT	180
CACCGTATTT GAAAGAGAAT AGTGGGAAGT CTGATGCTCA ATTTTGTGTA CAGAACAGTT	240
GCCTCTGTGA CATTGTAAC TCTGAAATAA GAAATCCCC TTTTGATTCA GGAGCTCTCG	300
AG	302

(2) INFORMATION FOR SEQ ID NO:824:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:824:

GAATTCGGCC AAAGAGGCCT AAATCAGCAG TGAATCAGA ATCAATTGAG TGACATNGAG	60
TCAGTAAATC TCTGACTGCC TCAGTTACCC CATATGATAG TTTTGAGGAT GGGAACATTG	120
AGAGAGTTGA TTTGGAAGCA TATCAAGAGT AAAAATTCCA ACATTTTtag TTCCTTTAAG	180
TTAAATCCAG GCACTGTCTT TTCCTGCAAG TCTCCTGTTC CTTTCAGATT GCACAGGTGA	240
GAGTGCTCAG ATTAGGGCTG GAGGTGTAA ACCATTGCTC CCGTCCTCGA G	291

(2) INFORMATION FOR SEQ ID NO:825:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 545 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:

GAATTCGGCC	AAAGAGGCCT	AAGCTTTTTT	TTTTTTTACA	GACTTCACAG	AGAATGCAGT	60
TGTTNTGACT	TCAGGTCTGT	CTGTTCTGTN	GGCAAGTAAA	TGCAGTACTG	TTCTGATCCC	120
GCTGCTATTA	GAATGCATTG	TGAAACGACT	GGAGTATGAT	TAAAAGTTGT	GTTCCCAAT	180
GCTTGGAGTA	GTGATTGTTG	AAGGAAAAAA	TCCAGCTGAG	TGATAAAGGC	TGAGTGTGA	240
GGAAATTTCT	GCAGTTTTAA	GCAGTCGTAT	TTGTGATTGA	AGCTGAGTAC	ATTTTGCTGG	300
TGTATTTTTA	GGTAAATGC	TTTTTGTTC	TTTCTGGTGG	TGGGAGGGGA	CTGAAGCCTT	360
TAGTCTTTTC	CAGATGCAAC	CTTAAATCA	GTGACAAGAA	ACATTCCAAA	CAAGCAACAG	420
TCTTCAAGAA	ATTAAACTGG	CAAGTGGAAA	TGTTTAAACA	GTTCAAGTAT	CTTTAGTGCA	480
TTGTTTATGT	GTGGGTTTCT	CTCTCCCCTC	CCTTGGTCTT	AATTCTTACA	TGCAGGGAAC	540
TCGAG						545

(2) INFORMATION FOR SEQ ID NO:826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:

GAATTCGGCC	AAAGAGGCCT	AGGTGGTGA	ATCAAGGCCA	TGAAGGACCT	GTTTATGCGG	60
TGCATGCTGT	TTACCAGAGG	AGGGCCTCGA	G			91

(2) INFORMATION FOR SEQ ID NO:827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:

GAATTCGGCC	AAAGAGGCCT	ACTAAGAAAT	GCTATTGGAT	CTTTAGTTTG	TTCAGCTTTA	60
TTTTTCTTAT	AAGGATGAAA	GTGTTGACTT	ACAAGCTCTT	TATATATCAG	ACCAGAAACT	120
ACTTTTTTAA	AAATATAAAA	TGTAATCACC	ATCTAAAGCA	CTTNGCACAA	TGCATGGCAT	180
GTAGTGAGCA	CATATTTTTA	GCTCTTACTG	TTATTTATTA	TTATTCCATT	GAGAAAAACA	240
TTTCCTAATA	ATAATGAAAT	GACAACATGA	TATGGTAGCA	TCACAAAAAT	CAATACATCT	300
TTCTAAACAT	ATTAGAAATT	ATTTCTGTAT	GAAATAACAG	GTTTAAGGAA	AAAAATTAAT	360
GTGGTCAGAA	GTGTGCAATC	AAAATAATGA	GATGACATTG	GCATGAAGAA	CAAACCTCGAG	420

(2) INFORMATION FOR SEQ ID NO:828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:

```

GAATTCGGCC AAAGAGGCCT AGAATTCTAG ACCTGCCTCG AGCTTAGGGT GACAGAGTGA      60
GACTCCGTCT CAAGAAGTAG AAGAGTCCTG AAGTTCCTTC TGGAGTATTG GTGTGATAGA      120
AGCATTAGTA GTTCTTTTA TGTCTGGAG AACTTCTGTG CACATAAATG TTTATAGATA      180
TATACCCCGT TTGTATACCA AAGGAATCTT CATTATTTT CACTGAACAA AACACCTTAG      240
AGAACATTTT GTTTGTGTTT CCAATCAATC TAATTCCTTT AAATGACCAC ATAGTATCCC      300
ACGGTAAGTT TTTTGTGTTT TTTTITTTAA AATCATGATT TGTTTAAACA TGTCTATTG      360
CTCTCGAG
368

```

(2) INFORMATION FOR SEQ ID NO:829:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

```

GAATTCGGCC AAAGAGGCCT AATGTTTTTC AATACCTCAG TATATTGTAG GGACTTGTG      60
AGAACTTGTT GAATGAATAT ATTGTTTCTG GTTTACCAT ACTCAGTATT TTAGTTGTCA      120
CATCTTAAAA TAGATAATCA TTTTACCAT CACTCCCT TCATAAGATA TAGAAATAAA      180
GCCCTTCTTG TTTGAAATG GTGGTATTTT GGTTTACTT TTTTAAAGT TACTGTGTGA      240
AGGTACTACT TTAATATTTT TATTTAACTT TATTTGTTG TCTTTAGTAG GACTAAGCTA      300
ATGAGAGCTT TGACTTGCTT AAACGTTGGG CAGGAAACT CGAG                          344

```

(2) INFORMATION FOR SEQ ID NO:830:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

```

GAATTCGGCC AAAGAGGCTT AGAAGACTTT TGTATTTTGT ACTTTGCTAG TTTGTGGCAG      60
AGTGGAGAGG ACGGTTGGAT ATTTCAAATT TTTTAGTAT AGCGTATCGC AAGGGTTTGA      120
CACGGCTGCC AGCGACTCTA GGCTTCCAGT CTGTGTTTGG TTTTATTCT TATCATTATT      180
ATGATTGTTT TTATATTATT ATTTATTTT AGTTGTGTG CTAAACTCAA TAATGCTGTT      240
CTAACTACAG TGCTCAATAA AATGATTAAT GACAGGATGG GGTTCCCTG TGCTTTTACC      300
AGTAGCATGA CCCTTCTGA AGCCATCCGT AGAAAGTACC TTGTCTCGA G                          351

```

(2) INFORMATION FOR SEQ ID NO:831:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:

GAATTCGGCC AAAGAGGCCT AAAACAAGAT CCACTGGAGG GTCATGTCG AGTTGTTCTC	60
TTGATGATT TGGCTGATTA TCTTAATGCC CTTTCCATT TCTGATGCTC TTGTTCTACA	120
TTTTGGGTGA AAATACCAAT ATTTCTAATT CTGTATCACA TCATCTCACT GTGTAGCAAG	180
GCAGGTCTCC ACAAATTACC CCGTTCCACC TGGAGAGCTC CTTATTGACT TAACGTGATA	240
TTCAGCCAGG TTTTCTTCC TGTAAATAGT GCTTTGCCTT TAGCAAATG CCTGGATCAT	300
TGACCTTTCT TAGCCCATGC ATAAAATGCC AACTCGAG	338

(2) INFORMATION FOR SEQ ID NO:832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:

GAATTCGGCC AAAGAGGCCT AATATTATAG AACCACCATA TGTACATTTT TCATAGAGTT	60
TGGGAATGAA ATAGTAAAAG GTATATAGAA AACTAAGAAA AGGGAAAATT CTGGGGGGCT	120
GGGATGAGGA AGTGATTAGC ACCAGGGAAA ACCAAGTTT ATACCAGAAA GGAACCTCTAA	180
TATTAGGCTG CCATATTAAG CCATGTGGCT GGGCTACATT GTGTTAAGTC ACTGATGAAT	240
GATCTAAACA AGAGTCTGGA TATAACCAA TCAGGAAGGC TTGAAGAATG TGTGTGTTAT	300
TGGGGGGAAC GGTGTCTACA GTAGGAGGTA GATGGTTATG TAAACTAGA GAAAAGGAAC	360
TAATATAAAG TGTTAGTTGG AATATATTAA TAATTGTCAG TGAAACTCG AG	412

(2) INFORMATION FOR SEQ ID NO:833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:

GAATTCGGCC AAAGAGGCCT ACTGTGGGTT TATATTGATG TGTAACAAGT TGATTGGAA	60
CACTGGACTC TCATTCTGTT ATTCTGGTTT TGTTTTTTTT GTTTGTTTT TTTCTTTTG	120
TAAAGGCAAT GAGCTAGTCC CAGATCTCGA G	151

(2) INFORMATION FOR SEQ ID NO:834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:

GAATTCAGCC TTCATGGCCT ACTCTGTTG AAGATGTGAA TATCTGTCTG CAGGCATGCA	60
GCAGTCTACA CGCTCTGTCC TCTTCCTTGC CAGATGATCT TTTACAGAGA TGTGTTGATG	120
TTTGCCGTGT TCAACTAGTG CACCGTGGA CTCGTATTCG ACAAGCATTT GAAAACTGT	180

TGAAATCAAT TCCTTTAGAT GTTGTGCGGA TTGAATTCTA GACCCGCCTC GAG

233

(2) INFORMATION FOR SEQ ID NO:835:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:

GAATTCGGCC TTCATGGCCT AGAACTGGGA GGTAGAAACA AAAATGACTG AACATCTTTT	60
TATCCCCCAA TCGTTACAAA GCCTAAATAA CTCTAAACGG GATGGGAGGG CAAATTTTAG	120
GTCAGTTGAC ATCCTGGAGA AGATATCCTA GGTCTGTCT CATTCCCTAG ACCGCATAAC	180
ACTCCAACCG TGTAGGCCAT GAAGATTGAA TTCTAGACCT GCCTCGAG	228

(2) INFORMATION FOR SEQ ID NO:836:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:

GAATTCGGCT TCATGGCCTA GGCTGGTGAT CCATGATGCA AATAATAATA ATAATGATGA	60
TTTTTTTAA TGTACAGCTC TCACACAAAT TTCATTTTGT GAACACACTG GTAAGTACAC	120
GATGCTGGGG CTTCACAAAT GTGGCGTATC CCACTGATGG CTCCAACCTG CGAGTGGGCT	180
CAGTTATGAA AAACCTCGGA GAGGACGGGT TGTCGCTGCT CGAG	224

(2) INFORMATION FOR SEQ ID NO:837:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:

GAATTCGGCC TTCATGGCCT AGGAGCTGTT GCACTTTGGG CCTTGGCAGG ACAAACACTA	60
AAACAACAAA AATATATGGC AGAACAAATT GGATACAGCT TTATAATAAA TATGCTTTTG	120
TCACCATCAG CTAAAATGCA GTATGTTGGT AAGTTATTTT CCTTATTTTA TTTTATTTT	180
TTAGAGACAG GATCTTGCTC TGTTGCCAG CCTGGTGTGC AGTGGCACAA TTATAGCTCA	240
CTGCAGCCTC AAACCCCTGG GCTCGAG	267

(2) INFORMATION FOR SEQ ID NO:838:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 514 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:

GAATTCGGCC TTCATGGCCT AATCAAATC AACTACGCC CTGATCGGCG CACTGGGAGC	60
AGTAGCCCAA ACAATCTCAT ATGAAGTCAC CCTAGCCATC ATTCTACTAT CAACATTACT	120
AATAAGTGGC TCCTTTAACC TCTCCACCCT TATCACAACA CAAGAACACC TCTGATTACT	180
CCTGCCATCA TGACCCTTGG CCATAATATG ATTTATCTCC AACTAGCAG AGACCAACCG	240
AACCCCTTC GACCTTGCG AAGGGGAGTC AGAACTAGTC TCAGGCTTCA ACATCGAATA	300
CGCCGAGGC CCCTTCGCC TATTCTTCAT AGCCGAATAC ACAAACATTA TTATAATAAA	360
CACCTCACC ACTACAATCT TCCTAGGAAC AACATATGAC GCACTCTCCC CTGAACTCTA	420
CACAACATAT TTTGTCACCA AGACCCTACT TCTAACCTCC CTGTTCTTAT GAATTCGAAC	480
AGCATACCCC CGATTCCGCT ACGACCATCT CGAG	514

(2) INFORMATION FOR SEQ ID NO:839:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:

GAATTCGGCC TTCATGGCCT ACTACATAGA CGTGGATTTT AGGGGGACAA AATCAACCA	60
CTACCGTCTC TTTGCTTGAA ATCACAACA ATTTCCAGAG GCCTAGAGAT GCCACTTTGT	120
CCGCAGATCT CTTCTGGCC CGCCTCTGT CTGGCAGCC TGGGTCTGAT TGTCTTCTG	180
TCTGCCACCC TCACAGTCT CAGCCGTGGC CTGGTTCCTG TCCTGGGGGC TGACCAGCCT	240
TCTGGGGCCT GGGACCTGGG GCATCGCTGC TGCCTGCCGG CTGACCTCGA G	291

(2) INFORMATION FOR SEQ ID NO:840:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:

GAATTCGGCC TTCATAGCCT ACCTAAATTA ATAATAATGT ATAGTTCAGA ATTGCTAAGA	60
GTACTTTTTT TTTTTTTTT TTGAGACAGG TTCTGCTCT GCCCTCCAGC CTGGTGACAG	120
AGCAAGATTC CATCTCAAAA AAGAAAAAAA ACACACAGCT AATAGAATTG CCATTGTTTT	180
TCATAATAGA ATCTAGCTGC TTAATCCAAC CTCACCTCGA G	221

(2) INFORMATION FOR SEQ ID NO:841:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:

GAATTCGGCC TTCATGGCCT AGTAAAGTTT CTCTCACCCC ACTTTAATTT CATGTGCCAC	60
ATTTTTTCCT TTCTGAACT ATATTGCTTC CCACATTCGG ATTTTAGAAT TTTTCTTTTT	120
AAAGAGATTG TATTTTAAAT TATATTGGC CTACTTCCCC ATTGTCAATG CTTGTACCGT	180
GTGAGAAAGTC CCTAGGATGA TAGTCATGGT TTTTCCCAT CTTATTAGCT TATTATTCTC	240
CTTGCCACC CCCCACCCT GGCAGCTTCC CACCCTCTCT AATGCTTCTG GAAGCTACTA	300
AGAAGTTTAA GTGGCCTATG TGAAAATATG TCAGTGTCCC ATTTTAGCAT ATATATGTAA	360
CATTTACAAT TTATACCCCT GCCTACATCC GAGAGGGTTG TGAGGTGGCT TATGATGATA	420
AAGAAAAAAA CCCACATATC TCGAG	445

(2) INFORMATION FOR SEQ ID NO:842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:842:

GAATTCGGCC TTCATGGCCT AAATTTATAA GGTACTCTTT AACAAATTTAT ATCAGAGTTA	60
GTGCTATCT TTAGCACCAT TGTCCTGATG GCCTCCACTT CTAGCTATAC ATTGCCTCTT	120
TGAAATGAGC CATTGCGGAG GCAATATAT CAATTAGAAT GCCTTTAAGA ATAAAAAAT	180
TAAAAAGCAA AGAAAAACAG AATGCCTTTA GGAAAAAATT TAATAAAACC AACTCAAAAT	240
TGTGCAACA AGGAAATTTT AGTGTTCCTC ATAATAAAC CTCGAG	286

(2) INFORMATION FOR SEQ ID NO:843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:843:

GGTCCCAAG TAATTATATT CCAAGGAACA TAGGAGGGGC AAAAATAATT CTAAAGACAT	60
AAAGAAAGAA ACAGGATATT TTCTAAATAT TTTTATCTTG AGACAGAACT TGGTTTTTTT	120
TTTGCTTTA GCTTGGAAAA TCTCGTGCA TAGATAAATC TTTCTCCTAT CTTGAAATTG	180
GTCTTATCAA GGAATACCC GCATTGAGAT ATGAAGCTCT GGGCCTCTCT GGTAGCCTTG	240
CACACCCTTC ATTCATCACC TGGTCCCCCA GATAAGACAG CCCTGACCTC AGAATACACC	300
TTGGATTAA CATTCTATGG GACATTTATT TCTAGTCTAC CCCCATCCCT CGAG	354

(2) INFORMATION FOR SEQ ID NO:844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:

GAATTCGGCC	TTCATGGCCT	AGTGGAAAA	ATAAGATATT	TCTTAAAGTA	ACAAGGCCTG	60
AATAAATGTG	TGGCAGTCTC	AAATTCTATT	CTATATCTCA	GGTGTAATCC	TTACATACTA	120
AAGATAGTGG	GATCATCCTT	GTAGATTCT	AGCAGACTGG	TACATTAAAA	AGTGACAATG	180
TTTGGGGTAT	GACAGTATAA	AAAAAGGTTT	AATTTGAGAA	AAAGGATTAA	GTTAAATAGT	240
AAACTTAGTG	TGAGATTTTA	ATCACAAGTA	CAAAAGAGTG	AAGAGCAGCC	TTCATGACAA	300
GGAATCATGT	GACCAGCCCC	CACCCCAAAC	TCGAG			335

(2) INFORMATION FOR SEQ ID NO:845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:

GAATTCGGCC	TTCATGGCCT	AAGAAAGGGT	GGGAACTAAC	ATTGATCACA	TTTATGGAAA	60
CCTGCCTTCT	CGTGCTGGGC	ACTTTATATA	TGTTATCTCC	CTTTGTGGTG	CAATCTCATG	120
ACATGCAGTC	ATTGTCCATG	TTTGTGGGTG	AGGAAACAGG	CTTAGGGGTG	GGAGGCTCGC	180
CTGAGGCCCC	ACACTGTTGG	CTGGAGACAG	CGTGGGGCCT	GAGTCTTGCT	CACAGCCTGA	240
ACGCTGCACT	CTGCTGCTCC	GCGTCCCAGG	AAGGAAAAGC	TGCTGCAGTG	GGTTTGTTTT	300
GCCAAATACA	TGGAGGCTTT	TTTCTGGGTG	AGTGCCCAGC	AGTTGATTGT	TCTGTATGCC	360
TCGAG						365

(2) INFORMATION FOR SEQ ID NO:846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:

GAATTCGGCC	TTCATGGCCT	AATCCATGTT	GTACAACCTGA	AATATAAATA	ATTTTGTCAA	60
TTATACCTAA	ATAAACTGG	AAAAAATTT	CTGGAAGTTT	ATATCTAAAA	ATGTTAATAG	120
TGCGTACCTC	TAGGAAGTGG	GCCTGGAAGC	CATTCTTACT	TTTCAGTCTC	TCCCATTCTG	180
TACTGTTTTT	TGTTTTACTT	TCGTGCGCTG	CAGGTCTAGA	ATTCAATCG		229

(2) INFORMATION FOR SEQ ID NO:847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:

GAATTCGGCC	TTCATGGCCT	AGGGGAGAGT	ATCATCTCAC	CAAAGGTGAA	AATGGCATT	60
CGGACATCAG	GACATCTCTT	ACTGGGAGTA	GTTTGAATCT	ATCACAGGAA	AGCCAAATAC	120
CTTCTTGCAG	ACTGTAATGA	AGCATTCAAT	AAGATAAAGA	TGGCTTTTCC	GCCAGGTGTG	180
GTTGACCTGC	CTGAGGAAAA	TCGGGAAGCA	GCTTATAATG	CCATTACTTT	ACCTGAAGAA	240
TTTCATGACT	TTGATCAGCC	ACTGCCTGAC	TTAGATGACA	TCGATGTGGC	CCAGCAGTTC	300
AGCTTGAATC	AGAGTAGAGT	GGAAGAGATA	ACCATGAGAG	AAGAAGTTGG	GAACATCAGT	360
ATTTTACAAG	AAAATGATTT	TGGTGATTTT	GGAATGGATG	ATCGTGAGAT	AATGAGAGAA	420
GGCAGTGCTT	TTGAGGATGA	CGACATGTTA	GTAAGCACTA	CTACTTCTAA	CCTCCTATTA	480
GAGTCTGAAC	AGAGCACCAG	CAATCTGAAT	GAGAAAAATTA	ACCATTTAGA	ATATGAAGAT	540
CAATATAAGG	ATGATAATTT	TGGAGAAGGC	TCGAG			575

(2) INFORMATION FOR SEQ ID NO:848:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 539 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:

ATCCTGGAGT	GCAAAAATAA	AATCCACTCA	AGAGTCACAA	GGCCCGCTGT	GCATAATCGG	60
TTTCACTTTT	ACCTTTTTTT	TTTTTTTTTT	TTTTNGAGAC	AGGTCTCACT	CTGTCACCCA	120
GGCTGGAGTG	CAGTGGCACA	TTCTCGGCTC	ACTGCAATTC	CGCTTCCTGG	GTTCAGTGA	180
TTCTCCCACT	TCAGCCTCCC	AAGTAGGTGG	GATTACAGGT	ACTCACCACC	AGGTCCAGCT	240
AACTTTGTGA	TTTTTAGTAG	AGACAGGGTT	TCACCATGTT	GGCCAGGCTG	GTCTCGAACT	300
CCTGACCTCA	GATGGTCTGC	CCACCTCCGC	CTCCCAAAGT	GCTGGGATTA	CAGGCGTGAG	360
CCACTGCGCC	CGGCCACTTT	CACACTTTTT	ACAGTGAGTG	GTGAATTAGC	AACAGTAACA	420
CTGATTATCC	AACATATATT	TTGGAATATC	TACTATGTGC	AAGGAATTTT	TCTTAAACTC	480
TAAGGTTATG	AATCACTGGG	CAAATCCATA	TAATTAGAGA	ATTTTAAGTG	CGTCTCGAG	539

(2) INFORMATION FOR SEQ ID NO:849:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:

GAATTCGGCC	TTCATGGCCT	AGGGGGAAGA	CGGGAAGCAT	ATAAATAAAC	AAATAATTTC	60
TAAGAGCAAC	TTTTTTAAAG	CAAGTGGGAG	GGGCATGCTA	GTTTTAAGAA	CTGTAATAAA	120
AAACACCACC	CATTGTTTTT	TTTTTGGTTT	TTCTTTTGG	AGACAGAGTC	TTGCTCTGTC	180
ACCCAGTCTC	GAG					193

(2) INFORMATION FOR SEQ ID NO:850:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:850:

GAATTCTAGA CCTGCCATGG CTGTGGGCGC GCTCCCCCTCT GACTGCGTCC CCTTCTCTCC	60
CTGCATCCCC TTCTCTCCCT GCATCCTTCT GTCTTCTGT GTGCCCTTAT CTGCCCTGGG	120
CTTCCTGTCT TCCTGTATCT TCTCACCTGC CTGTGTTGTT TCTAGCTGTG TCTCTGCCCT	180
TCCCTGTGTC ATCATGCCCT TCTGTGCACT CCTGTCTGAC TGTGGCCTCT TGCTTTCTTG	240
TGTCCCAGCA TCCACCTGCG TCTTCCTATC TGCACGTCCC CTCGAG	286

(2) INFORMATION FOR SEQ ID NO:851:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:851:

GAATTCGGCC TTCATGGCCT AATCTCGTTC TCCATGTCTT CCGTGTGCTG GATACACTGG	60
CAGAGCTCAC AGATGAGAAA CGCCCCCAGG GTGGCCTCCT CGTGGTTGTC CTGGATGTCC	120
ACATTGACCA CGTGACACAG CTGGCAGGTC TCCTGTTCTC TGGAAATCAG ATCTTCACC	180
ACCTGGTCAT AACTCTCTC TTCGCAAGTG AGGATCAGAT CAAACAGGTC TTTGCAGTTC	240
TGGAATCTTT CTGGCCGGGG CTTGATTCTC TTATTTCTGT CCAGCATATG TAAAATCCCA	300
TTCTGTGTAT AGAGTTCCTT GTCTTTCCTA AGAAGATCAT TGTACATCTG GTCATATGTG	360
GTTTGTGAAAT CATAAACATT GGGCTTGTG GAGCTGGTC CTGGAAGCTT CACGTGAGTC	420
CCTGTTCCAA AGGATCGGAC GCTGAATCCC CGTTTGCTGA GGATGTTGTG CGCCTCCATG	480
CTCCGGTTCT GGTGCTCGA G	501

(2) INFORMATION FOR SEQ ID NO:852:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:852:

GAATTCGGCC TTCATGGCCT AAGTTGTGCT GACACCAAAC ACATCCAGTT TATAATCAGT	60
ATATTGGAAA GCTGGTATG ATGTAGAACC AGTGCATAAC TTTTATGGG GTTTTGTAT	120
TGGTTTTTTT TTGTAAAGTG TGAATAAAAG GTATGTTTAC TCATTTTCC TGAACACTGT	180
GTTGGTAATG TGCATCATGA CAATTTCCAG TGAAGGTGAG CTGGAGCTGG TTGGACTAAT	240
GAGACTGAGG AAGCAGCTTT TCCTACGATC TGCATTATGT AATCACAGGT CCAGAGAGCT	300
TTATGGAAGC GGGAGAGGAG GAGCACTTAC TCATGTTGTA TTTGTTAATG GAGGATGTCA	360
TCTTTTCATA GATGCTGGAA CTAGAGTGCA CTGTTAGAT GCTAAAGGTT TGAGCTTTAC	420
ACAAAATGTC TTCATCTGTA TTTGTTATG TCTACAATAT ATTTGAATTT GGGGCAAGTC	480
TCGAG	485

(2) INFORMATION FOR SEQ ID NO:853:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 746 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

GAATTCGGCC	TTCATGGCCT	AGGTGGCTGC	ACCATCGGGA	TGTCCTGATC	CAACATCGAG	60
GTCGTAAACC	CTATTGTTGA	TATGGACTCT	AGAATAGGAT	TGCGCTGTTA	TCCCTAGGGT	120
AACCTGTTC	GTTGGTCAAG	TTATTGGATC	AATTGAGTAT	AGTAGTTCGC	TTTGACTGGT	180
GAAGTCTTAG	CATGTACTGC	TCGGAGGTTG	GGTTCTGCTC	CGAGGTCGCC	CCAACCGAAA	240
TTTTTAATGC	AGGTTTGGTA	GTTTAGGACC	TGTGGGTTTG	TTAGGTACTG	TTTGCAATTA	300
TAAATTAAAG	CTCCATAGGG	TCTTCTCGTC	TTGCTGTGTT	ATGCCCGGCC	TCTTCACGGG	360
CAGGTCTAGA	ATTCAAAAGC	AAGCATCTCC	GCATCGCATC	CTCTTCCATT	AACCAGTGGC	420
CGGTTGCCAC	TCTCCTCCCC	TCCCTCAGAG	ACACCAAAC	GCCAAAAACA	AGACGCGTAG	480
CAGCACACAC	TTCAAAAAGC	CAAGCCTAGG	CCGCCCTGAG	CATCCTGGTT	CAACCGGGTG	540
CCTGGTCAGA	AGGCCAGCCG	CCCACTTCCC	GTTTCCTCTT	TAAGTGAGGA	GAAGCTGATC	600
CAGTTTCCGG	AAACAAAATC	CTTTTCTCAT	TTGGGGAGGG	GGGTAATAGT	GACATGCAGG	660
CACCTCTTTT	AAACAGGCAA	AACAGGAAGG	GGGAAAAGGT	GGGATTTCATG	TCGAGGCTAG	720
AGGCATTGG	AACAACAAAT	CTCGAG				746

(2) INFORMATION FOR SEQ ID NO:854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:854:

GCAATTCTAG	TGGTAAGGTG	TTAATAATTT	CACTCTTTTT	ATGTAGACGA	GAGGTTGAGC	60
CTTGAAGGAT	GAGAGGTGTT	TACCGTCTTA	GGATGGGGTA	TAGTAGATAG	AACCATATGA	120
ACCGAAGAGC	TGAGGAATGT	GAGCATGTAA	CACCTGACGT	GTACAGTAGT	AGGTATGAAG	180
TCATATGGGA	GCAGTATTTT	TTTTTCTATT	TTGTTCACTG	ATTTTTCTCC	ACTGGTACTT	240
AATAGGCACT	CAATAAATAT	TTTGCTAAAT	AAATGAACTG	GTGATGTTGA	AATCCAGTTA	300
GTTTACATT	TGGTTGGTTT	TGGTATTGTC	TTTTAAAGGT	AGCAAAGACC	AAGTAATTAA	360
ATTTGTTAGA	TGAATATGAG	ATAAAATGGG	CTCTCGAG			398

(2) INFORMATION FOR SEQ ID NO:855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

GCCCTTTGCT	CCATTTCCAA	GGAAAGAAAT	TAAACCAAGA	TGGTGGCTGG	GATTACAGGC	60
ATGAGCCACT	GTGACCAGCT	CGCAAGATAG	AATTTTGAAA	AATGTATCTT	GAGCCTCTCT	120
TTCTCTTTCT	AGTTCTTTAA	GATTCAAGAA	ATCAAATAAG	GTGATAGCCC	TGAAGCCCTT	180
ACAGGCAGAG	GTGCCCTCGA	CTGTGGGTGA	GGAGGTATTG	ATCCCCAACC	AGTGAGATAT	240
TCTGAGTGGG	GAGAAGTGTT	TTCTATCGAT	GACACAGGGT	GGGCCCTATG	GGAGCAGCAG	300
CATGGCCCCA	CCTTCGACCC	AATGCTGAGA	GGAAAGGGGC	CTCAGGAAGG	GGAGACTGAA	360
GCCAGCACAC	TCGAG					375

(2) INFORMATION FOR SEQ ID NO:856:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:

GAATTCGGCC TCATGGCCTA TGAATTTATT TTATTTTACT TATTTATTTA TTTGGTAGAG	60
ACAGGGTCTC ACTATATTAC CCAGGCTGGT CTCTTACCCC TGGCCTCAAG TGATCCTCCT	120
GTCTCTGCAT CCCAGGCCTC CCAAAGTGGT GGGATTACAG GCATGAGCCA CGATGCCTGT	180
CAGCCTTATT GCACTTCACA CACACACACA CACACACACA CACACACACA CACACACACA	240
CACACACTGA TTCAGGCCTT GAGAGTCAAG CCCAAGAGCT CCCTTGGCCC TGTTCCCCAC	300
TCTCTCGAG	309

(2) INFORMATION FOR SEQ ID NO:857:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 564 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:857:

GGAGAAATAT GGCTTCAGTT TTTCACTACT TCCTGTTAGT TCTGGTCTTT CTGGATACAC	60
ACGCAGCTCA GCCTTTCTGT CTGCCAGGAT GCACTTGCTC AGAGGGAGTT TTNGCAGGAC	120
TCTGCAGTGC ACATCTGTCT CTTGGGAAA GATCCCTGGG AACCTTTCTG AAGAGTTCAA	180
GCAAGTGAGA ATNGAAAAAT TCNACCNTTA TTTGAGATGC CCCAAGGNTC TTTATCAAC	240
ATGAGCACCT TGAATACCT CTGGCTCAAT TTTAACAATA TCAGTGTGAT CCACCTAGGA	300
GCCCTGGAAC ACCTGCCAGA ACTGAGGGAG CTGAGACTGG AGGGGAACAA GCTCTGCTCA	360
GTACCATGGA CAGCGTTCCG TGCCACCCCT CTCCTGAGGG TCTTGATCT CAAACGCAAC	420
AAGATTGATG CACTCCCTGA GCTGGCTCTT CAATTCTTGG TCAGCCTGAC CTACCTTGAC	480
CTATCCTCCA ATAGGCTTAC AGTTGTATCC AAGAGTGTCT TCCTGAAGTG GCCAGCCTAC	540
CAGAAATGCC GGCAGCCACT CGAG	564

(2) INFORMATION FOR SEQ ID NO:858:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 680 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:858:

GAATTCGGCC TTCATGGCCT AGGTGGTTTG GAGTCATAAC ACAGAAGTGG TGAGAAGTGA	60
TCAGAGGCGG ATTCCTGTGT GCATTGAATA TGGGATGTGA GATAAGCAGA GGAGTCAGGA	120
TGGCTTCCCG GACTATGGTC CAAACAGTGG AAAGGATGCA GTGGCTGTAA CCTGAAGCAG	180
GAAGTCTGCA GGTGGGACAG AAATGTTTGT TAAGGGAAGT GTTTTCAGAG TTTGGTTTGT	240
GATATGTTAA GTTTGCCAGT GTAAATGGAC ATACTGTGTA GACATTTGGA AATATGAATC	300
TTGGAAATAT GAGGTTCTGG GTATGAGCAG AGTCCAAGGA TGAGCCTAGG GATTGGAGAG	360
CTGAAACCAG AAAAAGAAGC TAGAAGGAGA GGCCAGTTAA GACAGTGAAA AGAAGCGAGG	420

CATGAGGATC	ACTTGAGGCC	AGTAGCTCAA	CAGCCTGGGC	ATCATAGCGA	GACCCGTGTCT	480
CAGCAACAAC	AACAAAAACG	ACAGTGAAGA	GAGTATTTGA	AGGAGAGGGG	AACAGGCAGC	540
GTATTGCTTA	TTGCTGAGGG	GCAAAGTGAA	GACCAAGGAT	AGACTGCTGG	GCTTGACAGC	600
ATGGAGGGTG	CTGGGGGCCT	AGGCAAGTGC	AATATTCATG	TGGTGTTCATT	GGGCCAAAGG	660
TGTCATTGGA	GGTACTCGAG					680

(2) INFORMATION FOR SEQ ID NO:859:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:

GCAAAAGCAA	GTCACGTGGT	CATGCAGGGC	CTCAGTAAGC	AAGAAATATT	TACCCGCCCCG	60
GGGATGGACA	GGTAGGAAAG	GGTCTGTAA	GGAAGGGCAG	CAAATATTTG	GATAACAGTA	120
CTATGTGTTT	GTATGGAGCG	ATATTTAAGA	AGGTTTCCTA	GGTTTTTTGA	GGGGTATTGA	180
AGCTGAGAGG	TTGGGGGCAG	GCAGGAAGCT	CTGCAGCCTG	TAGCCTATGG	TATCAAGCTT	240
CATGAGAACG	AGAATTAACT	AGTTACATCT	TTATTACCAT	TTTTGGCATC	TCTGCAGACA	300
GTGGATCTAA	TGCATGATAG	CTGATTAATA	AATGTTTGTT	GAATTAATGA	ACAAAATAGC	360
AAGAAACACG	TGTTCTCGAG					380

(2) INFORMATION FOR SEQ ID NO:860:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:

GATTTTGAAT	ACACNACNAA	GTTAGAAGAA	TCTTATTACT	TAGATTCCAT	TAATATCTTA	60
CTATGTTTAA	TTACAAATCT	ATGTATCTCT	CTAGCCATCC	TTTAATCCAT	GTTATGTTTT	120
TGATGCTTTG	CAAAGTAAGT	TGCGAATATT	GGTTCATTTT	CCCTGAAATA	CTTAAGCATG	180
CAAAATCATGA	ACCAAGTTCC	AATATTGTG	TGAAATGCAC	AAATAAGTGT	AAATTGTCAG	240
AGTTTGGGCA	TATGCGTATA	CCTATCAAGA	CACGGAGCAT	TAATATCACC	CTGGAAGTCC	300
TCGAG						305

(2) INFORMATION FOR SEQ ID NO:861:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:

GAATTCGGCC	TTCATGGCCT	AGTGAACAAG	TAAAGACTGA	ATGGGGCTGA	GATGAAGGCA	60
ATGTTTCCAA	GGAAAGGAAA	TGTTATGAGC	AAGAGTGTGA	GGCAAGAGAA	GCTGGAACCA	120

CATTCAGAGA GTATCCTGTA GATTGCTCCA CCTAGAATCT CAGGTGGGTG GAGCAGTGGT	180
GGGAGAAGAC TGGAAAGGTA AGTTGAAGGT AAGGAATGTG TGGTGGGCCT CAGATCCCAG	240
GCTCATTCTT CAAATCACTT CTTACTTCCC TCACTTATCT TTGTTTAAAT AAGGTTAGCA	300
CACTCACTCG AG	312

(2) INFORMATION FOR SEQ ID NO:862:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:

GAATTCGGCC TTCATGGCCT AGTGGCGGGC ATCTTGTTT TATCTTCTGG AGTGAAATAT	60
GCTTTTCCAG TTGTCTTCGA AGTTTCACCT CTGCTCCATA TTTTCCAGTG GTCCCGTTGT	120
CAGCCAGAAT GAAGTGGGAA TGCATGCTGT TGAGAACAGT GAGCTTGCTC ATGGGATTGG	180
ACATGGTCTG GTATGGCCGG ACAACATCTC TTCCAATGAG GTCCTCCTGG TTTTCCACAA	240
TTCCCCAGGG GGCAATACCT ATGGTGCATA TCTTTCCTCG AG	282

(2) INFORMATION FOR SEQ ID NO:863:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:

GAAATTCGGC CAAAGAGGCC TAGGGTGCCT GTGGTTCCGG CTAATCGGGA GTCTGAGGCA	60
GCACAATTGC TTGAACCTGG GAGGTGGAGG TTGCGGTGAG CCAANATGGT GCCACTGCAC	120
TCCAGCCTGG GTGACAGAGT GAGACTCTGT CTCAAAAAAA AAAAGACCTT CCTTAATAAG	180
TGGAGTTGGA TAGACATTTT GCTTTGGAAA ACAGAAGCTA TTTACTGTCA ATATTAGGTC	240
TACTTCATTG ATTTACAGA ATAGGCAAAG ATGTCTGGGG CTTTGCTCAC TAGGGAATTC	300
TGGCCATGGC CTTTGTCTTC TCTTCTAACC AGGCCTTTTG CTTCTCTTCT CCCTTTTTCG	360
CAGATGTAGA ACCACCAGGC GACTCGAG	388

(2) INFORMATION FOR SEQ ID NO:864:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 115 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:

GAATTCGGCC AAAGAGGCCT AAAGTTTCTA AAGATTGTAA ATTTAAAAGG AAATGCCAAA	60
TGAATTATTT GTAAAATTGT TTAATAAAT TAATAATAA TGAGTGCGCC TCGAG	115

(2) INFORMATION FOR SEQ ID NO:865:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:

```
GAATTCGGCC AAAGAGGCCT AGATTGAGAA TGCTGACTCG CCTAAAAGCT TTATGCTTAT   60
CATGTCGTG GTGCTTGGAG CCTGTGGCCC AGGTGATTG GGGTTTGGG ACGCCTCATG   120
GGCAGAGACG GCTCGAG                                     137
```

(2) INFORMATION FOR SEQ ID NO:866:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:

```
GAATTCGGCC AAAGTAGGCC TAAATCCGT CCGGNAACTA TGAACAATGG CAGCTACAGC   60
GTANTCAGCT TCAAGGAGCA ATGCAGCAGT TTAACCAGAG ATTCATTAT GGGGAATCAA   120
GATTTATTTG CTACATCACA AAGTAAAGAA TTTGATCCTC TTGGTCCATT GCCACCTGGA   180
TGGGTCAATT AAATGAAAAG CCCTTACCTG AAGGTTGGNT TTNAGATTC ACAGTGGATG   240
GAATTCATA TTTGTGGAC CACAATAGAA GAACTACCAC CTATATNGAT CCCCACACAG   300
GAAAATCTGC CCTGTAAGTT TTCTAAACAT TGTAGATTAA GAGTAAATA CTAGTCCTTC   360
AGATTTTGAT ATAAAGATT GTATTAGCAA GGAGTGAAG TCTTAGTATT TCTTGAGTTA   420
GCTTGACAAT AGGTTTCTGT TCATTAAGTA TTTTGCAATT CCATCTCCCT CTTGGATATT   480
TTATCCTAGA GATTTTCATA TTTGTTACCA TTTGTTTACA CAGCACTAAA TGAAACTATT   540
TAGAATTTAT AGGTATTGTA CTGCTTACCA ATTAGTCTCT GATTTCTGAT TTTCAGCTTC   600
TTTCATTCCC TNAACACTCG AG                                     622
```

(2) INFORMATION FOR SEQ ID NO:867:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:867:

```
GAATTCGGCC AAAGAGGCCT GGCAGGCGTG TTTATTGACT CTTCCAATTA ATTTTAAAGA   60
ACCTGAAGAA ATGGACAAAG ACAGAGAAAA GNCNACCAGA TGTGATTCCG CCCTTCCAGN   120
AAGCAAAGAG CTTATTTTCAAT CCATATGAT CGATGCCAGT CATGGGGANG AGTGGCTGTG   180
TGGAATTAAT GGATTTTCAA CATCCATCAC AGAGGACACA CATGTATATT AGCNACTCTN   240
AAACCTCTTA AATAAACTGC ATTGCTTTTC ATTTTCATT CCAGTTATAA AACCAGTGGA   300
TGATGNAAG GCCATGTGAC NATACAGCAT GTACTCTCAG GNATGTTTGT GTGACAGGGA   360
TATTATATCT GAAGGGACAG GGCAACTGGG AGGGTGAAGT GCTCATAACT CTCAATTGTC   420
CAGGTAATGA AGCATTGGGA AAGCGACCTC GAG                                     453
```

(2) INFORMATION FOR SEQ ID NO:868:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:

```

GAATTCGGCC AAAGAGGCCT ACGAGCACCT CGCCGCGCG CCTCCTCCGC CGCCGCGGAC      60
TCCGGCAGCT TTATCGCCAG AGTCCCTGAN CTCTCGCTTT CTTTTTAATC CCCTGCATCG      120
GATCACGGCG GTGCCCCACC ATGTCTAGACG CAGCCGTAGA CACCAGCTCC GAANTCACCA      180
CCAAGGACTT AAAGGAGAAG AAGGAAGTNG TGAAGAGGC AGAAATGGA AGAGACGCC      240
TGCTANCGGG AATGCTAATG AGGAAANTGG GGAGCAGGAG GCTGACAATG AGGTAGACGA      300
AGAAGAGGAA GAAGGTGGGG AGGAAGAGGA GGAGGAAGAA GAAGGTGATG GTGAGGAAGA      360
GGATGGAGAT GAAGATGAGG AGCTGAGTCA GCTACGGGCA AGCGGNCAGC TGAAGATGAT      420
GAGGATGATG ATGTGATAC CANGAGCAGA AGACCGACGA GGATGACTAG ACNGCCAAAA      480
AGGGAAAGTT AACTNAAAAA AAAAAGGCCG CGTGACCTA TTCACCTCCA CTTCCTCTCT      540
CAGAATCTAA ACGTGGTCAC CTTCGAGTAG AGAGGCCCGC CCGCCACCG TGGGCAGTGC      600
CACCCGAGA TGACACGCGC TCTCCACCAC CCAACTCTCG AG                                642

```

(2) INFORMATION FOR SEQ ID NO:869:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:

```

GAATTCGGCC AAAGAGGCCT ACTCCTCCTC TTCGGTCTCA CCACAACCCA CCCTATCAAA      60
ATACTGCACC TCCACACAGC CGTTCTCTT TCATTGGGAA AGGCCAGCAC CTGGCTCTT      120
TCTCTTTGAT GCTTTTGTA ATTGAGTTT GGGGAGAGCG TTCCTGGTCT TTGTCTTAA      180
CCAGTGAAGA CAAACAGTGT ACTTGGTGTA AGCAGACACT GAAGGTTTGT CTAAGCTGTC      240
AGCCTGCTCT CCCAACACCT GTGCCTGTGC TGAGACCTGA TGGTCCAGGA AAGGCAGCT      300
GCCACACTGT GGATCCCCCG CCACCCACAC ACGCACCCCC CCTCGAG                                347

```

(2) INFORMATION FOR SEQ ID NO:870:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:

```

GAATTCGGCC AAAGAGGCCT ACAGAGAAGC GGGGCGAACT GAGGCGAGTG AAGTGGACTC      60
TGAGGGCTAC CGTACCGCC ACTGCTGCGG CAGGGGCGTG GAGGGCAGAG GGCCGCGGAG      120
GCCGCAGTTG CAAACATGGC TCAGAGCAGA GACGGGGAA ACCCGTTTCG CGAGCCCAGC      180
GAGCTTGACA ACCCTTTCA GGACCCAGCT GTGATCCAGC ACCGACCCAG CCGGCAGTAT      240

```

GCCACGCTTG ACGTCTACAA CCCTTTTGAG ACCCGGGAGC CACCACCAGC CTATGAGCCT 300
CCAGCCCCCTG CCCCATTTGCC TCCACCCTCA GCTCCCTCCT TGCAGCCCTC GAG 353

(2) INFORMATION FOR SEQ ID NO:871:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 426 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:

GAATTCCTTAG TTTGTTTTCA ACTGGAAAAT ATATAGAGAA AGATGAAGGG GCATTTTTCG 60
CTCTACTCAT CAATTTTGG TACCAAATTT CTTAAAAACC AGATGGTTTA AAGAAAATTT 120
TTCCAAAAAT TATGTTAACA TTCTGCTCAG ACATGGCTGC TAAAAAATA GCATATACAC 180
ATATAATACT GAACAGCTTC TGCAGTGCCT GTAAACTCTC AGCTCATTTC CTCTTTCTAA 240
ANAAAAATA TATTATAACT GATCCCAGAA CTCAATCTCT ATTGTGCAGC AGTATCAAAG 300
GTCCTTAAAT TCTCAACAAT GAAGGAAAAA CAAAAACCCA TTCCCGGAC CGCTTGAGCA 360
GGACTAGGGA AGGAGGAGTC CGTGGATGCA AAGGTTTCCT GCCCCGACGC CCTCAGANTC 420
CTCGAG 426

(2) INFORMATION FOR SEQ ID NO:872:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 430 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:

GAATTCGGCC AAAGAGGCCT AGGGAGGGCT GAGAGGGAGG GAGGGAGGAA GGAAGGAAAA 60
AAGGAACAAA TGCCGCCTGA CCGTCTTTG TGGAAATGACT ACACCTATGA TGAGTACCTC 120
CATGGACCAT GCACCTGCCT TGAAACAAGG AGGCACAGCA CACAGGGCCC TCAGCTAGAG 180
TGACAGGGAA AGGCGGGTGG ACATGGGGAA GGCTCAAACT CAAGCTTTGA AATCGGGGAA 240
AGCCCCGAAA TCTGAACCAC TCTTGGGCCC ATCCTTCTCT CTCCCACATT CACACCTTCG 300
CCTGCGCTCC CATAATTGCA AATTAATTCA TCCACACATT CACACATTCT CTCCTCCCA 360
CTCTCAANAG GCAGCCCCAA GCCCGGGGC CTCACGAAGT CTGGGTGGAT GACCAAGCTC 420
CTCCCTCGAG 430

(2) INFORMATION FOR SEQ ID NO:873:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 606 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:

GAATTCGGCC AAAGAGGCCT ACGGCGATGG TGGTAGCTCA GGAGTTCAAG GCTACAGTGA 60
ACTATGATTG TGCCACTGCA CCCAGCTTG GGTGACAGAC AGTGAGACCC TGTCTCTAAG 120

AAATAAATAA	AAATAAAAAA	TAAGAGGAGC	TTTTGGAATT	CAGCTATTAG	GAAGTTACTG	180
GTGCCCATGG	AGGGAAGTGT	TCCAGGCAAG	TGGTGGTGTT	AAAGGTNGAG	AGAAGAGACA	240
TTAGCTCAGT	GCTTCCCAAA	TAGGATANCC	AAGGCGCCAA	GCTGCANACT	GATCTCAGGT	300
GTGGCCCANT	GCCTCCCCCT	CAGCTGGAAC	CCCAGACCAG	ACTCCTGCAG	TTTCAAGCAG	360
CCTCCTCCTT	CTATCCCGGT	GTACCTTCCA	TATCTCAGTT	CCACCACGGG	GAACCTCAAA	420
CACCTGACAA	CCCATTTCAA	AAGCCTGGCT	ATGGAAAGAA	GAGGAAAGGG	AGGAGCCGCA	480
AGTTTGGGAG	AAAGTGTATT	TGGGATGCTG	GAGTGGGAGC	CTGTTGTAG	GAGCCATAGG	540
GCAGGCTTGA	AGATGAATGG	GAAAGAAGAT	GAGNGGAAGA	GGAGGTGAGA	CTGAGAGCAT	600
CTCGAG						606

(2) INFORMATION FOR SEQ ID NO:874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

GAATTCGGCC	TTCATGGCCT	ACTGGGGGTG	AACTATAAA	GAAAAGCAAG	AAGTGATTAT	60
CATAAAGAA	AGGTAATGAT	GTTTTTCC	TTTCTCGAG			99

(2) INFORMATION FOR SEQ ID NO:875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:

GATGAACAGA	TACGATTGTG	GGATTTTAT	CATCTGTGTA	GCAGGTGGTG	TATGCATCGG	60
GGTACTCCTC	GAG					73

(2) INFORMATION FOR SEQ ID NO:876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:

GAATTCGGCC	TTCATGGCCT	ACCAGAAGAT	GCCTGCCTTC	AATAGATTGT	TTCCCCTGCG	60
TTCTCTCGTG	CTTATCTACT	GGGTCAGTGT	CTGCTTCCCT	GTGTGTGTGG	AAGTGCCCTC	120
GGAGACGGAG	CCGTGCANGG	CAACCCCATG	AAGCTGCGCT	GCATCTCCTG	CATGAAGAGA	180
GAGGAGGTGG	AGGCCACCAC	GGTGGTGGAA	TGGTTCTACA	GGCCCCGAGG	CGGTAAAGAT	240
TTCTTATTTT	ACGAGTATCG	GAATGGCCAC	CAGGAGGTGG	AGAGCCCCCT	TCAGGGGCGC	300
CTGCACTGGA	ATGGCAGCAA	GGACCTGCAG	GACGTGTCCA	TCACTGTGCT	CAACGTCAT	360
CTGAACGACT	CTGGCCTCTA	CACCTGCAAT	GTGTCCCGGG	AGTTTGAGTT	TGAGGCGCAT	420

CGGCCCTTTG TGAAGACGAC GCGGCTGATC CCCCTAAGAG TCGGACTCGA G

471

(2) INFORMATION FOR SEQ ID NO:877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:

GAATTCGGCC	TTCATGGCCT	ACGGAAAAAT	AGTTATATTC	CAGTCTAAGC	CAGAAATCCA	60
GTACGCACCA	CATTTGGAGC	AGGAGCCTAC	AAATTTGAGA	GAATCATCTC	TAAGCAAAAT	120
GTCCTATCTG	CAAATGAGAA	ATTCACAAGC	GCACAGGAAT	TTTCTTGAAG	ATGGAGAAAG	180
TGATGGCTTT	TTAAGATGCC	TCTCTCTTAA	CTCTGGGTGG	ATTTTAACTA	CAACTCTTGT	240
CCTCTCGGTG	ATGGTATTGC	TTTGGATTTG	TTGTGCAACT	GTTGCTACAG	CTGTGGAGCA	300
GTATGTTCCC	TCTGAGAAGC	TGAGTATCTA	TGGTGACTTG	GAGTTTATGA	ATGAACAAAA	360
GCTAAACAGA	TATCCAGCTT	CTTCTCTTGT	GGTTGTTAGA	TCTAAACTG	AAGATCATGA	420
AGAAGCAGGG	CCTCTACCTA	CAAAAGTGAA	TCTCGAG			457

(2) INFORMATION FOR SEQ ID NO:878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:

GAATTCGGCC	TTCANGGCCT	AATAACATCT	CCCCAGACCC	AGAAAAACAG	AAAGCTCCAC	60
AGAAATTAAG	TGTTGAAGAG	AAACTCTCAA	AGGAAGTTAC	AGAAGAAAAAC	TATCTCTTTC	120
CCAGTAAGTT	CAGTGGAAAG	TGCACTAGAA	CATGAATATG	ACTNGGTGAA	TTAGATGAAA	180
GTTTTTATGG	ACCAGAAAAG	GCCACAACAT	ATTATCTCAT	CCAGAGACCC	AAAGCCAAAA	240
CTCAGCTGAC	AGGAATGTTT	CAAAGGACAC	AAAGAGAGAT	GTGGACTCAA	AGTCACCGGG	300
GATGCCTTTA	TTTGAAGCAG	AGGAAGGAGT	TCTATCACGA	ACCCAGATAT	TTCTTACCAC	360
TATTAAAGTC	ATTGATCCAG	AATTTCTGGA	GGAGCCACCT	GCACTTGCAT	TTTTATATAA	420
GGATCTGTAT	GAAGAAGCAG	TTGGAGAGAA	AAAGAAGGAA	GAGGAGACAG	CTTCTGAAGG	480
TGACAGTGTG	AATTCTGAGG	CATCATTTCC	CAGCAGAAAT	TCTGACACTG	ATGATGGAAC	540
AGGAATGCTC	GAG					553

(2) INFORMATION FOR SEQ ID NO:879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:

GAATTCGGCC	TTCATGGCCT	AGGTTCTTAG	GCTCTGAGAT	ACTTCTGCT	TCCCTCACAA	60
------------	------------	------------	------------	-----------	------------	----

ACATGCTTAT GTTTGGTGTG CATGCACATT TGCCTATCAG CACATATAAA GAGACAGTGG	120
AAAAGTCAGA AGTGTTTTCA GGTATTTTC CGATTGAATT CTAGACCTGC CTCGAG	176

(2) INFORMATION FOR SEQ ID NO:880:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:

GAATTCGGNC TTCATGGCCT ACTTCCTCTT CCTCCTCTTC CTCTTCCCCT TCCTGGTGCA	60
GGTACATGAC ATTCCGCACG TTCGGGACGG CCCGGGCAGT CGGAGACAGG ATCACTGTGT	120
CACAACTGTC ATCACTGTCC CCCTCACTGT CCAAAATGTA GTCCCGGGGA ACATGATTCC	180
ACAGCCCATG ATGTCCCCTT TGTAAACAGC TGGCCCAAAG GGTCCCCCAC ACCACCTTCC	240
TGCCCTCATG CTCGGGCTCT ATCTCTTCCC CATCCTCTTC CTCTTCTCTT TCCTCCTCTT	300
CCTCTTCCCC TCACTCGAG	320

(2) INFORMATION FOR SEQ ID NO:881:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:

GAATTCGGCC TTCATGGCNT AATCTGTAAC ATGAGGGAAT AAAC TAGTAT TATCTAAGCA	60
TTCTCTAGAC TTAATAATATG ATTCTAGAC CACTGAGGAG ATTAATAATG AGGTGAGAGG	120
GATTTCAAAA TGAAGCGACC TGCCAGACAT GGTGGCTCAC AGCTGTCATC CCAACATTTT	180
GAGAGACTGA GGCAGGGGGA TCGATTGAGC CCAGGAGTTC AAGACCAGCC TGGACAACAT	240
CGCAAGACCC TGTCTCTACA AAATAAAAAA AATGTAAAAA TAGCTAGGTG TGGTGGCACA	300
CACCTATAGT CCCAGCTACT CGAG	324

(2) INFORMATION FOR SEQ ID NO:882:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:

GAATTCGGCC TTCATGGCCT ACAGAAATTG AGAGTAAACA GAAACATTTA TAGGTCATTT	60
GCTATTGATT ACGAACGTCT AAGTGCAATT CAGTGTTTA TATTTTACAA ATGTGTTGGA	120
ATTTTACTTT ACTTATCTTT TTGAGACAGG TTCTCGCACT CCAGCCTAGG CAACAGAGTG	180
AGACTCCGTC CCAATCAGTC AATCAATCAA TCAATCAATA CCACAGCGGA GAAAATCTTT	240
ACAACTTTTG GTTAGGTAAT GATTTCTTAG GTAGGACACA CAAACACTC GAG	293

(2) INFORMATION FOR SEQ ID NO:883:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:

```

GAATTCGGGC CTCATGGCC TACCTACGGA GTGCTTCTTT CTCACCCTGC ATGCTCACCA    60
CCTCTCTATT CTGCCTAGTT GCGTCGCTA TATCCGCAGA CTCCGGGCTA TCCGGGAGCT    120
CAATAGGTAT GTGCCATGAT ACCGTGTCCT GGGATTGCCT GAGTTACCAC TTTTCTCAG    180
GGGCAGGCAA TTCCATTGTG AACAGTAGTT TTGAATGTTG GGGGAGGTAT GTACGTTATA    240
TAGTGTCTCT GTCTGCCTCC ACCGCCACAT CCATGTTGCT CAGTTGTCCA GAGTTCTTTA    300
CCTGGTGAAG TGATCCAAAC CTTGATTCTT GAGAGTTCTG AACCCTCGA G          351

```

(2) INFORMATION FOR SEQ ID NO:884:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:

```

GAATTCGGCC TTCATGGCCT ACCTGGTGTT TTTTGTTTT GTTTTACCC CTTGTCTTAT    60
GCCAGTGAGT TCCTTCGGGG TTA CTCTGTC AGTAGGTGGA CTATCATCTG GGACAGTTGG    120
GGAAGCTTGG ACAGCCCTGA GTTCAGCAGC CCAGGTAGCT TTGCAGTCTC TCTCTCATGC    180
AATGGCTTCA GCCGAGCAAC AGCTACAGGT GCTGCAAGAG AAACAGCAGC AGCTTTTGAA    240
GCTTCAGCAA CAGAAAGCAA AGCTGGAAGC CAAGTTACAT CAGACAACAG CTGCAGCAGC    300
TGCAGCAGCA TCAGCAGTAG GTCCTGTTCA CAACTCTGTG CCTTCCAACC CAGTGGCTGC    360
CCCTGGATTG TTCATTATC CATCTGATGT TATTCCACCC ACTCCAAAA CAACACCTCT    420
TTTTATGACT CCACCACTCA CCCAGCCCT CGAG          454

```

(2) INFORMATION FOR SEQ ID NO:885:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:885:

```

GAATTCGGCC TTCATGGCCT AGACGAATTT CAAGTATTTA TTACCTCTGT TGAATATAAT    60
TTATTGAACT GTAAGCTTAT ATATAATTCA ACTTTAAAA ATGGCCTGAG TTGAACAACC    120
AGCTCACCAC AATTCTATAA TCTAGGAGTT GGCTCTCGTG GGTCGGCACA GGTGAGCTAG    180
GGTGCTGGT CCTGGTGGAG GGCAGGAGGC CCCCTTCCCC TGGCCTCCCT AGCCAGTCCC    240
CACACACAGC CCCAGTGGCC TCCACAGCTC CACCCTCCTT TCATGGCCGT TCTTTTCTT    300
AGATGCCAAA AGCAGAAAGC TCGAG          325

```


(2) INFORMATION FOR SEQ ID NO:886:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:

```
GAATTCGGCC TTCATGGCCT AGGGAGAATT ATTTGATATT TGTGATACT TGACAGCAGA    60
TAATTTTTTA ACTGCAAGAC CACTAGAGGT CACCAGCGTA AAACTTTCAA CTTTGATTCT    120
GCTGGTAGTG AACTGAAAAG TTCAACTACT ATTCTGCAAT GTTTCCTTTG TTTCTTTTTT    180
TTTCTTTTTT TTGTTTGGAG ATGGAGTGTG GCTCTGTCAC CCAGGCTCGA G      231
```

(2) INFORMATION FOR SEQ ID NO:887:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887:

```
GAATTCGGCC TTCATGGCCT AGTTGCAGAA GAAAAAAG AAAATCCATC CCTGCCACTC    60
ACAAGCTGCT ACCTACAGCA GATTACTATC CTAAGCCTCA ATTTTGCCAT CTGAAAAAAA    120
CAGAAAAAAC AGTTAATAAT ACCTCACCAG GTTCTTGCTA ATTCTTTAGT AACACAGAGG    180
AATCTTTTAG CCCTTCTTTT TTTGTCTTAT AGCTTAAACC ATGCTGCAGG AAATGTATCA    240
ATCCAAGATA AAAGAGCTGA AATCCAAGAA CCTCCCCCTC ACATTTTGTG TGTGTGTTG    300
TTTGTGTTTG TTTGTGTTAG ACACAGGATC TTGCTCTGTC ACCCAGGCTC TCGAG      355
```

(2) INFORMATION FOR SEQ ID NO:888:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888:

```
GAATTCGGCC TTCATGGCCT AGCCACCACG CCCAGCCTCA ATTGCATTTC TACACACAAG    60
GAATAATCCA AAAAGGAAAT TAAGGAAACA ATTCCATTTA CAGTAGCATC AATATGAATA    120
AAATATTTAG AAATAAACTT AACCAGTGAT GTACAGTGAC AGTATGTACA CTGAAAGCTA    180
CAAAACATCA CTAACATAAA TGAAGACAAA TTAGACATCC TGTGTTAATA CATTGGAAGG    240
CTCTTAAGCT GTCAATACTA AAGGTGATCT ACAAATTCAG TGCAATCCCT GTCAAAATCC    300
CAATGATGTT TTTTGAAGAA ATAGAAAAAC TCATCTGGGA ATTCATACGG AATCTCGAG    359
```

(2) INFORMATION FOR SEQ ID NO:889:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 203 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:

GAATTCGGCC	TTCATGGCCT	ACTAAATTGG	AATAAAAGTT	TTAATAATAC	TAACTTGTCT	60
TTTTTTTTTT	TCTAAAATTG	ATTCCATTGC	TACTGTTAAT	AGTATAAATC	TTAAAAGGGT	120
GAATTTTTTG	GATGAAATTA	ATGCTTATTC	TTTTCTTTTT	AAACAGGGCA	ATAAATGTGT	180
TCGTAAGTGC	CAACCAACTC	GAG				203

(2) INFORMATION FOR SEQ ID NO:890:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:

GAATTCGGCC	TTCATGGCCT	ATAGGCCATG	AAGGCCGGCC	TTCATGGCCT	AGTTGATTGG	60
TTTTCTTAGG	TCAGCAATGA	GTCTTAAAGA	TAAAAATTCT	ACTGTGTAAT	CTTTAGTGTT	120
TTCTTTTTTT	TTTCAACTAT	CTTTAATCA	GTTTCAAACA	TTTCAGTGAT	TAAAAGAGAG	180
ATTTGTTGTG	GTTTTGTTGT	GGAGCAGAAA	TGGATTTCAA	GGAGTTTACC	TTCAGAGCTT	240
TTGTTTTTGT	TACGGTGGGT	CTCTCTAGTG	GAAAAAAAT	TTCCCCATCC	CTTTGGAAAT	300
ATTTTCTTTA	AAGGAAATCA	TGTTTTTAAA	ACAAATTATC	GAAATCAGCT	TTCTAATCAA	360
TTGAATCAT	CTCGAG					376

(2) INFORMATION FOR SEQ ID NO:891:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:891:

GAATTCGGCC	TTCATGGCCT	ACGCTTGTC	GTGGCTTCTC	TGAGAAGAAA	AGTTGAAAAA	60
GGGTAAAAGT	TTTCAGGAAT	ATTCGGGCTC	TCTATTGCTA	AGCATAGCGA	GTGTCGGTTT	120
TCTCTCTCCA	ACAGACATCG	CTATTGCGGT	TCCGAGGCAG	TGGGAAGAGA	TGCGGCCCTT	180
GGACATCGTC	GAGCTGGCGG	AACCGGAGGA	AGTGAGAGTG	CTGGAGCCCG	AGGAGGATTT	240
CGAGCAGTTT	CTGCTCCCGG	TCATCAACGA	GATGCCGCGA	GGACATCGCG	TCGCTGACCG	300
GCGAGCACGG	GCGGGCGTAC	CCACGGACCC	TCGAG			335

(2) INFORMATION FOR SEQ ID NO:892:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:

GAATTCGGCC	TTCATGGCCT	AGTATCTTTA	AAGTTAATGT	CTAGCCAAGA	GTTTAGTAAA	60
CGAAGAATTA	AACTGCACTG	TTGATCGGTG	CTTTGTGTAA	ATACATCTTT	AACATTGGG	120
TGGAGAGGGG	CCTTAAGAAG	GACAGTTCAT	TGTAGGAAAG	CAATTCTGTA	CATGAGTTTA	180
AGCATTCTTG	TTGCATTGTC	TCTGCAGATT	CTATTTTGT	TTACAATATT	GAAATGTATG	240
TTAGCAAAAT	GGGTGGATTT	TCAAATAAAA	TGCAGCTTCC	CACTCGAG		288

(2) INFORMATION FOR SEQ ID NO:893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:893:

GAATTCGGCC	TTCATGGCCT	ACTCATCGCT	AGTCCATATT	TGGCCTCCTT	TTAAGCAGTT	60
AATTAACAGG	TATTTTATA	GCATAATGGG	TTTCCTCAAA	CCACCACCCA	ACCAAAACCC	120
AGCCCTTGAT	GATGACCTGC	GCCCACCACG	CAGGGCGCCC	TTGATGCACA	CGCACCTGCC	180
GCCCCGCCC	TGTGACCACC	GCCCTGAGTG	CGGGGTCAT	CATCCCTTCC	ATGCCCTTTC	240
TACATTGCTA	CTAAGAATCT	GTGTGTATTC	ATTAAGACCA	TIACTTTCT	TTCAGATTTT	300
AAATTTATTA	AAGGCTTTAG	TGCTGAATGT	GATTTTGAGG	ACTCTTTTAA	AAAAATACTT	360
TTGGTTGGAA	TGTGGACATT	TCCCACCTAG	CATTGTGTTG	CTCATGTTCC	TCCATATTGA	420
TGTGTGTTTA	GCTAGAGTAC	CCCGTCTAA	CTCTGCGAAT	ATGCCACACT	GTGTGCACCT	480
GCATACACTC	GAG					493

(2) INFORMATION FOR SEQ ID NO:894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:

GAATTCGGCC	TTCATGGCCT	AAAAAAAGGA	AATAGAATCC	TATAATTTAC	CATGAAAAATA	60
TTATGAAAGA	TACAGGTCAG	CATGTATTGT	AGGAGCAAAC	TTAGTGGTCC	TGCTGGTCTT	120
TTGGGTTCAT	TGGTTTGTGG	TTAAGTTTCA	AGTAAGTTCC	CTCTTGGTCT	GGTGTGTTCT	180
GCTGCTGGTG	AGCTCCAGCA	GCTCAAACCA	GCTCTCTCCC	ATTAGTAAGC	CATGCTAAGT	240
TTAGTTTAAC	ACCCATAGTA	GGCCTAAAAG	CAGCCACCAA	TTAAGAAAGC	GTTCAAGCTC	300
AACACCCACA	TACTCGAG					318

(2) INFORMATION FOR SEQ ID NO:895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:

GAATTCGGCC	TTCATGGCCT	ACATTGAGTC	AGTCACCAGG	TGTTTTTTTT	TGGTTTTGTT	60
TTATTTTGT	TTGTTTCTGT	TTTGACCTG	CAGTATCTCG	GCAGGTCAGA	CTGTCATGCC	120
GTGCAGGTGC	CAGCCCTCTC	TCTGCTGTTT	TTGCTCTTGT	TGCTCTCAGA	GCCAAGAGCC	180
ACTCTGCACC	CAGAGGGCCT	CCCATCCACA	CCAGCCTGCC	CTTACTCAG	CTCTCACTTT	240
CGTCATCACC	TGTGGGATCC	TGCTGCAGA	ACCCCTCAA	AACTCTTTCC	TTCACGGTGC	300
AGCTCCACCC	ATCCTCGAG					319

(2) INFORMATION FOR SEQ ID NO:896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:896:

GAATTCGGCC	TTCATGGCCT	AAGACAGGGA	GGCAGACACA	TTGAGAAATA	ATACAAATTA	60
TTATCATCTT	CATAAATAAT	ATAGACAGCT	CTGACGATAA	AGGTGTGTAC	CAGATATGAC	120
AGGAGCAGAG	CTGAGGCATC	CAGCACCTTC	AGGGATGAGG	GGTAATGGTG	TTAGGAAAGG	180
TTTTCTGTAC	TTCTCTACG	TGGGTGCTTT	TCTCCATCTC	TACTTTCAA	TCCACCCAT	240
GCTAAGGCCT	TATCCAAATG	ACCACTGCCA	GAAAG			275

(2) INFORMATION FOR SEQ ID NO:897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:

CTCGAGTTCC	CCCATCAGTC	TATGTGCCCC	ATGAGAGCAG	GCACACATAG	GAACAGGTCA	60
GTCAGTTTCT	GATGCCCAGC	ACAAGGCCAG	GCACAGAGTG	GCAGGGGAGT	TGTGGGGCCC	120
CACAGACCAG	AGGCCAGCGC	CAATTCTGCC	CCTGCTATTT	GCATGCCCTC	ACCTCTGTGG	180
GCCCCTGTCT	GTCTGCGAGG	ATTGAGGAG	TAAGTCCTGG	AGCACAGCGC	GGGTTGGAGC	240
ATGCAGAACT	GCCAGGTGCT	ATCAGCACCA	TCATTCTTTC	CACTCCCTAC	TCCCTTTAGG	300
CCATGAAGGC	CGAATTC					317

(2) INFORMATION FOR SEQ ID NO:898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:

GAATTCGGCC	TTCATGGCCT	ATGACCTGGA	AGAGTGGTGC	GAAAGAGAGG	AAGGGGCAGA	60
GGCCAGGAGT	GTCATGCAAT	TGCTGTGCCT	CCTCACGGAA	TTATTGAGTG	TGTCCCCTGT	120
GTCATAGACC	CATCACAGTT	GTCTCTTCCA	GTACTTCGTG	AGCTCCCTAA	GGGCAGGGAC	180
TGTGTATACT	TCTGGGCGCT	AAAATGAGTG	TGAATCCATG	TCAGGCACTC	TGTGCCAGTC	240
TTTATTGGAA	ATATATGATT	TTATCTTAAA	TAGTTCTTCA	ATGTAGGTAC	TATCACTTGC	300
CCTGACTTTA	GAGATACAGG	CACTAAGGTT	TGTGGAGGTA	AATAACTTTC	CCAAGATCCT	360
CGAG						364

(2) INFORMATION FOR SEQ ID NO:899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:899:

GAATTCGGCC	TTCATGGCCT	AGGTGTTTAT	GGATATCCTC	CAGATTATTA	TGGATATGAA	60
GATTATTATG	ATTATTATGG	TTATGATTAC	CATAACTATC	GTGGTGGATA	TGAAGATCCA	120
TACTATGGTT	ATGAAGATTT	TCAAGTTGGA	GCTAGAGGAA	GGGGTGGTAG	AGGAGCAAGG	180
GGTGTGCTC	CATCCAGAGG	TCGTGGGGCT	GCTCCTCCCC	GCGGTAGAGC	CGGTTATTCA	240
CAGAGAGGAG	GTCCTGGATC	AGCAAGAGGC	GTTTCGAGGTG	CGAGAGGAGG	TGTCCAACAA	300
ACTCGAG						307

(2) INFORMATION FOR SEQ ID NO:900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

GAATTCGGCC	TTCATGGCCT	AATTCCATC	ANGAANTCNG	TGAGGTTCTC	AGATGTGGCA	60
ATGTCCACGC	AGTTTCGCAC	CANGGCATGG	CGGTTCTTGT	CTCCCATTC	TGGCTGTCCC	120
AGGTAGCGCA	GATGCCAGGG	TGCCCTGCC	CTGTCCATAG	AGCGTCGGGC	CCTGAGAACA	180
AATGGGCTGG	CTTGCTGGNC	CTTAAGGAGG	AATACCATCT	CATGGTCAAG	GAAAGTCTCA	240
GGTTCCATGT	TGTCACACAA	ACCACGAAGG	CGGTGGATGA	GGCTTTCCAA	ACTGTGATCT	300
AAAACACTTC	CCTGCAACAG	GTACTCCATC	ATGTTAATGG	TGCCCCCAGT	GACAGGGATC	360
ATGGTGACTG	GAGGTGCCTC	CATGGTGTCT	AAGTTGAAGA	CAACACAAC	GGACTCAGAG	420
CCCCAGTCA	GGTAAGGCAC	GGGATATACC	TCCTTGAGGC	TGTAGTGTCT	TCCTCGAG	478

(2) INFORMATION FOR SEQ ID NO:901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:

GTACCAGGCG	NATCCTGAAG	AGACACTACT	ACNACCAAAT	GGAACCCAG	AAGAAATAAA	60
ATGTTTGGAT	CNAATAAAGA	AAATTGAAAC	NACTGGTTGC	NACCNAGAAA	TAACATCATT	120
TGAAATTAAT	CTGAAGGAAA	AAAAGTACCA	GGAGGACTTT	AACCCGCTGG	TGAGAGGATG	180
TTCTGTTC	TGCTGTAAGA	ATCACACTCG	GGCATACTC	CACCATCTGC	TGGTGACCAA	240
TGAGCTGCTG	GCCGGAGTCC	TGCTTATGAT	GCACAACTTT	GAACACTACT	TTGGGTTTTT	300
CCATTACATC	CGGGAAGCAC	TAAAAAGTGA	CAAACTGGCA	CAGTTGAAAG	AGCTCATCCA	360
CAGGCAAGCA	TCTTGAGATC	TTGCAAATAC	AAGTCTCACT	CTTCACACTG	AGCCTGTACC	420
ACTGTTGTAA	CATGGGAAGA	CGTGAAGAAG	AAATAATCTG	AGCTCGAG		468

(2) INFORMATION FOR SEQ ID NO:902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:

GAATTCGGCC	TTTCATGGNCT	AGCCAGGGAT	AAAAATACAA	TCTTCAAAGC	GGTCAGAGAA	60
AAAAATGCAAA	TTATGAACAG	AGGCATCAAG	GTAACAATAA	CAGCCGAATT	CTGGTCAGAG	120
ACAATGCAAA	CCACACATGA	GCAGAGCGGN	CCCTTTAAAG	AACTCAAAGG	AAAGAAAAAG	180
TGAATCGACC	TGGAGCTCAG	AGCCAGATAA	AATATCTTGA	AAATATGAAA	GTAAAAAATA	240
GAGAAGAGGA	GCTCATGAGG	GGAGAGGGAC	TAGTGTAAGG	AAAGGTGTGT	AGGTGGGAAA	300
AGGNCCAGTG	TGTTTCAGCA	TAGATAAGAA	AAGNAGACCA	CGCNAAGAGG	TAGACGAACA	360
GGCAAGGTTG	GTATCAGGT	GAAAAGACAG	GTTAGTGGAC	GATCAAAGAG	GNTCTTGACT	420
GCCGTGCTAC	AATAAACTAC	ATATTTTTTT	TTCAGGCAAA	GTAAGGATTT	CAGAGATGAT	480
TTTTAACATG	GGATGATATA	ATGCACAGTA	TTTTAGAAAT	ATTGTTCTAA	ATCAAGAGTG	540
GAGAACCCAC	TGCGGAGACA	AATTCTGAG				570

(2) INFORMATION FOR SEQ ID NO:903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:

GAATTCGGCT	TCATGGCCTA	CTCCCATCAA	ACTCCAGAGA	AGAGAGTGAA	TACTGGAGAA	60
GAAAGGAGGA	AAATATCTGA	GGAAGCAGCA	AGAAAGAGAA	GGCTGGAATT	TATTGAAAAA	120
GAAAAGAAAC	AAAAGGATCA	GATTATTAGT	TTAATGAAGG	CTGAACAAAT	GAAAAGGCAA	180
GAAAAGGAAA	GGTTGGAAAAG	AATAAATAGG	GCCAGGGAAC	AAGGATGGAG	AAATGTGCTA	240
AGTGCTGGTG	GAAGTGGTGA	AGTAAAGGCT	CCTTTTCTGG	GCAGTGGAGG	GACTATAGCT	300
CCATCATCTT	TTTCTTCTCG	AG				322

(2) INFORMATION FOR SEQ ID NO:904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:

GAATTCGGCC	TTCATGGCCT	AAATGTATGT	AAGGTACAGA	GAGGATGTCT	GGAGGTGCGC	60
CCTGTGGATA	TCTTAAGCCT	TTAAGGGTGA	GCAAAAAACA	ATAGGTTTAC	AAAGGAAAAT	120
GAGAATGGGC	TATGAGAAAG	GTAAGAGGAA	AACCAAGGAA	AGAGAACGTT	TTGAGACAGT	180
AGTAGTGGTC	AGCAATGTCA	AATTGCTGCA	GAAATTTTCT	AAGAGTGAAA	TTGGGTTTAG	240
CAGCTGCAAG	AGGAGTTCAT	TTAATTGGTG	TAGCAGAAGC	CCATTAGATT	GCAGTGTGAT	300
GAGAAATTAT	TGGGAACAAG	GATACTCGAG				330

(2) INFORMATION FOR SEQ ID NO:905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:

GAATTCGGCC	TTCATGGCCT	AGATGCCGCC	ATCTACCAGG	CCTCTGCCCC	AGAACAGCAA	60
GGGCATTGTG	TCCTGCTCAG	GGGTCCTGGA	GGTGGGCACC	ATGACTGAGT	ACAAGATCCA	120
CCAGCGCTGG	TTCCGCNAGT	TGAAGCGCAA	GGCTGCGGCA	AAGCTGCGCG	AGATCGAGCA	180
GAGCTGGAAG	CACGAGAAGG	CGGTGCCTGG	GGAGGTGCGAC	ACTCTGCGCA	AGCTCAGCCC	240
CGACCGCTTC	CAGCGAAAGC	GGCGATTGAG	CGGGGCTCAA	GCGCCGGGCC	CCTCGGTCCC	300
TACCAGGGAG	CCTGAGGGTG	GGACCCCTGG	GGCTTGCCAG	GAGGCAGAGA	CTGAGACTGC	360
TCAGCACTCA	GGTTTGGGCC	TGATCAACAG	TTTGCTTCT	GGAGAAGTGA	CCACCAACGG	420
GGAGGCTGCC	CCCGAGAATG	GCGAGGCTCG	AG			452

(2) INFORMATION FOR SEQ ID NO:906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:

GAATTCGGCC	TTCATGGCCT	AGCCATGGAT	TTAAAGAAAT	TGTGACTAAA	CCAATGTTTT	60
AGCATTGATA	AATGGGAAAT	TGCGGAAGGA	TGTAAACGTA	GAGTTTAACT	CTACAACCTG	120
GCTTAGGGAC	TCAGGTATGG	ACAGTGAGAA	TAACTTGGTT	TAGGGACTCA	GATATGGACA	180
GTGAGACTGG	CCACATGAGT	GCCTTTCTCA	CTGTCACACT	CTTACCCAGG	TTGGAGTGCA	240
GTGGCTGTG	ACAGGTGTGA	TCATAGCTCC	CTGCAGCCTT	GAATTCCTGG	GCTCAAGCAG	300
TCCTGCCTCA	GCCTCCCAAG	GAGGTGGGAC	TAAAGATGGT	GTGCCACCAC	ACCTGGCTAA	360
TTTTTAAATT	TATTGTAGAG	AAGGGGTCTT	GCTATGTTGC	CCAGGTTGGT	CTTGAACCCC	420
TGACCTCCAG	GGATCTCTCC	TGCCTTGGCC	TCCTCAGGAG	CTGGAACTAC	AGATATATGC	480
TAATGTCTTC	AATTTATGGA	AATGCAGAAA	TGCTCGAG			518

(2) INFORMATION FOR SEQ ID NO:907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:

GAATTCGGCC	TTCATGGCCT	ACTTGCTGCT	GCGCTTTGAC	ATCAGCTTGA	AGAAGAATAC	60
CCACACCTAC	TTCTACACCA	GCTTTGCAGC	CTACATCTTC	GGCCTGGGCC	TTACCATCTT	120
CATCATGCAC	ATCTTCAAGC	ATGCTCAGCC	TGCCCTCCTA	TACCTGGTCC	CCGCCTGCAT	180
CGGTTTTCCT	GTCCTGGTGG	CGCTGGCCAA	GGGAGAAGTG	ACAGAGATGT	TCAGCTACGA	240
GTCTCTGGCG	GAAATCCTGC	CTCATACCCC	GAGGCTCACC	CACTTCCCCA	CAGTCTCGGG	300
CTCCCCAGCC	AGCCTGGCCG	ACTCCATGCA	GCAGAAGCTA	GCTGGCCCTC	GCCGCCGGCG	360
CCCGCAGAAT	CCCAGCGGTC	TCGAG				385

(2) INFORMATION FOR SEQ ID NO:908:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 630 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:

GAATTCGGCC	TTCATGGCCT	ACCCCTGTCC	ACTTTGGTCA	CTGTTGGCTG	GGGCCCCGTGG	60
AGCTGTCCAG	AGGGGACCGG	GGCCAGTAGA	GTAGAGGACA	GTATTTGTAG	AGCAGGCATT	120
TCCTCTGAGG	TTCTTTGGGA	TCCCCTGAGC	TATGAAAGCT	GGAAGCAGTT	GAAAGTTTTC	180
AGGGAGAGGG	ATGCTGGAGT	CTCAGAACTT	TAGAGGTGCT	GCAGGAGTCA	GTTCTGGCAG	240
TGAGAGAACA	CTTGGGCGGG	TTTCACACAC	ACACAGCACT	TGAGCCATTC	TTGGGCAGAA	300
GGGGCCTCAC	TTCCAAGCAC	AAGGAGTGTT	AACGAAAAAT	TATTAACATG	GTAAGGAAGA	360
CTTTATTTCAG	GGCCATTGCA	GTAGGCATCC	CAATAGTGGG	GAGAGATGGG	GCTCAATTCC	420
AAGTACAAGA	AGAACAAGTG	GGCACTTAGC	CAAGGAGCAG	GTGGGAGGGG	GTCAGAGGAT	480
AGAAAATTAC	TAAGAGGAGA	CGTCAAGGTT	AGGGGGATTG	TTGCTGAAGT	CAGGCCAAGG	540
AGCAGGTGGG	AGGGGGTCAG	AGGATGGAAA	ATTACTAAGA	GGAGACGTCA	AGGTTAGGGG	600
GATTCTTGCT	GAAGTCAGGC	CTTGCTCGAG				630

(2) INFORMATION FOR SEQ ID NO:909:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 678 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909:

GAATTCGGCC	TTCATGGCCT	AGACGGTGAT	GTTTTTGGTA	AACAGGCGGG	GTAAGATTTC	60
CCGAGTTTCT	TTTACTTTTT	TTAACCTTTC	CTTATGAGCA	TGCCTGTGTT	GGGTTGACAG	120
TGAGGGTAAT	AATGACTTGT	TGGTTGATTG	TAGATATTGG	GCTGTTAATT	GTCAGTTCAG	180
TGTTTTAATC	TGACGCAGGC	TTATGOGGAG	GAGAATGTTT	TCATGTTACT	TATACTAACA	240
TTAGTTCTTC	TATAGGGTGA	TAGATTGGTC	CAATTGGGTG	TGAGGAGTTC	AGTTATATGT	300
TTGGGATTTT	TTGAGGGGTG	TAGGGATGCG	AGCTCTGGAG	GGGACCTTCC	TTTCAGGACA	360
GCGCCCTGGC	CCCCAGTGCC	CCACTCACCT	TCCTGGGCGG	GAACCTCAAG	TGCAGCCAGG	420
CTGGGGGACA	GAGTTCCCCC	CAAGCTGAGA	CAGGAGGGGT	CTCAGGCGGC	AAAATTCTCT	480

CTCCAACCTCC	TGGTGGGGTG	GGGGTCATGG	ATGAGGGGGG	CCCCTTCCTT	CCCCAGCCCA	540
CTCAGGGCAC	CCCTGGCCCG	TCCCGCCCCA	CCTCCAGCTG	CTTCATGGTC	TCCTCCAAGC	600
TGAGCAGGTT	CTCCTGGATT	TCCTGGGTCC	GTGCTGGGCT	CAGGGGGCCG	CCCCCTGGGA	660
CCCCATCCCC	ATCTCGAG					678

(2) INFORMATION FOR SEQ ID NO:910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:

GAATTCGGCC	TTCATGGCCT	AAGAAGAGGA	GGAAGAAGAC	GGGGCTGCAG	TTGCTGAGAA	60
ATCACATCGA	AGAGCTGAAA	TGTAGCGGCA	CCCAATTTCT	AGACAACGCT	CAGCCAACGG	120
ATTCTTTTCA	AGCTGCTCAA	ACATAAATCT	GCCTACTGAA	CTCTAGGATA	TTTAATTACA	180
AAAATTAAGA	ACTTAGACTT	TTTTAAAAC	TTTGTATTAG	AAATGCGCAT	ACATTATAT	240
GAATATATTT	TGATAACGTA	GGTCTAGAGC	TTCTTTTATA	TTCAAGCTTA	ACATGANAAA	300
GAAGAAAAAC	AATAAAGTAA	ACCTGAGCCC	CCACGTCCCA	ATTTTTTAA	AGATTATGTG	360
ATGTTGGAAA	GCTCATTGAT	TTTGATATATG	TTTCAGCGTG	TTACCTTTCT	GGCTTCCAGT	420
TCCAGGTGT	TCTTTGTTTG	CCTTTGATAA	AATACAGGAT	TTAAGAACAG	AGAGTACTGC	480
AAAATGCCAT	GCAGACTTTA	AAGAGAATGG	CCTGTTTACT	AATTGCTGCC	CTTCTGATGT	540
CTTTATGTAT	AGCTCTGATA	GAATTTTCAC	CAGTCTATGT	ATCTCTGGAG	TGAGATCCTA	600
TGTACAAAGT	GACATACAAT	TGGAATCCT	CGAG			634

(2) INFORMATION FOR SEQ ID NO:911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:

CTCGACCTTC	ATGGCCTAAT	GAGCTGTTTT	GTAAACGAGA	TTTGTTTTGT	GGGAAAGGGA	60
ATTTTGTTTC	AAGACTTCCC	TAAGAACTG	ATAGCATCGG	GTAATTCTTA	AATTGACTT	120
ATCATAATGG	TATATCTGGA	AGGAATTTGT	CAACTGATAT	GTTATAATTA	TTTTTTAATT	180
TTTTTTAATT	TTTGAGATAG	GTCTTACTCT	CTTGCCCAGA	CTGGAGTGCA	GTGGTGTGAT	240
CATGTTTCAC	AGCAGCCTCA	AACTCCTGGG	CTCAAGAGAT	CCTCCCACCT	CAGTCTCCTG	300
AGTAGCTGGG	ACTAAAGGCA	TGTGCCACCA	TGCCTGGCTA	GTTAATTTTT	TTTTTTTTTT	360
TTAAGTAGAG	ATGAAGTCTT	GCTGTGTTGT	CCAAGCTGGT	CTCACACTCC	TGAGCTTGAG	420
CAACCTCCT	CTAGGCCATG	AAGGCCGAAT	TC			452

(2) INFORMATION FOR SEQ ID NO:912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:

GAATTCGGCC	TTCATGGCCT	AGCGGGCTAT	GTGGCTGATT	GAAGAGTATG	CAATGAGCGA	60
TTTtaggtct	GTTTgTCGTA	GGCAGATGGA	GCTTgTTATA	ATTATGCCTC	ATAGGGATAG	120
TACAAGGAAG	GGGTAGGCTA	TGTGTTTGT	CAGGGGGTTG	AGTTTGATGA	GTTTAGGCAG	180
GGCCTGGATC	ACCTCTTCT	TCTCCAGCCC	ATTGAGCACC	GGGATGAGGA	AGCGGACGTC	240
TGGCAGTCGC	TTGTGGTAGA	GATCCCGGAC	CCGCTTCACC	AGCTCTGGGG	AGGGTGGGAC	300
TTTGTCTGTG	AGGCTGTGCA	GACATCTCGT	GACCAGTGTC	TCTGCTCCCT	TGGGACAATT	360
TTCCACCAGC	AGGAGCAGCT	CCGGGGAGTT	CATGCCCAAT	CCTCGGATCG	GCTGCTCAAT	420
GACCCTCAGC	ACCGTCCGCT	TGATGTCGGC	GATGGCTTCA	GTGTACACGG	CCGCCAGTTC	480
GTGGATCAGC	TTGTGGGCTC	GAG				503

(2) INFORMATION FOR SEQ ID NO:913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:

GAATTCGGCC	TTCATGGCCT	AAAAGATATT	ATTTTAAATT	AATTTTGAAC	TATAGAAAAG	60
TAGTACAAAT	AATTCAGAAA	ACTCCCATAT	TTACTTTACA	TGGATTCACC	AATTTTTAAC	120
ATTTTGCTAC	ATTTGTTTGC	TTCTCTCGCT	GTCTCTACAC	ACACATACAC	ACACAAATT	180
TTGGGAGGTC	TAGTGACGCT	CCCGGCCGGC	CCAGGAGGAC	AGGAAAACAT	CACTCACGAA	240
GTCACTCCTT	GCCCCGAGCC	GCTTTGTCCT	GTCTTCTGTC	AGGAGGCCCT	CCAGGAGGTG	300
TCTTGCGGAA	TTTGTAATAT	TTGGTTTCAT	CTCGAG			336

(2) INFORMATION FOR SEQ ID NO:914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:914:

GAATTCGGCC	TTCATGGCCT	AGACAGTCAA	TGTGGATGAG	AACTAATCGC	TGATCGTCAG	60
ATCAAATAAA	GTTATAAAAT	TGCAAAAAAA	AAAAAAAAAA	AAGAAGTGAG	GATGACAGGA	120
GAAGGTAGAT	GGTGCAACAT	GAGGGTGCTT	TCTACCAACA	AGGTGTGCAG	CATTGGACAC	180
GCAAGACCAC	GTGACCTGCA	GCTCTGATGG	TGCAACATGA	GGGTATGTCC	TACCAACAAG	240
GTGTGCAGCA	TTGGACATAC	TTGACCACGT	GACCTGCGGC	TCTGAAGGTC	CCACCTGTTC	300
TCGTTCTAAA	GTCAACATTT	CTGACCGCTG	TGCTGTGGAA	GGGGAGGCAA	TCAACCAGAA	360
CTCGAG						366

(2) INFORMATION FOR SEQ ID NO:915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:

GAATTCGGCC	TTCATGGCCT	AGGCAACAAG	AGCCCTGAAG	TGCTCCGGGC	ATTGATGTA	60
CCAGACGCAG	AGGCACGAGA	GCATCCCACG	GTGGTACCCA	GTCATAAATC	ACCTGTTTTG	120
GATACAAAGC	CCAAGGAGAC	AGGTGGAATC	CTGGGGGAAG	GCACACCGAA	AGAAAGCAGT	180
ACTGAAAGCA	GCCAGTCGGC	CAAGCCTGTC	TCTGGCCAAG	ACACATCAGG	GAATACAGAA	240
GGTTCACCCG	CAGCGGAAAA	GGCCAGCTC	AAGTCTGAAG	CCGCAGGCAG	CCCAGACCAA	300
GGCAGCACAT	ACAGCCCCGC	AAGAGGTGTG	GCTGGACCAC	GTGGACAGGA	TCCGGTCAGC	360
AGCCCCTGTG	GCTAGAGGAA	CACCACTCGA	G			391

(2) INFORMATION FOR SEQ ID NO:916:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:

GAATTCGGCC	TTCATGGCCT	ACGGGTGTTT	GAGGAGTACA	TGCGGGTTAT	TAGCCAGCGG	60
TACCCAGACA	TCCGCATTGA	AGGAGAGAAT	TACCTCCCTC	AACCAATATA	TAGACACATA	120
GCATCTTTCC	TGTCAGTCTT	CAAAC TAGTA	TTAATAGGCT	TAATAATTGT	TGGCAAGGAT	180
CCTTTTGCTT	TCTTTGGCAT	GCAAGCTCCT	AGCATCTGGC	AGTGGGGCCA	AGAAAATAAG	240
GTTTATGCAT	GTATGATGGT	TTTCTTCTTG	AGCAACATGA	TTGAGAACCA	GTGTATGTCA	300
ACAGGTGCAT	TTGAGATAAC	TTTAAATGAT	GTACCTGTGT	GGTCTAAGCT	GGAATCTGGT	360
CACCTTCCAT	CCACACTCGA	G				381

(2) INFORMATION FOR SEQ ID NO:917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:

AGATGGACTG	GCTTCAGCTG	TTTTTGGAGG	TGCTTGTGTT	TGGAANAAAT	GCAGGGATGG	60
CAGANGCCTG	GCTCTGCAGC	CAGGANCCAC	TGGTGCGCAG	CGCTGAGCTG	GGTTGCACGG	120
TCGACGAAGT	TGAGAGCCTC	ATCAAGCGGC	ACGAGGCCTT	CCAGAAGTCA	GCAGTGGCCT	180
GGGAGGAGCG	ATTCTGTGCG	CTGGAGAAGC	TTACTGCGCT	AGAGGAGCGG	GAGAAGGAGC	240
GAAAGAGAAA	GAGGGAGGAG	GAGGAGCGGC	GGAACAGCC	GCTTGCTCCC	GAACCCACAG	300
CCAGTGTGCC	TCCAGGGGAC	TTGGTGGGCG	GCCAGACAGC	TTCTGACACC	ACCTGGGACG	360
GAACCCAGCC	ACGGCCACCA	CCATCCACAC	AAGCACCCAG	TGTTAATGGA	GTCTGCACAG	420
ATGGAGAGCC	CTCACAGCCC	CTGCTGGGAC	AACAGAGACT	TGAGCACAGC	AGCTTCCCCG	480
AAGGGCCGGG	ACCTGGCTCA	GGGGACGAAG	CCAATGGGCC	CCGGGGAGAG	AGGCAGACCC	540
GGACTCGGGG	CCGGGCCCCA	TCTGCAATGC	CCCAGAGCAG	GTCTACCGAG	TCAGCCCATG	600
CTGCCACCCT	GCCGCCTCGA	G				621

(2) INFORMATION FOR SEQ ID NO:918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:

```
GAATTCGGCC TTCATGGCCT AACATGGGTG ACACGGATGT CTATAGTGTC CACCACATTG      60
TCTGGCATGT GGAGGAAGGA GGCCCAGCCC AGGAGGCAGG ACTCTGTGCT GGGGACCTCA      120
TCACCCACGT GAATGGGGAG CCTGTGCATG GCATGGTGCA TCCTGAGGTC GTGGAGCTGA      180
TCCTTAAGAG TGGCAACAAG GTAGCAGTGA CCACAACGCC CTTCGAAAAT ACCTCTATCC      240
GCATTGGTCC CGCAAGGCGC AGCAGCTACA AGGCTAAAAT GGCTCGGAGG AACAAAGCGAC      300
CCTCCGCCAA GGAGGGCCAG GAGAGCAAGA AGCGCAGCTC CCTCTTCCGG AAGATCACGA      360
AGCAGTCGAA CCTGCTGCAT ACTAGCCGCT CGCTGTCGTC GCTGAACCGC TCGCTGTCAT      420
CCAGCGATAG TCTCCGGGGC TCGCCTACGC ACGGGCTGCC GCGCGCTCG CCCACGCACA      480
GCTACCGCTC CACGCCTGAC TCCGCCTACC TAGGCGCCTC ATCCCAGAGC AGTCCCCCAG      540
CCTCGAG                                     547
```

(2) INFORMATION FOR SEQ ID NO:919:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:

```
GAATTCGGCC TTCATGGCCT ANACACTCTT CCTCTTCTCC TTTTTCCTTT AGAGATATGA      60
ATCAGGTTCT TGATGCCTAT GAAAATAAGA AGCCATTTTA TCTGTACACG GGCCGGGGCC      120
CCTCTTCTGA AGCAATGCAT GTAGGTCACC TCATTCCATT TATTTTCACA AAGTAAGTAT      180
NGGATCTTAT GGCTTTTCTT ACTCTCTTAG TGAATTGAGA ATGTTGCTTA TAAACCATGT      240
TTAGAAGTGA CAAGATCATG CTAGTTTCAAT TGCTGAGCAA CCAAGATGTC AAGAGTTGGC      300
ACTTTTTTGG CTTCCATTCA CTTTGTTCCT GGGCTCACTT TAGAGGACCA TGGAGTGATG      360
GGGAGAGCGC AGCTTTGGAG TCAGCCAGGC CTGCTCCTCT TCTCATCCTG CTCCTGTCT      420
GCATGGCCAT GGGCCTGCTA CTTCTCTGAG CCTAAGTTTC CACATCTGCA AGATGAGAAT      480
GAAGATACCT ACCTCATAGA ACTACTGTAA AGCTTCAAAA CAAAGTGTGT AGAGCAGCTA      540
ACACAGAGCA CACAGGGCCA CCTGGTCGAT AAATGGTAGT AGACCTTATC ATTATCCATA      600
GTCCCTCGAG                                     610
```

(2) INFORMATION FOR SEQ ID NO:920:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:

```
GAATTCGGCC TTCATGGCCT ACTAACTCTC CTTCTCAAAA CACCAAAAGT AAATTTTAAT      60
ACCCAAAACG AAATTCATTT TGTTAATCAC AGCTTAGAAG GTTTCATATG ATCTGGCCAA      120
ATCTGTATCT TGCATCACTC TTATCACTCC CCCTCTCTGC TCACTGTATC TGCATGATAG      180
```

GAATCAGCTC ATCTTCCTAT ACATCAGTAC TAAACAACC TCACTCCTAC CTGAGGCCCT	240
GTGTGCTGTC TGTAGATGGT CCATCTTCTC ACTTCACTCA GGACTIONAAT GTCCCTCTT	300
CACTCGAG	308

(2) INFORMATION FOR SEQ ID NO:921:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:

GCAACCGGGT TTTGCCAGGG CCTATTGCAC CAGAGAGCAG CAAGAAGCGG GCCCGTAGGA	60
TGCGACCAGA CCTTTCTAAG ATGATGGCCC TCATGCAGGG TGGAAAGCACT GGGTCTCTAT	120
CTCTGCATAA CAGTTTCAA CACAGCAGTA GTGGCCTACA GTCTGTGTCA TCTTTGGGTC	180
ACAGCAGTGC CACTTCTGCA TCTTGCCTT TTATGCCATT TGTGATGGGT GGTGCACCAT	240
CATCCCTCA TGTAGACTCC AGCACCATGC TTCATCACCA CCACCACCTC GAG	293

(2) INFORMATION FOR SEQ ID NO:922:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:

GAATTCGGCC TTCATGGCCT AGTGGGGCCT GTTATAGTT GACTGACAGT AAGTTCTATA	60
TGGTATATAA CACTAATTCT CTAGTCTTCT GGGCATATCT ACGAACAAAT ACAATCCAAA	120
TATTATGAGT AACTGGGTTG TGACCACTGC ATGCATTACA CTGAAAGAAA CACCAACTCG	180
AAGCACAAT ATATTATTAT TATATTTCCG CTCAGCTCTC AGTGGGGAGA GCAGCTACCT	240
CGGACCACAA TGCCATTTAA ACCAGATTCT TTTCAAATAA AATTCTCAAT CTAAGTGGAA	300
AGCCCCCTCA GAGAATGCCT TATCCCCTA CTAAGCAATC CAGGCTTGT TAAAACGTCT	360
GATAAGGCCT GTAGTGCCCA TTGAGTATGA GTCTGCTGTT TACATTCTGC ACAGGCCAGG	420
AGGGGAACAG AAGGTGTGAG CCACAGGTGC TCCTGGGTCT GACCAGCAAG TCTAACCCAT	480
GAAGATCTCG AG	492

(2) INFORMATION FOR SEQ ID NO:923:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 650 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:

AAATAACCAC AAATATNAAG AAATTATAAT CAGGGCAACA GATTAAATG AAAAGGGGTA	60
TAGAAAGATA TATTTTAGAT AATATAAAT CCTGACAAGC TATGCCCTAG AATTGCAGCC	120
TCCAAACCTT GCCCANGATT TCCACCTTC CATAGCCTCA CTTCAAGTTC AAATGGAAAT	180

GAACAACAAA TAAAGTGAAC AGGTGGTTGA GCCAGCCNAA GCCTCCCAAG TTATGTTAGG	240
TGGACAGTAA GACCAGGTGG ACAGCATTG AGAAACTGGC TGGACACAGG GGAGCTGCTA	300
CTGGTAGTTA TATTTAATTT GGAGGAATTT CCAGCCCACT GATAAAGAGA GAAACCAAGG	360
AACCAAATGA CTTTTCTAGT AACATATAAT ATATGAGATG AAATATAATT CTGTTAGAGA	420
GGACATGGTG GTGAGATGGG AAAGAAAAGA GAAGAGAAAC AGGCAGACTT CGGGCACCAT	480
CTCCCTTTGT TTTCTACAAAT GCATTGGTTT CTTTCTGTG CGGAGCATTG TTAGGATTA	540
GCTACAGACC CCAATGTCCT CTGAGTAAAT ATATGTCAGC TCAGTCTCTG ACATGATATC	600
CATGCTTATT GGCCTCCTGG AGGGCTGGGT GGTTCCTCAGG GTCCTCTGAG	650

(2) INFORMATION FOR SEQ ID NO:924:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:

TGAGCTGCGC TAAACTCCAC CGTGACCTCA AACTCTTTGG ACTGTTTGAA AAAAAAAAAA	60
NTNGGAAGAA ANTCCATCCT CCAANANAAT CGGCTTAGGA GGAGATGGAA CTTNCCCCT	120
TTCTCTNGGT TTNGTCCGTC TGGTGGTCTC GAACCTGGGA TTGGGCGAAT GCGGATTGGA	180
TCATTACAT CGGAGCAATT TTTGATGAAT CTGCCAAAAA GGATGATGAG GTATTTGCA	240
CTGCGGTTGG TGACCTTAAC CAGAATGAGG AGATCTTACA GACTGAGAAA ATCACATTTT	300
CAGTGACGTT TGTGATGGC AACAAACCTT TCCAAGCAGT TCAAGAAGCC TGTGAACCTA	360
TGAATCAAGG CATCTTGCC CTGGTCAGCT CCATTGGCTG CAGTCAGCA GGATCCCTCC	420
AGTCTTTGGC AGACGCCATG CATATCCCC ACCTCTTCAT TCAGCGCTCA ACAGTGGA	480
CCCCAAGGAG TGGCTGTGGA CTCACCGGA GCAACAGGAA TCTCGAG	527

(2) INFORMATION FOR SEQ ID NO:925:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:

GATTCGGCCT TCATGGCCTA GAACTTTCTA CTTGGACAAC TAACACCCAC AGTCCTCCAG	60
ACAGAAAGAC AACAGGTACA AAGCCCTAAG GATTATAAAG GTATGCTGCT TACCATCATC	120
TTAGTGACCA AGGCAGCGAA GCTGTTTCTG TACCTTGGA CAGTCTTCCC TGACAAGCCA	180
GAGAACAGTG ATAAAGCCAC CAGCCTTGGG ATCAGGACTG AAAAGGCAAG AGTGATGGAG	240
ATTCTCTCTG CGCTAAGCCA AGAGAAGTT TCAGCACTTC AGACAGCTCC CACCGAAGTA	300
GCCGATCTCG AG	312

(2) INFORMATION FOR SEQ ID NO:926:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:

GAATTCGGCC	TTCATGGCCT	AAGATGTTTG	TCTTTATCCA	GTAAGGTGTT	TGTATGCTCC	60
TTAAGTGGCA	GCGGGGAGTG	AGCAGAGCAG	TGAAGATAAA	CATGAAAGCT	GGTGGTAACA	120
AATCCTGATA	CCTCCTCTAT	TCCAAAAGGA	AAGGCAGAAC	TCAGAGGCAC	CATCCTCCTG	180
TTGTGTTTGC	AAGCTGTTGA	CACAACCTGG	AAAGGTAAAA	AGTTTTCAAC	AGACTTGTCA	240
GAGTTTGTGT	TCAATGGAAA	CTGACAGAGC	CTACCGGCTG	AGGGGCTAAT	TTTAATAGAA	300
ATAACCTAGG	TGCGCGCTCG	AG				322

(2) INFORMATION FOR SEQ ID NO:927:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:

GAATTCGGCC	TTCATGGCCT	AGTGGAACCTA	GACTGCCAGC	TGTGAGCCTC	AGAGCTCCTG	60
GCTGCCTGTT	GCTGAGTCTA	TCAGCTGCTG	AGCCTTTCTC	ACCNNAAAAA	AAAAAAAAAA	120
AAAAAAAAAN	TGNGCTTAAT	AAAATAACCC	TGCACAGAAA	TTTTCTGAAA	TTAAGATAAC	180
ATTCAATGGA	AAACAGAATT	TAATCTACAG	AAATACACTT	CACAGATGTT	TTAGGAACAG	240
AACCTAGAGA	AAATGAAAGT	CAAAATTTAA	TAAAAGAATT	TGTCAGGAAC	TTCAAGGTAA	300
AGACTCCATG	TATTTTGTGG	CAACTATAAA	ACACTAAGAA	GGCTTTTAA	ATATTAAAAA	360
GCCATTAAAA	CATTCAAAT	TAAGATTCTT	CAATATACTT	CAGATTCTG	TACTGAGTTA	420
CCCTCTOGAG						430

(2) INFORMATION FOR SEQ ID NO:928:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:

GAATTCGGCC	TCATGGCCTA	CGTTAGTGTG	TGGATAGTAT	GTGTGTGTCC	GCACTCATGA	60
TAACCTGAAA	CCAGACATAG	GGTTCATTTT	TGAAAGGTTA	AACCACACTG	TTTCAGGAAC	120
TTGCTCCAAA	TACTACTTGG	TTATCCCTTC	CTTTACCAGT	TAGAACTAAA	GAGTGTGATG	180
TATGAACACA	CTGGGTGGG	ATTTTCTGTT	GAGGATATGC	AGGGCATTIT	GGCATGAGGC	240
AAATACAGAA	GCAAGATTTC	ATTCTACTTG	GTGATTGAA	TCATGACAGT	CCTCATTCCA	300
ATCTCTCTTT	AATTCTCTCT	GGCCCTGCCC	ACACTCTGTA	TTTGAAAATC	TTGTTTTTGC	360
TCTTTCGGGA	GCTTCACCCC	TCTACTTACA	TATTGTAAAG	TTGTATAAAT	CTATCATTGA	420
AAGGTCCTCT	CTGCCAGCAG	TGGTGCCACC	CTTTGGTTTG	CTGTGGTACT	TTGCTGTGTA	480
CTCCGTGGCA	TACTCGAG					498

(2) INFORMATION FOR SEQ ID NO:929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:

GAATTCGGCC	TTCATGGCCT	AGTTAAGGGC	ATTTACTCAT	GTTGAACCTA	GTTTATTTTA	60
CAGTATATTT	GTATGCATAG	AAGATGGAGG	TCCACCAAAG	TGTTAATTAT	GCTTAGTTGT	120
AGGTCAGGTA	TAGCTAACTT	TCCTTTTTTA	ATATATATAT	TTACATTTGT	GTTTCCTTTA	180
TAATTTATGG	CATAGATTGC	CACGATTTTC	TTAAGTATAC	TTTATAATC	AGAAAAATGA	240
TATTAAGGAC	TCATTTTAAG	TACACTAAAT	CAAATATTAG	AAGGCTTCTT	TATTTTAAGC	300
TAATGTGAG	GATTATTTGT	CATTTAAAC	TTTTGCTTCT	ACTTATTACC	CTGAAGTATC	360
TTTGGGTGC	TTATGTTTTT	CACAGACTGT	ATAAATTGAT	ATACTCTCCC	GCCCCATGGT	420
AATGTTGCTA	CACATAAGCT	CTAATAATTA	TCATTTTTAA	TGTTTAAAGA	TTAATTCAAC	480
TAAGTTTTAA	AAATAATCCA	TTGGTTACAT	ACATAAGAAA	GTACTGTATA	CAGATTCCCC	540
TGACTTATAA	TGGTTCGACT	CTCGAG				566

(2) INFORMATION FOR SEQ ID NO:930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:

GTGATATGAC	ACTGACAGAA	TTCAAGTTCA	TCTGGTACAT	GGAGTACTCA	CACCGAATGT	60
GGGGTCGCCT	TGTAGGCCTT	GTGAACATCC	TGCCTGCTGC	CTACTTTTGG	AGAAAGGGCT	120
GGCTCAGCCG	TGGCATGAAA	GGACGTGTTT	TGCCCCCTCG	TGGCCTCGTC	TGCTTCCAGG	180
GTCTGTTGGG	ATGGTATATG	GTGAAAAGTG	GACTAGAAGA	AAAATCAGAC	TCCCATGACA	240
TCCCTCGGGT	CAGTCAGTAC	CGCCTTGCTG	CCCACCTGGG	ATCAGCCCTG	GTTCTTTATT	300
GTGCCAGCTT	GTGGACCTCA	CTGTCACTGC	TACTCCCTCC	GCACAAGTTG	CCTGAAACCC	360
ACCAACTCCT	ACAGTTGAGA	CGATTGCTC	ATGGAACAGC	AGGTCTGGTG	TTCTTTACGG	420
CCCTCTCAGG	GGCTTTTGTG	GCAGGGCTAG	ATGCTGGGCT	TGTTTATAAC	TCCTTTCCCA	480
AAATGGGAGA	ATCCGGATCC	CTCGAG				506

(2) INFORMATION FOR SEQ ID NO:931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:

GGGAAATTAG	AAAGGGAGGG	CCTGAGTTGG	TTGCTATTCC	TGAAAGTTTC	TTTGAATGGA	60
ATACTGGATC	ATCGTTTTTG	AAGAGGTCTG	TTGTTACTTC	ATTATTACCT	CCTTTAGCAG	120
CACCTTGTT	TTCTCCAAC	CTCTGCCAAG	ATTAGTGTC	TGTGTCTACA	TTTGCCCTT	180
CTGTTTCTCA	TACTCCCAGA	TGGAAATATT	ATATTTCTTA	GGACTTTTCG	CTCTATTGGA	240
ATTAGTATTT	TCTACTCGAA	ACACCCTCGA	G			271

(2) INFORMATION FOR SEQ ID NO:932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:932:

GAATTCGGCC	TTCATGGCCT	ACATTTACTT	TTGTTACACA	GGGCACTACT	TTGATTCTA	60
TTAGTGCTGT	TTGTGATTGT	GTATGTCTTT	CACTTGAAAT	CCACCATGAA	GGTGAAAATT	120
TGTTTGAACC	GTGGCACTAT	ATGGCAGTGC	AGTGTAGTCA	GTTGTGTTTG	TAGTCCGGAT	180
TATCAGAGCT	TGAATTCTGG	TTCTGCTGCT	CACTAGCTTC	TTCTTGCACA	CTGTTTCAGT	240
GTACTCAGCC	TCACCTTTTA	TTTTATTCT	ACAGAGTCCC	ATTTGGTGTG	TAAGCTGGTC	300
TCGAG						305

(2) INFORMATION FOR SEQ ID NO:933:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:

GCGGTGGCAC	GATCTGGCT	CACTGCAACC	TCCACCTTCG	TTCAAGCGTC	CACCATGCCT	60
AGCTAATTTT	TTTGTATTTT	TGGTAGAGTC	AGGAGTTCGA	GACCAGCCTG	GGCAACATGG	120
CAAAACCCCA	TCTCTACTAA	AAATACAAAA	TGTACTCAGG	CGTGGTGGTG	CCGCGCTGTG	180
ATGCCAGCTA	CTCAAGAGGC	TGAGGTGGGG	ATCACCCTGAG	CCCAGTATGT	CGAGGCTGCG	240
GTGAGCCATG	ATTGCGCCAT	TGCACTCCAT	CCGGGTGAGA	CTGAGACCCC	GTCTCCAAAA	300
AAAAAAAAAA	AAAGAAAGTG	AAATAATTTG	TGGACAACAC	AGAATTACAA	ACTTTTATT	360
TTGTCTTTT	AAAGTTACCA	CAAATTGTCA	CCACCATTCT	CTGAAAGGAC	ATTAACACCT	420
GAATATATTT	AGTTTCATGA	AAATTTCACT	TTTAACACTC	GAG		463

(2) INFORMATION FOR SEQ ID NO:934:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 290 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934:

GAGCATCCTG	GGGAGCACCC	ATTTCTGGG	AACAAGCTGA	CCCTTTTGCG	TCCTTAAAAA	60
AAGTCGGCCA	AGATTCCATA	GTGCTGCTGA	TCTGCATTAC	AGTGTTCCTC	TCCTACCTAC	120
CGGAGGCAGG	CCAATATTCC	AGCTTTTTTT	TATACCTCAG	ACAGATAATG	AAATTTTCAC	180
CAGAAAGTGT	TGCAGCGTTT	ATAGCAGTCC	TTGGCATTCT	TTCCATTATT	GCACAGACCA	240
TAGTCTTGAG	TTTACTTATG	AGGTCAATTG	GAAATAAGAA	CACACTCGAG		290

(2) INFORMATION FOR SEQ ID NO:935:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:935:

GAATTCGGCC TTCATGGCCT AGTTTTGCCC GGCAGCCTCT CAGGTTGGAC TTCTCAGGAT	60
TTGCCATTTC TTTAATCCC TGAGACCACA CAGTTGATGT TTAGAGCCTG CCCTGCATGT	120
GATCGTTCCA GTGGAGGATA CAGCATGGGG TCTGGCCTCC AGCAGGGTCC TCCCCAGGCC	180
ACCCCTGGGT GCCGGGAGGG CAGCCCCTTG GCCTGAGGCC CACTATGACC TGCCCCCTGC	240
AGCTGCACCG TGATGGTGGC TTGCCTTTGT GGCTCCCTGG GCTCTGGTGG CCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:936:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 337 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:

GTTTAATGAA GAGTAGTCAG TCTTCTAGAT TGTCTTATA CCACCTCTCA ACCATTACTC	60
ACACTTCCAG CGCCAGGTC CAAGTCTGAG CCTGACCTCC CCTGGGGAC CTAGCCTGGA	120
GTCAGGACAA ATGGATCGGG CTGCAGAGGG TTAGAAGCGA GGGCACCAGC AGTTGTGGGT	180
GGGGAGCAAG GGAAGAGAGA AACTCTTCAG CGAATCCTTC TAGTACTAGT TGAGAGTTTG	240
ACTGTGAATT AATTTATGC CATAAAAGAC CAACCCAGTT CTGTTTGACT ATGTAGCATC	300
TTGAAAAGAA AAATTATAAT AAAGCCCCAA ACTCGAG	337

(2) INFORMATION FOR SEQ ID NO:937:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937:

GAATTCGGCC TTCATGGCCT ACATAGTTAT TCAGATTTAG GACCAGTAAG GATAGAAGTT	60
TCTCTTATTT ATGAAAAAAA ATGCTAATAA TTTTGGGGCA GTTTTTCN TTAATTATTT	120
TTTTCAATTT CAAGTTTAAT TTTATTTTAG CTGATCTGAT GTGGTTTCAA CTAACCCAAG	180
GTCTCACCAT GTTAAAANGC CGGCGGACTC TACGGCGTTT TGATAGATCCC CCCCCCCCAC	240
CCACTGTGAA GGGGTGCCAT ACTACCTTAA ATGCTAATGC TAGATATGCA ACCCTCGAG	299

(2) INFORMATION FOR SEQ ID NO:938:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:

CTCGAGTGGT GTGTCATTAT AGCGGACAAA GGTCACGATC ACAAAGGTGG TGGCGATGAT	60
TCCCAATATT GCAACAAACA CAGGCACCAC AGCCCAGGGA GAATGCCACT CCAATTGAT	120
GATGGGGATA AGCTGGCAGC CTGTGCGGTT CATGTTGGGT CTCTGATCCA GAGGGCAAAG	180
TTACAGGAC AGCTCATCCA CCTGGTAGTT GTAACCTTCA CAGCGTTCAC AGTGCCAGCA	240
GCAAGGGACC CCTTTCACCG TTTTCTTCCT CTCCCCTGGC TTACACGGCA GGCTGCAGAC	300
AGACGCCGGG TGAGTATGTT CTCTATGAGC CCACTGCATG TCTTCCACTT TTAGATGAAG	360
CTGATTGGTC CAGTGGCCGA TGACTTTGTA CTCTGTGCTT TTC	403

(2) INFORMATION FOR SEQ ID NO:939:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:939:

GAATTCGGCC TTCATGGCCT AATTCTTTTC TGTCCTTCAC ATGCATGTCA CAGTTCATCT	60
CACATTTCTG TGTAGAGGGC TCCATTTCTC TGCATATGGC ATTACCATTG TGCCTGATGT	120
ATTCCAATTC AGATAAACAT AAGCTCCTTT CTGCTGCTTT CCTGAGACC CCTGGTGTGG	180
ACTTCTCTAA TGTTCCTATA ATATCTATGC ATCTCTCTAT GATTATACCA TGTTATACTC	240
TGTGTGGCCT TAGGCTTTGT GAGGAGAGGT TCAGAGTAGG TTTTGCTCTA GAGTGTGGTC	300
CTTACTCCTA AGGTGACCCC TTCNGGTGT CTCTGCTGGT GTATGGCATT AATGTGATTG	360
CTTCACTCTC GAG	373

(2) INFORMATION FOR SEQ ID NO:940:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:

GCAAGCTCTA ACCTAAATCA CAGAGACATG CATGTTTCAT GCATTAACAC TGATTTGCT	60
CTGTGGCCCC CCAGAGGGGT GGGCTCATGT CCCCTGACTC CTCACATGAG TGCCTCAGCT	120
CTAAGNCCCG TGGAACGGGG GGTAGGGAAG GTTTGCGATC TGGAGCTCAG CAACTGGCTC	180
AGCAACGTTT TCTCCATTTC ATTAGCACTA AACAAGTTTC TTGCTCTCAG GAATTTGTCA	240
GAAAAAAGAA TAACATCACC TGAGACTCCA CATACCAGAT TATAAACTCT TTCTCGAG	298

(2) INFORMATION FOR SEQ ID NO:941:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:941:

GAATTCGGCC	TTCATGGCCT	AGGTTTCCGG	ACACTTGGGA	CACGCGTTTC	CATCCTGGCT	60
CACTGAAGCC	TCGATCTCCC	AGGCTTTCTT	TGACGGTGTT	CCCTCAAAGA	AAGAGGCCCA	120
AAGCCCTCCC	CCGCAAAAAA	AGCCAGAAAG	GAATGGAGGT	GCCTCCGCAG	AAATCCAGAG	180
CATCTGCAAG	ACATCCTCGA	ATTCTAGACC	TGCCTCGAG			219

(2) INFORMATION FOR SEQ ID NO:942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:

GAATTCGGCC	TTCATGGCCT	AAGCAAGATG	GGTCTGAGGA	TACCTGTGAG	AAGTAATTCA	60
ACACATCTTT	CACACATGGG	CCAATTGCT	GGTCTAAGTT	AAATNGGAGT	GACAAGGACA	120
GCTGCTTAAA	GAGTGAGTTC	TAAAGCCCCA	GGAATTAGGT	GATGTCTTGA	GCTGGGGTGA	180
AGCAAGNCAA	GTGGGATGGG	GAAGAGATGG	CTGGNTTCTG	CNGGAGTGAG	TTTAAGGGAG	240
GAAGGCAGGG	TTGCCCGGCA	GCCCCGATGT	TCCAGAAGAG	CCCACGAGAG	ATGTCTGTCC	300
CACAGGGCTT	ATAGCACNTN	GCANTCCNTC	AAAGGGCGGT	GTCTCATGTC	CCNTCTGTTA	360
GGCTCTGGGT	GGGCTTTTGT	GACAGCTTTG	ATAATGTTCT	GGAAGAGATG	CTGCTGGGCT	420
TCTGGGCTCC	CGCGACCCCT	TAGAGAAAAGT	GGTGCAGCTT	CTCATTGGCT	CTGTCTCTCT	480
CCGAACACGC	CCCTTTTGGG	GCCCTCTGGA	AAGGAAGACA	CTGAGCAACC	AAATAACATA	540
TTTTGACACT	AATTTCCTGA	GACCGTCTCG	AG			572

(2) INFORMATION FOR SEQ ID NO:943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:

GAATTCGGCC	AAAGAGGCCT	AAGGAAATGT	GTGTCTCTAA	AACAGATTTG	GATTTTATTT	60
ATTTGGGACA	TATAAAAGAG	GAAGGAAGAG	TTGATAAAGA	TTCTTATTTG	ACTCTTCAAA	120
GTCAGTGTTC	ACCAGAAATT	CAGAGAATCA	ACATACAAAT	TACAATGGTA	GTTTGTTTTT	180
TGGAAGGCCA	GTGAAATACA	GCTCCTTAAT	TTATAATGAA	ATTACTTTC	TAACAAATTA	240
AGTCTTTCTA	ATGAGACCAA	CATTGAGAAT	TCAGCCCTTA	CCTCGGGATG	GTCTGAGAAA	300
ACCAAAAGGC	CAACTGTTTT	ATTGCTTTAG	ATCAGTTAGG	TGATGATAAC	TATGAGCATT	360
TATAATAATA	TTTTAAATTG	GCCCTGAGAG	GCTTGAAGAC	ATAGAACTCG	AG	412

(2) INFORMATION FOR SEQ ID NO:944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:

GAATTCGGCC	AAAGAGGCCT	ACAAAAA	AAAAA	NNACTTGAAC	TGAGACCTGA	60
AANNGTAAAA	CTANNGNAAC	AAAACCTAGG	GAGAAAGCTT	CTTGACATTG	GCCTGGGCAA	120
AGATTTT	GGATATGGCC	CCATAATGAC	ATAGGACAGG	CAACAAAAA	AAAAATGGAT	180
AAATGGGATT	GCATCAAAC	AAAACCTCTGT	ATAGCAAAGA	AAACAATCAA	CAGAGTGAAG	240
AGACAACCTA	CAGAAATGTGA	GAAATATTT	GCAAACCACA	CATTTCATAG	GAAATTAATA	300
TTCAAAATAT	ATAAGGAACT	TATGTAACTC	AATAGCAAGA	AAACAAATAA	CCTGATTAAA	360
AAATGAGCAA	AGGTCAGTTG	AGAGAGGAAG	AGAAAAACAA	TATGAGTAAA	AGACTTTAAT	420
AGACCTTTCT	CAAAGAAGG	TATGTGCATG	GCTGATCTGT	GCATGAAAAG	GTAATTAACA	480
TCATTAATCA	TCAGAGAAAT	GCAAATTAAC	ATCATCTCGA	G		521

(2) INFORMATION FOR SEQ ID NO:945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:

GAATTCGGCC	AAAGAGGCCT	AGGTACACAA	AAGCAAACAG	AAAAACTCTT	AAGTTTTTCT	60
GCAATACTAA	AGAAAGTGAG	ATAAGACTTT	AAAGTTAAAG	ATCTATAGAC	ACTTTAGGCA	120
AAACAGGCTC	ATAAAGCAAT	TAAAAAATCA	ACAATTTAGT	AAAAACAGGC	TACATAGTAT	180
TTTGTTTTTA	CGTTTCATTT	GTCTATTGAT	CTTTAAATTA	AATTAGACAT	TTCTACTGTT	240
TTCTGTACT	CTTATACACA	CCTGTTTTCT	CCAATGTTCT	CCTTAGTAT	GGCTGGTAAT	300
TGTTTTGGTG	ATTGCCACCC	CCTCGAG				327

(2) INFORMATION FOR SEQ ID NO:946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:946:

GAATTCAGG	GCTAGGCGAG	TTATTGCAGT	CACGTCCTTA	AGTCAGCCGG	GTCCTCTTCT	60
TTTCCCTCAA	GGTGCTGTG	TTTTCTATTT	CCCGTCCAG	TCGGTGGCCC	CACCCAGCCC	120
CAGGGTGCTC	CCTTCCCCC	TTTCGGGTTT	CTGCCTGGAG	GGTGTGGTTT	TCTCTCCCAC	180
CTCGGTGCCT	GCCAGTAGAC	TGGAGTTCCC	CGCCACGCTG	TCGGTCCCAT	CTCATCACCT	240
TTCCGCTTTC	ACGCCGCTAG	CTAGTCTTGG	GACTGGCCCT	GTTATAGCCC	CAACTTATGC	300
GCTCTCTAAC	CTTTCCTGGC	TTACCCGGAG	TCACAGTTCA	GTTCTACTTC	TTTCAATTC	360
TGTAGGGCAT	TGGTCTCAAT	TGGGACTCAG	TTTTCTCCA	CACCCGCCGT	TCCTGTAGTC	420
TGGTTATATC	ACAGTTCATT	ATTTAATGTA	GGTTTTTGAG	CGCTTTGTAA	ACGGCAAAGC	480
TCTCTCTGTT	AATAATACAT	ACTCAAATG	TTATCTTTTC	ATTGGTGCAT	TACAACTCAG	540
TTGTTTGCTT	CTGAATCACT	TTCCCGACTC	GAG			573

(2) INFORMATION FOR SEQ ID NO:947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:

GTTGAAGTCA TTTATTATTT TATAAATTGA GAACAACCAC ACCACCAAAT GTCACACCTT	60
CTTATAAAGT GTGAACAAGG AAGGTCATGT TTTTGTGGGT ATTTTGTGAG ACTTAGAGGT	120
TTCAATTTCAG GGCATAGTCA AAGGCATCAT CCTCCCAACT ACCCACTTGA TTATGTATTT	180
CAGATCCCTC CGTGGGGGCC TTCTTCTGAC AGAGAATTCT TTGAGGTACG CAGTAGTGCT	240
TTTGTACAGCA CAGACTGCTA ATCTACATCT TGCTGCGTTC TGTTTGCTGA GGTGGGGCTT	300
ATTCATTTAA CACGTACCAA CCATTATCAC TCGAG	335

(2) INFORMATION FOR SEQ ID NO:948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:

GAATTCGGCC AAAGAGGCCT ACGGCCAAAG AGGCCTAGTC GGAGGAGGAA ACATATGTAG	60
GGAACAGCCT GGGTCTGTG AATCCGTTTC CCAGCTATGA TGCCTATTTT CTCAGCAGAA	120
TGAGTGTAGC ATGTCTCCCA GGTCTGTTTT TTATTTGTTT GAGAGGTGAT TTCAAGCAGA	180
ATCTCACAGC TTA CTGTTGG AAATGCTATC AGTTGTAAAG ATAGGGAAAA TCTCTCTTCC	240
ACTACGGTGG TAGGAAATGA ATACATATCA TTTCCAGCT TCCAGGATGT CCTGTCATCT	300
TAACTGTGCG TCCCAAGGA CCTACAGATC ACAGGGCAAC AGGGGCTGTG AAAGAGTAGC	360
CCGGGGCTCG AG	372

(2) INFORMATION FOR SEQ ID NO:949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:

CTAGCATTAC GAATCTCTTA GGATTTTAA GATTGTATTT GATAATACTT ATATTTTACA	60
GGGCACACTT TTGGCACACC TCAGAGCACA CTGCTGCTAT TTTGGGTCAT ATCACTGTAA	120
AATACATAAT AAGTACTACT TAACTGTGAC ATGAAGAATT GGAATCCCAG AGGGCAACAT	180
TTGATTGAC TAAGATCAGG CATAAGATAG AATTTTGTG ATTTTTCCTT GCAGTTTAT	240
TGACTTAGTT TATGAGCTTG GATAAAATAA TTTTGTGATG AATCATGTCA ATAAAAGGAA	300
AAATAATGTA ACTACCTCAT AAGTCTGATA AAAGGAAGTT GCTAGTGTTT TATAGAATTT	360
CTGAAGGTGG TTAAATCAAG TATGATTTCA AAATATCAAC TAGTTCCACT TTTGTGATTG	420
CAGGATGCTT CTTATACTAA AGTTCTGAG	450

(2) INFORMATION FOR SEQ ID NO:950:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:

GAATTCGGCC	AAAGAGGCCT	ACGTAGGCAA	AGGTTGACCC	AATCAAAGAT	AAAAGAAAAT	60
CGACAGCAAA	TCGTTCTGTC	TCGAAAATAT	TATGATGATT	ATAGAGTTCA	GTGTGTGTGCA	120
AAAATGATGA	GAATGAGGAC	CCGGGAAGAA	ATGATATTTA	AGAACTGTT	TGAAGAAGGT	180
TTAAACATT	AAAAGCAAAG	ATTACGAGAC	CTAAGAACT	ATGCCAAGA	AAAGCGAGAT	240
GAACAAAGGA	GACGCCACCA	GGATGAACTG	GACTCCATGG	AGAACTACTA	TAAGGACCAG	300
TTTTCATTGC	TGGCAGAAGC	CATATCACAG	GAACAACTCG	AG		342

(2) INFORMATION FOR SEQ ID NO:951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:

GAATTCGGCC	AAAGAGGCCT	ACCCTGTTTT	AATCACATGA	CTACCTGTCC	CAGTACACGA	60
AAGGGCGCTG	GTTGGCATT	TTCTTAATGT	ATTTAGTAAA	GATTATAAGA	CATCCTTTAA	120
GAGTTTAAAT	GTCTCTGAAA	CAGGCATACA	GGCTCTAGTC	AAGAAATGAAT	TAGAGTGAAG	180
GAAAGCTGTG	TGACACCTGG	CATTCTCTCT	TGTTTCATGGA	GCTTCTTTGA	GGCTTGAAGT	240
TTGATTTTAC	TATCTAGACC	TCTCTGGCTA	ATACCTATT	TTCAACCACC	TCGGTTACTC	300
TGACATAGGA	ATTTACTTCT	TTTCCTTGAG	TGGAAAACAC	TTTAGAAAAT	AATAACAAAC	360
ATTATTATAA	ACTAATATAT	GTGAGAGTAC	TTAGTTGAAA	CAAAAAGGAA	TTTTAGTAGA	420
CAGTATTATA	TTATCTTTGA	AAATCAAGGA	GAAGTTTATG	CAACTGAAAA	TGTTTACACA	480
CTGTGCTACT	CGAG					494

(2) INFORMATION FOR SEQ ID NO:952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:

CAAAGAGGCC	TAGGGAGTGT	CGCTCTGTCA	CCCAGGCCGA	GATTGCACCC	CTGCACTCCA	60
GGCTGGGCAA	CAGTACGAGA	CTCTGTCCAA	AAAAAATAAA	AAAGAACAGC	CTTTTATAGGC	120
CACAGTGACC	TGCGCAATGT	TTATATGCTT	NGACCTACTA	ACTTTCTCCT	AACTAAATAT	180
TTGATTTTAG	GAGAGTGT	TTAAATAATTA	CAGTATGTCT	ATATGATGAA	ATGTTATTTT	240
GCCATTAAAA	TTTTGTTTAC	AAAGATAATT	TTTATTGACA	TAAAAATNAC	TTTAATGTAA	300
TTTATGTTGA	AAAAGCTGAA	TACAAGTCTT	TATATAGAGT	AATATTTGAG	CTGTGTTCAA	360
AAATACATAG	GAAAAGACTG	ATAAAATGAA	ATATGGCNAA	ATGTTAATAG	TTTTCCCTGG	420
AATAGGATAA	TAGGCAATTT	TAAAACAGAC	TCCTTTAAAA	AAACAAACAA	ACNAAAAAAA	480
CATAGACTTC	TTTATATCTT	TTGAGCTCCC	CCCCNACTCG	AG		522

(2) INFORMATION FOR SEQ ID NO:953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:

GAATTCGGCC	AAAGAGGCCT	AGTGTGTTAT	ACAGTTGTTG	CCACTGCTGT	TTTCCAAATG	60
TCCGATGTGT	GCTATGACTG	ACAACTACTT	TTCTCTGGGT	CTGATCAATT	TTGCAGTAGA	120
CCATTTTAGT	TCTTACGGCG	TCAATAACAA	ATGCTTCAAC	ATCATCAGCT	CCAATCTGAA	180
GTTCTTGCTG	CATTGTGTCA	AAAGAAATTT	CCTTATTTTC	TACTGCCATT	CCCATAAAAG	240
TAAGTAGTCT	CATTTTGGCC	ATATTCTGTT	CATGTAAACAG	GCCAAGTGAA	TCAATGAAGT	300
CTTTATTATT	CTGATAAAAC	TTGACATATG	ATGCCAATTT	AGCACTCACA	AAAATGGTTA	360
AAAGATCATG	AATAAGCTCG	CCTTCCAAAA	ACTTGACTGG	TTTTAAAGTA	AGAAGGTGGT	420
CAAAAAGAAA	TGCATTTGGA	TCTTCAATG	CTCGTACAAT	ACACCTGTGG	GCATCAACTC	480
GAG						483

(2) INFORMATION FOR SEQ ID NO:954:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:

GAATTCGGCC	TTCATGGCCT	AGGTGCCCTC	TGTGAAGCCA	GTGTTCTCTG	CTCCCCGGGT	60
CAGAGGTCAC	AGGTCAAGTT	CAGTCAGTCC	GAAGAATCAT	GGGCGGGTGC	TCGCTGTCCT	120
CATCCAGGCG	CAGGGCGCTG	GCCTCGTCCT	CCAGGCAGGC	GCCACCCACA	GCACCCAGGT	180
CGTCTGTGTA	GGCTGCAAAG	AGACGACGAA	GTCACCCTTC	AAAGGCTGGG	GACACACCAC	240
AGACCCCATG	ACACACACTG	AGGACTGTGT	TTTGGAACA	CTGGTGTATA	TTTATAAAT	300
GAAGCCTGTA	CTAAGACGTT	CTGAATTCTG	ATTGCTTTCT	AATGAACTCT	TTGCAGCCTT	360
AGGCAGCTCG	AG					372

(2) INFORMATION FOR SEQ ID NO:955:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 436 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:

GAATTCGGCC	TTCATGGCCT	ACTATTACCA	TTATATATCA	CCCATCTGCA	ACAAGGTACT	60
GTACAGACAA	GTAAGAAGTA	TGTTATCTAG	TTCCCTTTCC	CCCAGAAGGT	TGAGGCTCAG	120
GTATAGGGGT	AATTCTCCTG	TGCAGTCTTT	ATTTATGCTG	ACTCAGTGAC	TTCAACAGGC	180
TTAATCATGT	GGTCAGGTTT	GTGCCCAGCT	GCATAATGCT	CCCACATCTG	TAGATAGAGC	240
CGCTCTAGTT	CCATTGTGTA	TTGTTTGGTG	TTGAACAGAG	GGCTAGATAT	TCTTTGCTTC	300
CAGACTTTGC	CACGAACCTT	CTTCAGGTAT	TCTAGATCAG	TTCCCAGCTT	CACAGCTATG	360
TCTTCATATT	CTTGTCTGTT	TTAGCAATA	AGCTCAAGAC	AACCTAAGCA	AGTGAGCTGG	420
GATGCTGCAA	CTCGAG					436

(2) INFORMATION FOR SEQ ID NO:956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:

```

GAATTCGGCC TTCATGGCCT AAGGAGATGG GAGAATGTCC GGGGAGGGGC TGGCAGGAGG      60
GGCCAGCCAA ACTGCACGGA CTTTGCTGGT TAGTGAAGGA TTTTAAGTCC TCTAGTGGAA      120
TTAAGTGATT AGATTTTTCG CTTACAAAGG AAACCTCTCT ATGGAGAACA AACTACCATA      180
TGAAGCTAGC GGCCTAAACC AGGAGAATGT GGGGAAAGAA GAGAGGTGAG GATAACTGGA      240
GGGTATTAT  GTAACAACAG AAAGCATCAC AGTTCAATGA ACAGGGCAAG GTGGGCAAAT      300
GAAGAGGGCA GAGGAGGACT GGGCCCTCGA G                                     331

```

(2) INFORMATION FOR SEQ ID NO:957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:

```

GAATTCGGCC TTCATGGCCT AAGACTGTGA GTTCTGGGGC CAAGAAAAGT TTTGAATTGC      60
TCTCAGAGAG CGATGGGGCC TTGATGGAGC ACCCAGAAGT ATCTCAAGTG AGGAGGAAAA      120
CTGTGGAGTT TAACCTGACG GATATGCCAG AGATCCCCGA AAATCACCTC AAAGAACCTT      180
TGGAACAATC ACCAACCAAC ATACACACTA CACTCAAAGA TCACATGGAT CCTTATTGGG      240
CCTTGAAAAA CAGGTCTGTC CTCCACCTGA ACCAGGGGCA CTGCATTGCC CTGTGCCCCA      300
CCCCAGCTTC CCTTGCTCTG AGCCTACCCT TCCTCCACAA TTTCTAGGG TTCCATCACT      360
GCCAGAGCAC ACTGGACCTA CGCCAGCAC TGGCTTGGGG TATATACTTG GCCACCTTCT      420
CGAG                                     424

```

(2) INFORMATION FOR SEQ ID NO:958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:958:

```

GAATTCGGCC TTCATGGCCT AGATATGGCC AGGATGCTAT AGCATTGTCA GTGAGGAGAC      60
ATCAGAGCTT TCCCAGATCG GGAGGAAAAA TATGGAATGT GTTTTACCGC TGAAGTGAACA      120
CAACCAAAATG AACTGTCTTG ACAGTAGTTT GCAAACCAGC AGCTAGCAGT TTGTCCAGCC      180
TCTAACATTG TCCAGCACTT TCCAGAGCAA ACTCACTGTT TACAAGAACT CTTGGCCTTA      240
CGAAGTTTAT AACCTCAAGC TTTGTTTATT TAAATATTC CTGCAAAAAG AAAGTACCCG      300
GCCCATGACC ATTCGTGACA GGCCCTTTGA ACGGACGATT ACCATGCATA AGGATAGCAC      360
TGGACATGTT GGTTTTATCT TAAAAATGG AAAAAATAACA TCCATAGTGA AAGATAGCTC      420

```

TGCAGCCAGA AATGGTCTTC TCACGGAACA TAACATCTGT GAAATCAATG GACAGAATGT	480
CATTGGATTG AAGGACTCTC AAATTGCAGA CATACTGTCA ACATCTGGGA CTGTAGTTAC	540
TATTACAATC ATGCCTGCTT TTATCTTTGA ACATATTATT AAGCGGTGGC ACTCGAG	597

(2) INFORMATION FOR SEQ ID NO:959:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:

GAATTCGGCC TTCATGGCCT AGTGTCTTCT TGTCAACTTC ATTCTCTTCT CTTGTTTCT	60
ACGTCTGAGA TCTTTCTGAA CACATTTTGT TAGAGGCTGC TGTCTCCTGC TGTCTGGAGA	120
ATGATCTTTA GAGGGAACGG AAGCTTTCTT CCTGTGCGTG TGTGTCTTCC TGTGTCTAG	180
CACTTGGGGG TGGAGAGTCT CGGGGCGGGG ACACCACTGT CATCAGCGCC TCTGTGTCTG	240
TGCTTCTCTT TTGCATGTTT GGAAAGCCTC AAGCGGGAGG CGGACTCGAG	290

(2) INFORMATION FOR SEQ ID NO:960:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:

GAATTCGGCC TTCATGGCCT AGTGAGTGAG TAAGACAGGT TGCTCTTTGG AAAACAAGGA	60
AAATCCCTTT ATTAGAACAA GGCATGAAAT TCTGCCACTA GGTGGCGATG CCCTATAACT	120
TTACAACTTA GTGTACATCA CACGAGCACT ATGGAAGATT TCTCCATTCT GCGCCCCACC	180
AACTCCCTCC CCTCCTTCAT TTTTCAGGAT GACAACACCT TAGAGGTTTA TGGCCATCAG	240
GAGAATTAC TACTAAGCTA TATACTGATG TAATGAAATC TAATATATGT TGTGCTCGAG	300

(2) INFORMATION FOR SEQ ID NO:961:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 503 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:

GAATTCGGCC TTCATGGCCT ATTTTCCCTT CAGGATTGTG TGTGGGGTG GGGGCATACT	60
GGGGATGACA GAGGGAGAAA GAAAGATTTT TATTTTCCTT TCTAATAAAT GTTCATTGAG	120
AAAGTTATAG AATATGGAGA AAATGAAATT TATACTCTC CTGCGCAGAA ATACTGTTAG	180
CTGTGAGTTT CTTTCTATA TATGCTTATA TAGTTGAGAT TATGCATGTA TACAGTTCTG	240
CATCTTAGCT TTAATAATAA TGTACATCT TGATAATTTT CCAGTCATTA AAATTATTTG	300
AAGATATCAT TGATGTATCA CCTTATTTTA TATTCTATTT GAATAATACA TCCAAGGTCA	360
CCAAAAGATG ACAGTGAAAT GTATTGTTTG TAATCTACAT TAGCATCAGT AAATATGGAC	420

CATTTAAATT GTGTTAAGTC AACCTCTCTG ATCTTATTTT ATTAAAGTTT AGGATAGGCA 480
CTACATTTGA TGGGACTCTC GAG 503

(2) INFORMATION FOR SEQ ID NO:962:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:

GAATTCGGCC TTCATGGCCT AAGCAGCTGC TGCCTGCCAG AGAGGCGCCT TCAGAGACCC 60
 AGCGCTTACA CAATACCCAC CATGTCCCAG GCTGGTGCTC AGGAAGCCCC TATCAAGAAG 120
 AAGCGCCCCC CTGTGAAGGA GGAGGACCTG AAGGGGGCCC CAGGAAACCT GACCAAGAAC 180
 CAGGAAATCA AGTCCAAGAC CTACCAGGTC ATGCGAGAGT GTGAGCAAGC TGGCTCGGCC 240
 GCCCCGTCGG TGTTCAAGCG CACCCGCACA GGTACCGAGA CTGTCTTTGA GAAGCCCAAA 300
 GCCGGACCCA CCAAGAGTGT CTTCGGCTGA GAAGTGTGCG CCACTCCCCT TGCTGCCCGA 360
 ATGCTCGGAA ACAGGAGCCT TACCCAGGCT CGAG 394

(2) INFORMATION FOR SEQ ID NO:963:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 497 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:

GAATTCGGCC TTCATGGCCT ACCCTTCATG GCCTAGGAAA CTCACAAAAT GAAATATCCT 60
 TCTCAACGTC ACTAGAGAGT GGCAGAGTTT AGAGACAAAG CCATCTGATT TTGGAGCCTG 120
 TGCTCAGCTT TTAGCAGACA CACTGATTTT CAAGAATTGC TAGGATGTTT CTCAGTGCAG 180
 TTGACCACAG GACTCTCTGG AAAGCCTTCA GGAAGTAACT TCCTCCAGAC AGTTTGGGAA 240
 AACTGTCATG TGTCTATTAT GAAGCCATCA GCTGAGCTCA TCCCCCGTGC ACTCCACAAC 300
 GCTGAGGCTC TGCACATGGC TCACCACTGC CAGGTGCTGC CAGTCAGCAG TGCCGCTGCTG 360
 TTTCCACAGC AGCCTGCATA CGTCTATATT GCCCAGCCTG TTTCACCTGG CGGGGTCACA 420
 CAAACCAACC CCTGGTATTG TTAGCAGGTC CACATAATGG CATCTCCACA GCTGTGTCAT 480
 CCAAAGAAA CCTCGAG 497

(2) INFORMATION FOR SEQ ID NO:964:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:

GAATTCGGCC TACATCTTTT GATGACTCTG ATACCTTCAT TCATTTTCA AAGGAATTTA 60
 CTGATCATGA GGTGGAAAA TCTGTATTTT TCTTGCTTAT TATGTATTAA TAATCATAAA 120

TGTCTAGATT CACCAGAAGT CACCAGAAGG TCTGTCTCAG TGAAGAAAAC TTATAAAGCC	180
ACTTTGTTGC ATTTTGTGTT TCAGTGTTAC AGTTTGAGAT CTGTATATTT GTACACAGCT	240
ATGTGTTTTT CATTGAAATA ATGTACAAAG ACTGATCTTG ATGCTGTGTA TTTTATGAG	300
TTGTCTTAGG CATTCTGAG CTCAGCTTCA GTTGGATGGT GGGTCAGCAC CCTGCGTTTC	360
TGAACATACT AGACTTCAGT TAAAACTGC TCGAG	395

(2) INFORMATION FOR SEQ ID NO:965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:

GAATTCGGCC TTCATGGCCT ATAGTAAATG CCCACTAGGC ACCCTGGAGT CATTGTGTA	60
GAGTGGCATC TCTATACAAC TGTTGACTA ACTGTGCGAG ACACCCTAAT CACCCAGCC	120
ACAAACAAAT AGAACATTGT ATGTGTGCTG AATCCACAA AGGCCAGACA TGATGCCATG	180
AGACCAAGAA GGAAAAGAAA TAATGTGGAA AGGGTTTGGG GTGGAAAGGT GGGGAACCTG	240
GAGGCGGGCC ACATGGGGCC CCAGAAGCCA TGTGAGGGT TTTGTCTTCA CCAAAGGATC	300
AGTGGGAGAT TAGTGTAGAA CATTAAACAG AGGTGGGGTA TGTGTATAT TTCCATTAAA	360
AAATTCATCC TGGCCACAGT GTAAAGAATA GATTAGGGAG GAAGCCAATC AGGAAGCAAT	420
TGGAGTAGGC AATGCAAAAG GCAAAGTGAA CTGGACTAG TGGTCTCGA G	471

(2) INFORMATION FOR SEQ ID NO:966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:

GAATTCGGCC TTCATGGCCT AAGCCAGCTC AGNTGCNTCA GAGATTTTGT GTGTCCTTGC	60
ATACACAAC TAATTTCTCT AGGATTCAGT CTCCTCGTNT TATTTTAAAT ATNATTTTAT	120
TTGTAAATAC CTCATCGTGG ACTCCAAAAG CATGTCCTCT CGTTTTAAAA ACTGGCATAA	180
TACCTACCAC AAAGGTGGAT GTGAGAAATTA AATAGAGCTT TATACAGAAT TCCCTCAGGC	240
ATTTTAAAGT TTATGTAATA GGGATGTATC TTACAGTTGA TGGGTACATT TAGTGTAGTC	300
CCCCTACCTC CCAAGCTAAT AATGGTGCCT CGTACAATTG ATGGTACCAA ATTGAGGTGA	360
TAATAACATA GAAAGAGTTT AATGCAACGT GAAGTACAAA ATGCATTCAA TAAGTAGCTG	420
CTATCATTTT TTTAAAAATT AAATATGGCT GCTTGTTAAG GCCATATCCC AGGAGGAAAG	480
TGTGGTCTCT GCTGGGAGGT TGGTCTACAT ACAGGAAGCC AGATGTGTGA GATGGCTCTA	540
GATAGGCAGA AGGGGAGAGC TCGTGCCCTC TAGGAACCTA TTAATAGATA TCAAGGGAGG	600
GATAGCTCGA G	611

(2) INFORMATION FOR SEQ ID NO:967:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:967:

GAATTCGGCC TTCATGGCCT AATTTAAGTT TTTCTAGCAG ATCGCTCAGG TTGCTCTTAA	60
CTGGAATGTA GTGTTTCCAG GGCTGCAGCT CATTGTAAAA ATGTTTCATAG TAGATGGAAT	120
CCTGCTTCAG CACAACACTG TCACCAACTA GCAAATATGG CAGGCGATAA GCTGCTACAG	180
TGCCATCGAT ATTTATTTGA TACTTATGCT TGAAGAAATC AAAAAATGAA ATATGTTTCA	240
CAATGGGACC ATACAGGTTT TCATCGTGTT TAAAGAAGAA AAAGTTGGTG AAAGCAGCGT	300
CTATGAGTTC TGGGTGTTTT CTACTGAGTT TAACCAGCTC GAG	343

(2) INFORMATION FOR SEQ ID NO:968:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:

GAATTCGGCC TTCATCGCCT AGCCAGGANC TTTCTCGGAC GCCTTGCCCA GCGGGCCGCC	60
CGACCCCTCG CACCATGGAC CCCGCTCGCC CCCTGGGGCT GTCGATTCTG CTGCTTTCCT	120
GACGGAGGCT GCACTGGGCG ATGCTGCTCA GGAGCCAACA GGAAATAACG CGGAGATCTG	180
TCTCCTGCCC CTAGACTACG GACCTGCCC GGCCTACTT CTCGTTACT ACTACGACAG	240
GTACACGCAG AGCTGCCGCC AGTTCCTGTA CGGGGGCTGC GAGGGCAACG CCAACAATT	300
CTACACCTGG GAGGCTTGCG ACGATGCTTG CTGGAGGATA GAAAAAGTTC CCAAAGTTTG	360
CCGGCTGCAA GTGAGTGTGG ACGACCACTG TGAGGGGTCC ACAGAAAAGT ATTTCTTTAA	420
TCTAAGTTCC ATGACATGTG AAAAATTCTT TTCGGTGGG TGTCACCGGA ACCGGATTGA	480
GAACAGGTTT CCAGATGAAG CTACTTGAT GGGCTTCTGC GCACCAAGA AAATTCATC	540
ATTTTGCTAC AGTCCAAAAG ATGAGGGACT GTGCTCTGCC AATCCGACTC GAG	593

(2) INFORMATION FOR SEQ ID NO:969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:

GAATTCGGCC TTCAAGGCCT AGTTGTTTG TTTTCGTTTG GTTAAAGCTT ATTGCCATGC	60
TGGTGCGGCT ATGGAGACTG TCTGGAAGGC TTGGAATGGT TTATTGCTTA TGGTAAAATT	120
TGCGTGATTT CTTACAGGCA GCGTTTGAA ACCTTTTATT ATATAGTTGT TTACATACTT	180
ATAAGTCTAT CATTTAAAGA CATGTACTGA AACAAATGTA TTGTTTCAT AAGCATCTTC	240
CTGTAATCTA TTATAAAATT GAAATTAAT ATAGAGAATG TTTTAACAAT TTTTAACTC	300
AAAATTGTG AATCATTTT AATAGTTCTT TTTTATAAA AAGAAAAAGG AATTAAAGGA	360
CAGGCAGTAG TCTCTTTTAA AATTATTCA CAAAACCCAT TAACTCGAG	409

(2) INFORMATION FOR SEQ ID NO:970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:

GAATTCGGCC	TTCATGGCCT	AAGATTATAT	AAGATTATGC	CAATAAAACT	CATGCCTGAG	60
GAAGTGGTTG	CTCCCTTTCT	ATGGGTCACT	ATTGGTGCAA	GAAGTGGAAA	CCAGCCCTTG	120
GAGAATAGTT	ATACATTGGC	CATGATTTTC	CACAGCCCTG	GAAATGCACA	ATTCTATCCT	180
CCTACCAGGA	TGATTGTAA	GTITTAGCTA	ACATTTGATT	ATAAAAGGCC	GTAAGTATGA	240
GTATCTCTGA	GATAATTTGT	GTATTGGAAA	GAGGTGTGTA	ATAGCACTTT	TTTAAAAAAA	300
CCTAGGTGTG	AAGGAATTAC	AAGTCCAGAA	GGCTCAAAAT	CTATAGTGGA	AGGAATCATA	360
GAGGAAGCTC	GAG					373

(2) INFORMATION FOR SEQ ID NO:971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:971:

TGCGAACTCC	TGACCTCAGG	TGATCGCCCC	ACCTTGGCCT	CCCAAAGTGC	TGGGATTACA	60
GGCGTGAGCC	ACCACGCCCG	GCCTATCTCT	TGTTTTTAAA	TCAGTCTAGG	GTGCCAAAGC	120
ATCAGGGTTC	CGGCCTGCA	AGAAAGGGAG	ATTCTGTTC	ATGTTAAAGT	GTCATATTTA	180
TGAAACTGCC	CTTTTGGAA	TCTTTGAGGT	TGTCTGTACT	ATAGGACTGG	GGAAATGCAA	240
GTGAGTCTAA	GAAGAAACCC	AGATGTGTCC	TACCCTGGCT	GGCAGTAGTG	AGAAGGGAGG	300
AAGTTCCTCC	TTGGACACTA	GTAATATTGG	AAAGTTCCTT	ATGTCTGGTT	CACTGATGAA	360
GCTTGAGGAT	AGAATTGGTG	AGGAGGGAGG	GGAGAACAGG	TCACAGCTGG	AGGGGAGCCT	420
GGGCCCTATA	GGGTGTGAGG	CAGAGCAGAG	TGGCAGATAG	GACATGTGGA	CGGTGGGGAA	480
AATATTCCTC	ATGGGACAGA	AGATACCTGG	CACATGTACC	CACAACCTGT	ACACAGATGA	540
TCTGTACTGG	ACACACGTGG	AGATATGGCC	ATGCCACGCA	TGTGCAAACA	GAGGTGTACA	600
CACAGGAGTG	CAGTGATACA	GGACACAGAT	AAACAGAATG	TACACAGCTT	CTCGAG	656

(2) INFORMATION FOR SEQ ID NO:972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:

GCAGGAATAG	AGTTGGAGCG	GTGCCAGCAG	CAGGCGAACG	AGGTGACGGA	AATTATGCGT	60
AACAACTTCG	GCAAGGTCCT	GGAGCGTGGT	GTGAAGCTGG	CCGAACTGCA	GCAGCGTTCA	120
GACCAACTCC	TGGATATGAG	CTCAACCTTC	AACAAGACTA	CACAGAACCT	GGCCCAGAAG	180
AAGTGCTGGG	AGAACATCCG	TTACCGGATC	TGCGTGGGGC	TGGTGGTGGT	TGGTGTCTCG	240
CTCATCATCC	TGATTGTGCT	GCTGGTCGTC	TTTCTCCCTC	AGAGCAGTGA	CAGCAGTAGT	300
GCCCCACGGG	TCCTCGAG					318

(2) INFORMATION FOR SEQ ID NO:973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:

GGAAAAATAC AAAAATTAGC CGGGTGTGGC GACGTGCGCC TG TAGTCCCG GCTATTCAGG	60
AGACTGAGGC AGGAGAATCG TTGAAACCTG GGAGGTGGTG GTTGCCAGTGA GCCAAGATTG	120
CGCCATTGCA CTCAGCCTG GGCAACAGGG TGAGANTCTG TCTCCAAAAA AAAAAAAAAA	180
AAAAGCTGGA TTACAGGCGT GAACCACCGC ACCCAGCCAA TTCATAGGTG TTTTAAGTGT	240
GACACTTGA TGGTTTAAGT CTGATAGAAC TTTTACATTT ATTATACATT TAAATATATA	300
CCAGGGGCTC GAG	313

(2) INFORMATION FOR SEQ ID NO:974:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:

GAATTCGGCC TTCATGGCCT ATTCTTCGCA GATTATGAAG ACTACATTAA ATGCCAGGAG	60
AAAGTCAGCG CCTTGTAACA GAACCCAAGA GAGTGGACGC GGATGGTGAT CCGGAACATA	120
GCCACCTCTG GCAAGTTCTC CAGTGACCGC ACCATTGCCG AGTATGCCCG GGAGATNTGG	180
GGTGTGGAGC CTTCCCGCCA GCGCCTGCCA GCCCCGATG AGGCCATCTG AGCCTCCAGA	240
CCAGACCCCA AACCAGCCCT TGAGTCTGTC AACTCTCTT GGGCCAGCCC CAGCACCTCA	300
TGCAGAGGGT GGGGTACTGG AGTTAGATCT CTAAGCCCCT CCTGGAACCC TCATTTTCCC	360
CACGTGCTCG AG	372

(2) INFORMATION FOR SEQ ID NO:975:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:

GAATTCGGCC TTCATGGCCT AAAGGATTTG ATTCAGAGTG ACATAGCTGC TCTCCATCAC	60
TTTTACTCCA AGCATCTCGA ATTCCCTGAC AATGATAGCC TCGTAGTACT CTTTGCACAG	120
GTAACTGTA ATGGCTTCAC AATTGAAGAT GAAGAATTT CTCATTTGGG ATCAGCGATA	180
TTTCCTGATG TTGCATTGAT GAATCATAGC TGTGCCCCA ATGTCATTGT GACCTACAAA	240
GGGACCCTGG CAGAAGTCAG AGCTGTACAG GAAATCAAGC CGGGAGAGGA GGTTTTACC	300
AGCTATATTG ATCTCCTGTA CCCAACGGAA GATAGAAATG ACCGGTTAAG AGATTCTTAT	360
TTCTTTACCT GTGAGTGCCA GGAGTGATACC ACCAAGGACA AGGATAAGGC CAAGGTGGAA	420
ATCCGGAAGC TCAGCGATCC CCGCTCGAG	449

(2) INFORMATION FOR SEQ ID NO:976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:

```
GAATTCGGCC TTCATGGCCT ATAGTGCTT CCTNGGCGCT GCGACAGCCA ATGTAATGGC   60
CTTCTGTTT CTCATAAGCA GTTTGTACA GATAATCACT GGCAATATCC CTGGAAGCCT   120
TGGCATGCTG GATCCCAATG GCATCAAACG CGAG                               154
```

(2) INFORMATION FOR SEQ ID NO:977:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:

```
GAATTCGGCC TTCATGGCCT AGAAGAAATC TCTCTTCCAT TCCTGAAAAC AATTTTAGTC   60
CATTCTCTT CATTAACTA AGTATAAAC TACTAATATC TTTCAAGTGC CAGAAGTTCC   120
TCAAGAAGCC GCAGAAAAG AAATTCCCGT GGCTCCACCC AAAAAACCAG AAGCTCCGAT   180
TGTCCAGGT ACACCTTAGC CTGACTTCA TCTGCAGAA GAGATATCTC CTCTCCTACT   240
GTAAACAATT TTAGCCCAT TCTCTTCAAT AACTTAAGTC TAAACTACT AATATCTTTC   300
AAGTGCCTGA AGCTCAAGAA GTTGTCCAG AAAAGAAAGT TCCTAAGGCT CCTCCACAA   360
AACCAGAAGC CCCACCTGCC ACAGGTATTT TTTACCCCTG TCCTTTTCT GCAGAAAGAA   420
TATCTCTTCT GATCTTAGAA ATATTTTACT CCATTTGTCT CATTAACTA AGTAAAAAC   480
TCGAG                               485
```

(2) INFORMATION FOR SEQ ID NO:978:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:

```
GAATTCGGCC TTCATGGCCT AGAAGATTG CTACGTGGGC GACGAGGCTC AGAGCAAGAG   60
AGGTATCCTG ACCCTGAAGT ACCCTATCGA GCACGGCATC ATCACCACCT GGGATGACAT   120
GGAGAAGATC TGGCACCACA CTTCTACAA CGAGCTTCGC GTGGCTCCCG AGGAGCACCC   180
CACCTGCTC ACCGAGGCC CCCTCAATCC CAAGGCCAAC CGCAGAGAAG TGACCCACCA   240
ATCACCTAGG CCATGAAGGC CGAATTCGGC CTTATGGCC TAGCGCGACC GGCAGGGGAG   300
GAAGAAGCGC GAAAAGCTCG AG                               322
```

(2) INFORMATION FOR SEQ ID NO:979:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:

```
GAATTCGGCC TTCATGGCCT AGCCGCATCT TCTTTTGGCT CGCCAGCCGA GCCACATCGC      60
TCAGACACCA TGGGGAAGGT GAAGGTCGGA GTCACCGGAT TTGGTCGTAT TGGGCGCCTG      120
GTCACCAGGG CTGCTTTTAA CTCTGGTAAA GTGGATATTG TTGCCATCAA TGACCCCTTC      180
ATTGACCTCA ACTACATGGT TTACATGTTT CAATATGATT CCACCCATGG CAAATTCAT      240
GGCACCGTCA AGGCTGAGAA CGGGAAGCTT GTCATCAATG GAAATCCCAT CACCATCTTC      300
CAGGAGCGAG ATCCCTCCAA AATCAAGTGG GCGATGCTG GCGCTGAGTA CGTCGTGGAG      360
TCCACTGGCG TCTTCACCAC CATGGAGAAG GCTGGGGCTC ATTTGCAGGG GGGAGCCAAA      420
AGGGTCATCA TCTCTGCCCC CTCTGCTGAT GCCCCCATGT TCCTCATGGG TGTGAACCAT      480
GAGAAGTATG ACAACAGCG                                     499
```

(2) INFORMATION FOR SEQ ID NO:980:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:

```
GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGGCC TTCATGGCCT ACTTGCCCTCC      60
TTTGCTGTTT TAGGAACAAT TCCATGGGAG GGTCTATTCT GGATTAGGAA TTCCTTCTTG      120
AGTAATTTTT ATTACCTTTT AATTGTGTCC ATTTCTTTGG GAAATAGCAA GCTCTCCCTG      180
CTCCGCGCAA TCTCTCCTCT TACTTTTGG ACCAGTTCTT GTACCTCTTA GCTCACCTCA      240
TTCAGTGAAT ATTGACAAA GAGACGTGAG TTTCTGTACC TGTGAGACAG CTTATTTTGG      300
TGTCTTTATG GTTCTAAGC CAAAATCTC GAG                                     333
```

(2) INFORMATION FOR SEQ ID NO:981:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:

```
GAATTCGGCC TTCATGGCCT ATCGAGTAAT CCTGATGTTT TCACTTTCTC TAATCACTTC      60
TTCCTATTTT TGTCCAGTGG CTTTCTCGA G                                     91
```

(2) INFORMATION FOR SEQ ID NO:982:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:

GGCCGCTCGT GGCTGCGTTC CCGCTGATGC TTGTGCCTGC AGAGCCTCTC CAGGCTGCTG	60
GTGGGGGAGC ACTCCCTTCC CCGAGGTCTG GACGCTGATC TCCTTTTCTT CTCTTCCTA	120
CTCTCATAGT GCTCATAGGA AGAGCTGCCA GGGCTCCCCG ACCGCGACCG GGACGTCCTC	180
CGGCTGTGGC CCCAGGGGCC CCGCTGTGTC TCCCTGCTCT TGTCTTGGC TTTCTTCCTC	240
TTAGCTCGCT CTCGGCTGCT GGAGCGGTCA CTGGAGGACC GCCGGCTCTT GGCCTTGGAC	300
CGCTGCCTCC TGGGGCGCTC CTCACCCACT GATGGTGACG CCGACCTCGA G	351

(2) INFORMATION FOR SEQ ID NO:983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:

GAATTCGGCC TTCATGGCCT ACACAAATAT TGCTGTTCCA TGTCTCCAC TTTCATTTTC	60
CACTACAAAT GAAAAGCAAT TTTTGAGACT GAATCTGTG CTATTTTAAA GGTATTGTG	120
GGAAACTGAG CTAAAGGAGT TAGCATCTTT ATTTTGTAT CAAAAATAAA GGTATTTTG	180
AAATTATTAG GATTTTACA CAATTCTGAA ATCTGTTGCT TTTGTAAACA AATTGTTGA	240
TCTTAGTGAT CCCCTACTA CTACCACCAA TTCACCTCAC AAAGTCAGTT ATGAGTCTAC	300
CAGACTTTGT TCTGAAAAAT AGAAACAAA CACCTGATTA AGCTCTTGAG TATGGCATAG	360
GAATTTTTTA GAAGAATGCA TTCAAGGATT CTTTCCTTT CCTTCAGTG CATTAAATGT	420
AAAAGAGCAG CCACTGTTTT GTTGAAACAA ACAGCTTAAC TTCAGAAATA AGAACTAGCA	480
CACTCGAG	488

(2) INFORMATION FOR SEQ ID NO:984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984:

GAATTCGGCC TTCATGGCCT ACCTCCTGGC TCAGCAGGCT CCCTCCTTTT ACCAAGACTG	60
CTGGGACGTT GAACTCCGCT GTCTGATCAT CTCACCTACT CTCCTCCTAA CTCCCACTG	120
AAATCCATCT CCTCTCTTCC TCCCAACAT CCATCTCTT CCAACATGC CTTGACCT	180
AGAGCAGGTG AAGAAAGCCC ATGACTAAAA CTAAAGACTC AGAATGAAAC AAAAGGTGTG	240
ACAAGTTATT TGTGGGGAAG GTTTTCAGAT ATGTTCCAAG AGAAAATAAG GTAAAACAAC	300
CTTGTTTCATC AGACCAACAG TGCTGGAAG GGCTCGAG	338

(2) INFORMATION FOR SEQ ID NO:985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:

GAATTCGGCC	TTCATGGCCT	ACCTGAATTG	GGTGGCGAGT	TCCCTGTGCA	GGACCTGAAG	60
ACTGGTGAGG	GTGGNTTGCT	GACAGTGACC	CTGGAAGGGA	TCAACCTCAA	ATTCATGCAC	120
AATCAGTGTT	ACCTTTTATC	TCTCAGTGGA	CATTCTTAA	GCTAATTCCT	TTCTGAGGCC	180
AGCGCATCAT	CCCAGGAGCG	GAAGGTTTTC	ATAGAGCTGA	ATCACATTAA	AAAGTGCAAT	240
ACAGTTCGAG	GCGTCTTTNG	TCCTGGAGGA	ATTTGGTAAT	TACACTATTT	TGCTCTTAGG	300
TCTGGACTCA	CATGGCAGTA	ACTCAAACCT	CGGAGCTCCA	GAGGAGGGTC	TAGGGGCAGG	360
GAGAAAGA	ACCTCTGTAG	AGAAGTCTGG	AGGAGCAGGA	GTGACAAGGA	AGAAAAGGGA	420
CCCCTGAGAT	GAGAGCCGGG	ATGTGGAAGG	GAAAGATAGA	TAATGGATCG	CAGAAGAGCA	480
AATGGGCCT	CNGGTGGTAC	TCGAG				505

(2) INFORMATION FOR SEQ ID NO:986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:

GAATTCGGCC	TTCATGGCCT	ACACCTTCAC	ACCTGTCCTT	ACCTCCATTC	TCACCTCCAC	60
TGCTTTCAC	AACTCCACCA	TCATCACTTC	AATCTTCCCT	TCCATTCTCA	CTCTCTTCTC	120
ACTCACTGTC	CCTCTTTCAC	CTCCATCCTC	ATCTCTGTCC	TCCGCTCTAT	TCTCCTCTCC	180
AACCTCACTT	CTGTCTCTCC	CTTCTCTCTG	CTCTCCATCC	TCACCTCCAT	CCTCACCTTC	240
AACCTCACCT	TTATCCTCAC	CTCAACCTC	ACCTTTATCC	TCACCACTCG	AG	292

(2) INFORMATION FOR SEQ ID NO:987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:

CTCGAGTATC	CACCTGCCTC	GGCTCCCAA	GGTGTGGGA	TTACAAGCAT	GAGCCACCAT	60
GCACGGCTGT	AGATGTAAAT	TTTGAAAGA	GGAAGGCATC	AAATTAGGGG	TGGGGGGATG	120
GAGGTACATC	CAGCTTAGCC	TTCAGACCTT	AATGGAAATG	CTTTCTAAAC	TAGCGATCCC	180
AGAGCAGTTG	ACTCTCCTGA	AATAAACAG	GATCTGAGTA	GGCCATGAAG	GCCGAATTC	239

(2) INFORMATION FOR SEQ ID NO:988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:

GGCAGACTGC	AATACCTGCG	TGGAAATAGA	AGACAGAAAG	GTTTCAAGAC	AACAGATGAA	60
TTGTGAAAGA	GAGCAGCTAA	GGGGTAATCA	GGAAGCAGCC	GCTGCCCTCG	ACACAATGGC	120
TCAGCCTTAC	GCTTCGGGCC	AGTTTGCTCC	CCCGCAGAAC	GGTATCCCCG	CGGAATACAC	180
GGCCCCTCAT	CCCCACCCCG	CGCCAGAGTA	CACAGGCCAG	ACCACGGTTC	CCGAGCACAC	240
ATTAAACCTG	TACCCTCCCG	CCCAGACGCA	CTCCGAGCAG	AGCCCGGGCG	ACACGAGCGC	300
TCAGACCGTC	TCTGGCACCG	CCACACAGAC	AGATGACGCA	GCACCGACGG	ATGGCCAGCC	360
CCAGACACAA	CCTTCTGAAA	ACACGGGGCT	CGAG			394

(2) INFORMATION FOR SEQ ID NO:989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:

GAATTCGGCC	TTCATGGCCT	ACTTCGGGGC	TTTGACTCAA	TTCATGGGAA	ACAGGAAAAG	60
CAAACTAGT	TGATCTTGCT	ACTAAGGCGG	ACTGAAGTTT	CTTGCTTCA	TTGCTAAACA	120
ACTTCCAAAT	CACTTTGACT	CTTTGACCAT	ATTCATGTCT	ATTTCCCAT	AAAGCATCAC	180
AAAATAATGA	AGGAATTCTT	AGGAAGAGCC	TCAAGATGCC	CATGTGGCGT	CTGTGTGGGC	240
TGCCTCGTCT	GGTAGTTCAG	GGACCCACTG	GGCCATTTGA	AGGGCAAAGA	GAAAGCCCCA	300
GGTCTCATGG	CAGGAGACAA	GACTTCCACA	GTGGTGAGCC	AGTAAGGAAC	AGGGCACGTA	360
CTCGAG						366

(2) INFORMATION FOR SEQ ID NO:990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:

GAATTCGGCC	TTCATGGCCT	ACATGTTTCT	TATGAAGTTA	TTAGTAATAC	TTTGTGTTTC	60
TGGACTTATA	ACTGGTTTTA	GAAGTGACTC	TTCCTCTAGT	TTGCCACCTA	AGTTACTACT	120
AGTATCCTTT	GATGGCTTCA	GAGCTGATTA	TCTGAAGAAC	TATGAATTC	CTCATCTCCA	180
GAATTTTATC	AAAGAAGGTG	TTTTGGTAGA	GCATGTTAAA	AATGTTTTTA	TCACAAAAAC	240
ATTTCCAAAC	CACTACAGTA	TTGTGACAGG	CTTGATGAA	GAAAGCCATG	GCATTGTGGC	300
TAATTCCATG	TATGATGCAG	TCACAAAGAA	ACACTTTTCT	GACTCTAATG	ACAAGGAGCT	360
CGAG						364

(2) INFORMATION FOR SEQ ID NO:991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:991:

GAATTCGGCC	TTCATGGCGG	GGAAGAAGAC	AAGAAAATTA	ATGAAGAACT	GGAGTCTCAA	60
TATCAGCAAA	GTATGGACAG	TAAATTATCA	GGAAGATATC	GGCGACATTG	TGGACTTGGC	120
TTCAGTGAGG	TAGAATACCA	TGATGGAGAA	GGTGATGTGG	CTGGAGATGA	TGATGATGAC	180
GATGATGATT	CACCTGATCC	TGAAAGTCCA	GATGATTCTG	AAAGCGATTG	AGAGTCAGAG	240
AAAGAAGAAT	CTGCTGAAGA	ACTCCAAGCT	GCTGAGCACC	CTGATGAAGT	GGAGGTCTCG	300
AG						302

(2) INFORMATION FOR SEQ ID NO:992:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:992:

GAATTCGGCC	TTCATGGCCT	AGGTGCAGCA	GGTCCTCTGG	GAAGTGTCGC	ACAAAGGAGT	60
CGCCCACTGG	AAGTTTCTGG	GCAGGCGAGA	TGCCCAGAGG	TGATCCCTGC	CCGCCCCCTCC	120
CACCTCCCTT	CCACACAGC	CCATGGAGGT	GTTTGTGGAC	GACGAGACCA	AGCTCACGCT	180
GCACGGCCTG	CAGCAGTACT	ACGTCAAAC	CAAAGACAGT	GAGAAGAACC	GCAAGCTCTT	240
TGATCTCTTG	GATGTGCTGG	AGTTTAACCA	GGTGATAATC	TTCGTCAAGT	CAGTGCAGCG	300
CTGCATGGCC	CTGGCCCAGC	TCCTCGTGG	GCAGAACTTC	CCGGCCATCG	CCATCCACCG	360
GGGCATGGCC	CAGGAGGAGC	GGTGAGTNCG	AACCGCCCGC	CAAGGCTGCA	GGGNGCACCA	420
CCAGGAGCCC	AGTGTCTGAC	GGCCTCCACT	TGTTTCTCCT	GCACCCCNNC	CCATCACGCT	480
CGAG						484

(2) INFORMATION FOR SEQ ID NO:993:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:993:

GAATTCGGCC	TTCATGGCCT	AAAGGAATTT	ATCTATTTAA	TCATTGAATG	TATTGAACAT	60
TCATTGTGTT	ATAATTTTGT	TTTGTATTG	AAAATGTCTG	TAAGATTTAT	AGTGATGTTT	120
CCTTTTCTAT	TCCTGACATT	GTAAATTTGT	GTTCTCTCTC	CCTCCATCCC	TCTCTCACAT	180
CTCGAG						186

(2) INFORMATION FOR SEQ ID NO:994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:994:

GAATTCGGCC	TTCATGGCCT	AGTGTTCCT	TAAAGGGGTT	GAGGCCACCA	GTACTGCAGC	60
GAATTTCTCT	TTCTTCTCCC	TCCTCCTTCC	TTCTCTGAGC	TTGCTTTTAG	GGAAGGTTAA	120
TCTTACAGGC	TACCTATGTT	TCTCTCCACC	TTACTAAAAT	CTAAATAATG	ATAGAAAATT	180
TAAAGTTTTA	AAATTGAGTAG	TTCTGAGTAA	TCCTAGAATA	TTTTTCCAAA	TTAAATAATC	240
CTTTATTATT	TGCAAGTTGG	GCCAAATTTT	TTTTTTTTTG	GAGACGGACT	CTTAACAATC	300
TAAGATTGTT	TCAACAGGAC	TTCTTAATC	CCATTCCCTC	GAG		343

(2) INFORMATION FOR SEQ ID NO:995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:

ATCTTTAACA	GAATTATTAT	TATTTAATAT	AGAAGCACAA	GCAGGGGAAA	AATACGTCAT	60
CAAAATTTTC	AAGTAGTCAA	CTCATTATTG	GAGCCATTTT	ATTTTATAAT	TTTATTATATC	120
AGCTGGTTCA	GAATTCAAAA	GGGCATGTAA	TGAAGTCGCT	ATCCTGCTTC	TGTTTCCCAG	180
CTATCCAGCT	TCCCTCCCTG	GAGGCAAACA	GTGTCATTGG	TTTTCAATAT	ATCCTTCCAG	240
ATGTATGTTA	TCCGTAACCTC	TCGAG				265

(2) INFORMATION FOR SEQ ID NO:996:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:

GATTCGGCTT	CATGGCCTAC	AGCAGACACC	CTCCTGCCCCA	CACCTACTTG	TCCGCGCGGT	60
CTGAGGTTTG	CTTCGAG					77

(2) INFORMATION FOR SEQ ID NO:997:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:

GAATTCGGCT	TCATGTCGCT	CTTCCTGCAG	GTCAACATGT	ACAGCAGCGT	CTTCTTCCTC	60
ACCTGGATGA	GCTTCGACCG	CTACATCGCC	CTGGCCAGGG	CCATGCGCTG	CAGCCTGTTC	120
CGCACCAAGC	ACCACGCCCG	GCTGAGCTGT	GGCCTCATCT	GGATGGCATC	CGTGTGAGCC	180
ACGCTGGTGC	CCTTACCCGC	CGTGACCTG	CAGCACACCG	ACGAGGCCTG	CTTCTGTTTC	240
GCGGATGTCC	GGGAGGTGCA	GTGGCTCGAG				270

(2) INFORMATION FOR SEQ ID NO:998:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:

```
GAATTCTAGA CCTGCCCCCA GGCCACAGTC ACACCCCCCA GGAAGGAAGA GAGAATGGAT      60
TCTGCAAGAC CATGTCTACA CAGACAACAC CATCTTCTGA ATGACAGAGG ATCAGAAGAG      120
CCACCTGGCA GCAAAGGTTT TGTCACTCTA AGTGATCTTC CAGGGTTTTT AGGTGATCTG      180
GCCTCTGAAG AAGATAGTAT TGAAAAAGAT AAAGAAGAAG CTGCAATATC TAGAGAACTT      240
TCTGAGATCA CTCACAAACT CGAG                                         264
```

(2) INFORMATION FOR SEQ ID NO:999:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:999:

```
GAATTCGGCT TCATGGCCTA GCGGATTGTA ACTGCCTATG AGAATAGCTC TCAGCATGAT      60
CCCAGTTCAA ATAAGCTAT GCTTGGGGTT CATGCATCAG CTTCAGCGAT CATCCAGTAT      120
GGAAAAATCG CCCGGAAACA AGGACTGGTC AATGTAGCTC TGGATATATT AAGTCGGATT      180
CATACTATTC CAACTGTTCC TATCGTGGAT TGCTTCCAGA AGATTGACA GCGTACTCGA      240
G                                         241
```

(2) INFORMATION FOR SEQ ID NO:1000:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:

```
GAATTCGGCC TTCATGGCCT AGAATTGAAT TTAGACTTTA CAGAGTTACT GGTTCGTAAA      60
TCTTTGAGTT GTTTAAATTT TAATGTTAGA GTTTTACTGT TTGATCAGCA CATTTTITTT      120
CTCTTTTGTC TATAGGCCCG AAATGTTTGA GACGGCGATT AAGGAGAGCA CCTCCTCTAA      180
GAGCCCTCCC AGAAAAATAA ATTCATCACC CAATGTTAAT ACTACTGCAT CAGGTGTTGA      240
AGACCTTAAC ATCATTGAGG TGACAATTCC AGATGATGAT AATGAAACAC TCGAG      295
```

(2) INFORMATION FOR SEQ ID NO:1001:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 248 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:

GAATTCGGCC TTCATGGCCT AGATATTTAG AAATTTTGTG TATTATATGG AAAAAGAAAA	60
AAAGCTTAAG TCTGTAGTCT TTATGATCCT AAAAGGGAAA ATGCCTTGG TAACTTTCAG	120
ATTCCTGTGG AATTGTGAAT TCATACTAAG CTTTCTGTGC AGTCTCACCA TTGTCATCAC	180
TGAGGATGAA ACTGACTTTT GTCTTTTGA GAAAAAAAC TGTACTGCTT GTTCAAGAGG	240
AGCTCGAG	248

(2) INFORMATION FOR SEQ ID NO:1002:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:

GAATTCGGCC TTCATGGAGT CAGCCTTCCA GTCCTCATCT CAGAAATGA CTAGCCAGAA	60
GGAACAGAAA AACTTAGAGT CTTCAACAGG CTTTCAGATT CCATCTCAGG AGTTAGCTAG	120
CCAGATAGAT CCTCAGAAAG ACATAGAGCC TAGAACAACG TATCAGATTG AGAACTTTGC	180
ACAAGCGTTT GGTTCCTCAGT TTAAGTCGGG CAGCAGGGTG CCAATGACCT TTATCACTAA	240
CTCTAATGGA GAAGTGGACC ATAGAGTAAG GACTTCAGTG TCAGATTCTT CAGGGTATAC	300
AAATATGATG TCTGATGTAA GTGAGCTCGA G	331

(2) INFORMATION FOR SEQ ID NO:1003:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1003:

GAATTCGGCC TTCATGGCCT ACAGTATTGG ACTTTCAGAA GCTGAACAGA TGATGGGTGA	60
GCAAACTGGT TTAGCAGACC CAAGAGAGCT GAATCCTAAG CCAGCAAATA GAGAAATCCA	120
AGATTGAGCC CAAATTATGC TTTAGAATTC CTCAAAGGCT CAGAACTGG CTGCACTAGT	180
TCCCCGACA GGAAGCATGG ATTGAGGAGG TACCAAACCC ACTCCCCACC AAAAACCCAA	240
AACTCGAG	248

(2) INFORMATION FOR SEQ ID NO:1004:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:

```

GAATTCGGCC TTCATGNCCT GGNGAAGAGN AACAAAGAGAA CAAAAAAN ANAAGTCGAG      60
AGTCAGTAAT TTTCTTACTT AATATTGNGG GGATNTTACT TNATACATAA AGTTANTGAA      120
ACTAGAAATA GTGGTTTAAAT ATATTACTTN TAATTCAAAA ATTAACCTAT ATTTACAGAT      180
GCTCTACACA GTTCTTTTGT GAATCCACCT ATGGTTTTAT TTTNATTAAT TTTTNTTNC      240
ANAGCNATGA AATGTTGCTT TGTGGNGCCA GCGCACTCGA G                        281

```

(2) INFORMATION FOR SEQ ID NO:1005:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1005:

```

GAATTCGGCC TTCATGGCCT ACATAAACCA TCACATTTAA TCTGGCAGCT GCCCTGTTTT      60
TGAGGTTTTT TTTGTATTTA TCTTTCCTTG GTAAATGAAA GCTCTCATCT TTGTTTACAG      120
GCCAGAAAAA CTGAAAAAGA CACAGGCTCT TCCACTTACT GGATGTTTGA CAAATGATA      180
TTTGGGGGCC AAAACATTGG CATTACTGGT AAAGTTGGTA GAGATTCAGT AACTCAGACT      240
TTATTCAGA TCTCCTGAAA AAATAATCTG CATTAACTG ATGACTCGAG      290

```

(2) INFORMATION FOR SEQ ID NO:1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1006:

```

GAATTCGGCC TTCATGGCCT AAATTTTCAC ATATATGTAT ACTTAATTTT CAGCAATTAT      60
GACACAATAA AAAGAATATG CAAATTTAAT GTTGTTCAG AAGGTTTTGC AGGACTGGGA      120
ACGCTTTAGT GTCATCAACA GTAAACCTCA GATACTGTTC TGCACAGTTC AGAAGTACCA      180
TACCAGGTAT TGTGAGTGGC AAGAACGCCA GGGGACAGAG ATGCTTCTGG TAGATGAGGG      240
CCAGAGAAAC CAGCTCTCCT CCATTTTGAC AGCAATTTCT CACTGTGGCC ATTTGGCCTC      300
CATTATGTTT TGAGAGGAAC GCTCGAG      327

```

(2) INFORMATION FOR SEQ ID NO:1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

```

GAATTCGGCC TTCATGGCCT AAAAAAAT ATAGTGTTTT ATGCCACAGA GAATCAAGTT      60

```

GCATTGTGTA TACTAAATGG TCAAGCATTT TCAAGAACAT GACAAAATAA AAACATACAA	120
ATTTATATCT CAAAAGGAAA GTATCTTCTT TCATGTCAGA TCATCAGCAC AGAAGCCCTC	180
GATGCATGCA AAGGCAAGCA CAGGCTCTGC AGATGAGATG TGAAGAAGCA ATTAGGGAAA	240
TTCTCGAG	248

(2) INFORMATION FOR SEQ ID NO:1008:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 460 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:

GAATTCGGCC TTCATGCCTA CATCAAACCC TTTTCTTGTA GCAGCACAGG ATTCTGAGAC	60
AGATTATGTC ACAACAGATA ATTTAACAAA GGTGACTGAG GAAGTCGTGG CAAACATGCC	120
TGAAGGCCTG ACTCCAGATT TAGTACAGGA AGCATGTGAA AGTGAATTGA ATGAAGTTAC	180
TGGTACAAAG ATTGCTTATG AAACAAAAT GGACTTGTT CAAACATCAG AAGTTATGCA	240
AGAGTCACTC TATCCTGCAG CACAGCTTTG CCCATCATTT GAAGAGTCAG AAGCTACTCC	300
TTCAACAGTT TTGCCTGACA TTGTTATGGA AGCACCATTG AATTCTGCAG TTCCTAGTGC	360
TGGTGCTTCC GTGATACAGC CCAGCTCATC ACCATTAGAA GCTTCTTCAG TTAATTATGA	420
AAGCATAAAA CATGAGCCTG AAAACCCCC AGAACTCGAG	460

(2) INFORMATION FOR SEQ ID NO:1009:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:

GAATTCGGCC TTCATGGCCT ACGACAAGTT TTAAATTTA CTCTTGAGTA TGGTTCCAGT	60
GATTTACCAG AAAAACCAAG AAGACAGGCA CAAAAAGCA AACGGCATT GGCAAGATGG	120
ATTATCAACT GCAGTACAGA CTTTGTAGTAA TAGATCTGAG CAACACATGG AGTATCACAG	180
TTTCTCAGAG CAGTCTTTC ATGCCAATAA TGGGCAGCA TCATCAAGCT GCAAACCTGA	240
G	241

(2) INFORMATION FOR SEQ ID NO:1010:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 241 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:

GCGATTGAAT TCGACCACCT TGTTCAAATT TGTTATTATT TTTCTACTTT TGTATTGATT	60
CTGTTAATTC TTATCTATTG GTTCAGCTTA CTTTTTATG TTGGTCACAT TTCTCTTCAT	120
TGATTGTGTT AATTTTCTA TGTTGATAGA CACATTTTAT GTTCATCACT TTTTCTCTC	180

CTCCTTCAAT TATTATCCTT CTGATTTCCT TTTGTTTTCT CATAGTGTG GCCATCTCGA 240
G 241

(2) INFORMATION FOR SEQ ID NO:1011:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:

GAATTCGGCC TTCATGGCCT AGGCCACAAC TCAAAAGCAT TATCTTTTTT AGGGTTAGTA 60
 GAAATTGTTT TATGTTGAT CGAGGTTTGT TTGATTGTCA AAATGTACAG CCACAGCCTT 120
 TTAATTGGG AGCCCTGTT GTCAATCAA TGTGTACCTC TACAGTTGTA AAAAGTATTA 180
 GATTCTACTA TCTGTGGGTT GTGCTTGCCA GACAGGTCTT AAATGTATA TTTTGGAA 240
 AAGTTTATAT ACTCTCTTAG GAATCATTGT GAAAAGATCA AGAAATCAGG ATGCCCATTT 300
 ATTTAATATC CATTCAATTC ATGTTAGCGG AACTCGAG 338

(2) INFORMATION FOR SEQ ID NO:1012:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:

TGAATTCTAG ACCTGCCTCG AGCTCCAGCT GCCAACACCC TTGGACACAA TATTCCAGTC 60
 TCCACTGCCC ATCTCATGTG GTTGCAGGNT CCTCGAG 97

(2) INFORMATION FOR SEQ ID NO:1013:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 412 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:

GAATTCGGCC TTCATGGCCT ACACATTCTG GGGGAAAAAA ACTGGAATTG TTGTATTTT 60
 GTTTTTTGG GGGGGATCT TTATGTGAAA AATCAGAGCT ACTTGTTACC ATAAGCCCTT 120
 ACTATCAACA AGATAATTAT TTGTAATCAC TTTTATATCC CAGGTTGGAA TTGCTTTCCC 180
 CTCTAAGTT ATCTCCCTT AATAATATT ATGATACCAG GACAGTGAGG GTATAAGAGC 240
 AAATGTAGTG AGGTATTCAA AATCCTGCA TATATGGACT CAAAAGTTCT TTAGTTATTT 300
 GAATTATATA TAGCTATATT ATTTATTAG CTGCGGTGT CAGAAGATTG CCAATTTTAA 360
 GAGTAAAGAG GAGAGAGATA AGTAATAAAA ATAGAGGAGG GGTACTCTCG AG 412

(2) INFORMATION FOR SEQ ID NO:1014:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:

GAATTATGTC TCCCATCTGT GCTTTTCCTA AGTGGGGCTC CCGTGCCGTT CACCTCACAT	60
TCCTGGTGTG TTA CT TGGCA GGC ACTCCCA CCACTCCGAA AGGGAGGCC TTCCTGGGAG	120
GGAGGCAAGA AGGCTCCCA GGCCTTTGC CCCCTTTCCT GGGCCTGCGT TCCCAGGGCC	180
TCCCAGGCC CTCTGGCTAC CCCGTGACCT GCCTCGAG	218

(2) INFORMATION FOR SEQ ID NO:1015:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:

GAATTCGGCC TTCATGGCCT ACCTTATTAC CAGACAACCT TAACCAAACC ATTTACCCAA	60
ATAAAGTATA GGC GATAGAA ATTGAAACCT GGCGCAATAG ATATAGTACC GCAAGGGAAA	120
GATGAAAAAT TATAACCAAG CATAATATAG CAAGGACTAA CCCCTATACC TTCTGCATAA	180
TGAATTAACT AGAAATAACT TTGCAAGGAG AGCCAAAGCT AAGACCCCG AAACCAGACG	240
AGCTTCGGGG GAAGTATGTA GGAGTTGAAG ATTAGTCCGC CGTAGTCGGT GTACTCGTAG	300
GTTCAGTACC ATTGGTGGCC AATTGATTTG ATGGTAAGGG AGGGATCGTT GACCTCGTCT	360
GTTATGTAA GGATGCGTAG GGATGGGAGG GCGATGAGGA CTAGGATGAT GGCGGGCAGG	420
ATAGTTCAGA CGGTTTCTAT TTCCTGAGCG TCTGAGATGT TAGTATTAGT TAGTTTTGTT	480
GTGAGTGTTA GGAAAAGGGC ATACAGTCTC GAG	513

(2) INFORMATION FOR SEQ ID NO:1016:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:

GAATTCGGCC AAAGAGGCCT ACCAAAATAA AACAGAAAT TATGAGATTG CCTCAACTCC	60
CACATATGCT CGAG	74

(2) INFORMATION FOR SEQ ID NO:1017:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:

```

GAATTCGGCC AAAGAGGCCT AAAGACCTGA GGTCCAGGAT GAGCTCTTTC CCACAGAAAC      60
TTTGACAAAT GTGTGGACAA TAAAGNAGCA CTGCTTCCCT CATTACCAT AGCTCAGCTG      120
GATTTATAGA TTAAATCTT TTAACGAAAA AGTTCATGTT GAGGTATTTA GATACTTTTT      180
AGAGGGTTAA ATACCAAGTT ACAGTGACAT TTAAACCGAG TGTCTAGAAC ATGAAGGCCAA      240
AGAGTCTGCT ATTCGGAGGT AAATTTTATC AGTGTTTGAA AGGTGAAGCA TTTGCTCATG      300
AAATGTTGAA TGAATTTCTG TGACATGGCA CGAGGCTGGT AAGAAAAAGT GGGAACTCGA      360
G                                                                                   361

```

(2) INFORMATION FOR SEQ ID NO:1018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:

```

GAATTCGGCC AAAGAGCTAC GAGAGTGTCA TGAAATATCT CCGAGAGTCC TTCAGTGAGA      60
GGTTGTTTTT TTTTCCTATG GCTGGTGTCA CTTCCTCTGG AGCATCTTCA TCGTTTCATC      120
ACAGTCACCT TCTAACTGGA GTCAGTAACT TCACCTTCTT TAAGCTTCCC AGGCTGCAGA      180
TACAGAGAGT GTCCACATTC CACAGTCAGC TATTTCTACG ATCACTCCAT TTACGCTTGG      240
TTCAAATTTT ACTCCAGTG TTACCACTTC TCATTCTTTT GCTGTGTTTC ATCTGGGCCA      300
TTTGCTTCTT ATGATTACCT GTTTTGTAA ACTGTCATGT GGGTTTATCC CTGGGAGACA      360
AGGAGACAGC ACAACCCCTT GGTTCGCTGT CTGTGAGCGA ACTCGAG                      407

```

(2) INFORMATION FOR SEQ ID NO:1019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:

```

GAATTCGGCC AAAGAGGCCT ACTAAGTTCT GTGAAGTGTA TGTAGCATCT GGGCTATAGA      60
TTTGGAGCTT TTAAGTACTC TNGAGAGTGG TGAAGGAGTA TCTGCAGCTC TGATGACAGG      120
NACAGAGAGA GAGAGAGAGA GATGGGTATG CCATCCGTGG ACACCAGGAA GAGTACCGAG      180
GACTGCTGTA GGCTCCTTCA GTTCTAGTTT CCAACTCAAA GCAATTTTIA AGTTTTTGTT      240
TAATTATGNN TCGGCTCTGC TAAGANANNA AGGTACCTTA CATAAGTCCC TCAAAGACT      300
TGTGTGTTTG AAGATGGCGC CCTCGAG                      327

```

(2) INFORMATION FOR SEQ ID NO:1020:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:

GAATTCGGCC AAAGAGGCCT ATGAATGCTA TATACCTTT TTATATCAAA AGTCTCAAGC	60
ACTTATTTTT ATTCTATGCA TTGTTTGTCT TTTACATAAA TAAAATGTTT ATTAGATTGA	120
ATAAAGCAAA ATTACTCGAG	140

(2) INFORMATION FOR SEQ ID NO:1021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:

GAATTCGGCC AAAGAGCTAC GGCCAAAGAG GCCTAGACTC GCGCTGNTC TCACACCACT	60
GTGGAACGTC CCGGCCNTC CCCTTGGGTC CCTTATCTTA GGGGACCGG ACGTCCATCC	120
CTTCTGCAGT GGCAGCNTCT GAGCCAAAGC GCCTCTCCA GAAGCCGGAC TTTCCAGGAC	180
CCTCACTCCC AGCCACACCC TGACACGGCC TGACTGGGGT CTCCTGTGAG TCCCATGCTC	240
GGCTTTGTCT GACACCTCCC AGGACAAGAC CGTCCCTTCT CCCCAAACTG GGCTCTCCAC	300
CAAGAGCCGC GTTCACCAC GGGGGAGTGG GCTCCACACA GGCCAGTCCT CGAG	354

(2) INFORMATION FOR SEQ ID NO:1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:

GAAAGAGGCC TAATCGTCAC ATCCATCAGA GGATTGCTGA TCACTCTTAC CAAGTTCCTT	60
TATGCCATCT CTAGCAGTAA GTCCTCCAAT GTCATTGTCC TGCTATTAGC ACAGATAATG	120
GGCATGTACT TTGTCTCCTC TGTGCTGCTG ATCCGAATGA GTATGCCTTT AGAATACCGC	180
ACCATAATCA CTGAAGTCCT TGGAGAACTG CAGTTCAACT TCTATCACCG TTGGTTTGAT	240
GTGATCTTCC TGGTCAGCGC TCTCTCTAGC ATACTCTTCC TCTATTTGGC TCACAAACAG	300
GCACCAGAGA AGCAAATGGC ACCTTGAAC TAAGCCTACT ACAGACTGTT AGAGGCCAGT	360
GGTTTCAAAA TTTAGATATA AGAGGGGGGA AAAATGGAAC CAGGGCCTGA CATTTTATAA	420
ACAAACAAAA TGCTATGGTA GCATTTTICA CCTTCATAGC ATACTCCTTC CCCCTCAGGT	480
GATACTATGA CCATGAGTAG CATCAGCCAG AACATGAGAG GGAGAACTAA CTCAAGACAA	540
TACTCAGCAG AGAGCATCCC GTGTGGATAT GAGGCTGGT TAGAGGCGGA GAGGAGCCAA	600
GAAGCTAAAG GTGAAAAATA CACGAACTC GAG	633

(2) INFORMATION FOR SEQ ID NO:1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:

```

GAATTCGGCC AAAGAGGCCT ATCTTGCGAG TGGAGTGTCC GCTGTGCCCC GGCCTGCACC      60
ATGAGCGTCC CGGCCTTCAT CGACATCAGT GAAGAAGATC AGGCTGCTGA GCTTCGTGCT      120
TATCTGAAAT CTAAAGGAGC TGAGATTTCA GAAGAGAACT CGGAAGGTGG ACTTCATGTT      180
GATTTAGCTC AAATTATTGA AGCCTGTGAT GTGTGTCTGA AGGAGGATGA TAAAGATGTT      240
GAAAGTGTGA TGAACAGTGT GGTATCCCTA CTCTTGATCC TGGAAACAGA CAAGCAAGAA      300
GCTTTGATTG AAAGCCTATG TGAAAAGCTG GTCAAATTTT CCGAAGGTGA ACGCCCGTCT      360
CTGAGACTGC AGTTGTTAAG CAACCTTTTC CCACGGGATG GATAAGAATA CTCCTGTAAG      420
ATACACAGTG TATTGCAGCC TTATTAAAGT GGCAGCATCT TGTGGGGCCA TCCAGTACAT      480
CCCAACTGAG CTGGATCAAG TTAGAAAATG GATTTCGTAC TGGAAATCTCA CCACTGAAAA      540
AAAGCACACC CTTTAAAGAC TACTTTATGA GGCACCTGTG GATTGTAAGA AGAGTGATGC      600
TGCTTCAAAA GTCATGGTGG AATTGCTCGG AAGTTACACA GAGGACAATG CTTCCCAGGC      660
TCGAG

```

(2) INFORMATION FOR SEQ ID NO:1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:

```

GAATTCGGCC AAAGAGGCCT ACTTGATTG GATTCACATT GCTTTCATTT CTAAAAATGC      60
TTCACCTCAG GTTCTTGGTC TTGGAATAA ATTTCAAGGT GCATTGTATC CATTTTAAGC      120
TGCTTTATTT TATTTTCACT TGTATGAGCA AATTCTTGGG GGAGCTTGC TTTTCTTCTG      180
CCAGAAAAAC AAAAGGGGGA AATGAAAATC TTTTTTGGAA TGAGTTCGTG GGGTTTTCTT      240
AACAGCCACC ATGTTTATTA GTTACATTGT GTTTTGGCCA ATCAGTGCAA TGTAACAAAT      300
TTTACAGTTA ATTGCTTTCA ATTGAGTCAG TAAACCTGTG ATAGATAATT TATTTAACTG      360
GAAAACCTAG GTACCCATAA GAAAAAAGAT TCATTCTCTG TGAAAACGTG AGGAATCTGT      420
TGTTGTTTTT ATTTGAATAT GCTCTACTTC TGCTCTAGTA TTGGTTTGG AATATATTTT      480
GTGGCTCTAA TTAAGTATT TTTAAAAACC CTACCTCCAT TAACAGTTGG TAAAGGCCCC      540
CTTCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:1025:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:

```

GAATTCGGCC AAAGAGGCCT AGTTAAGTCT GAACTAGTCT TTTCCTTTGT GATGTGGTTG      60
GAAAGTCTTC CCTGTTCCAA GGACTCCTCG AG

```

(2) INFORMATION FOR SEQ ID NO:1026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:

```
GAATTCGGCC AAAGAGGCCT AGTTAAAAAC TAATATTTAT ATGACAGAAG AAAAAGATGT   60
CATTCCGTAA AGTAAACATC ATCATCTTGG TCCTGGCTGT TGCTCTCTTC TTAGTGGTTT   120
TGCACCATAA CTTCTCAGC TTGAGCAGTT TGTTAAGGAA TGAGGTTACA GATTCAGGAA   180
TTGTAGGGCC TCAACCTATA GACTTTGTCC CAAATGCTCT CCGACATGCA GTAGATGGGA   240
GACAAGAGGA GATTCTGTG GTCATCGCTG CATCTGAAGA CAGGCTTGGG GGGGCCATTG   300
CAGCTATAAA CAGCATTGAG CACAACACTC GCTCCAATGT GATTTTCTAC ATTGTTACTC   360
TCAACAATAC AGCAGATCTC GAG                                     383
```

(2) INFORMATION FOR SEQ ID NO:1027:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:

```
GAATTCGGCC AAAGAGGCCT ACATGTGGAC TGCACTGTTT ACTTTTGGTT GGACTGGGAC   60
AATTGCGGGA ATATCTACTA TGTTTATTCT TCAAGAACCC ATCATCCAT TAGATGGAGA   120
AACCTGGAGT TATCTCATTG CTATATGTGT CTGTTCTACT GCAGCATTCT TAGGAGTTTA   180
TTATGCCTTG GACAAATTCC ATCCAGCTTT GGTAGCACA GTACAACATT TGGAGATTGT   240
GGTAGCTATG GTCTTGAGC TTCTCGTGCT GCACATATTT CCTAGCATCT ATGATGTTTT   300
TGGAGGGGTA ATCATTATGA TTAGTGTTTT TGTCCTTGCT GGCTATAAAC TTTACTGGAG   360
GAATTTAAGA AGGCAGGACT ACCAGGAAAT ACTACGACTC GAG                                     403
```

(2) INFORMATION FOR SEQ ID NO:1028:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1028:

```
GAATTCGGCC AAAGAGGCCT AAAACCGAAA CTTGATGAA AATGAAATTC CTCAAGAGAA   60
TGGCACTCGA G                                     71
```

(2) INFORMATION FOR SEQ ID NO:1029:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1029:

GAATTCGGCC AAAGAGGCCT AGAAACATGT CTAAGGTNGC ACACAGCTAG TANGCGTTAG	60
AAACGTGTCT CAAACCCAAG AGGTCTGGCT CTGGCATCCG TGATCATAAC CACTNGCTTT	120
GCCTGATCTA ACGTAAAGA TGGATGAAAA AATAAATCAA GTGTGATGAG TGTATATAA	180
GAAAGGGGAA ATAGCAGGGT TCAGTGTGGA ACATAGGAGA GTGGGCCTTC ATTCCCTCCA	240
GTTGAGGGCC AAATAAGGCA TCCCTGAGGA AGAGACATTA AGCTGAGATC TGAAAGGTGA	300
GCCTGAATAA GTTAGGTGAA GGACCATGAG TAAAGGGAAG CCGCTCGAG	349

(2) INFORMATION FOR SEQ ID NO:1030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

GAATTCGGCC AAAGAGGCCT ACTGATGATA ATAAACAGA GCTTTACTTG GGAGAAATTA	60
GCCTTGAAAG TGTGACATCC AAAACAATTT TTTTAAAAA ATTTAGACAA CTAAAAGGG	120
AAATGTCAAA AGGGAGAAAC TTA AAAAACA AAAGGAAAGT AGTCAGAGAA TCAGAGAGAA	180
AATATGAACA GAACACAGTA AAAAGGAATG GCTACAAGAG GGATCAGCAA CTCGAG	236

(2) INFORMATION FOR SEQ ID NO:1031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:

GAATTCGGCC AAAGAGGCCT ATTAGAAATA AATATCTTCC TTCAATAGAT GAAAATGAAA	60
ATACAGAAAA AAGAGAGCAG TTGTCAAATT TAAAAGTTTT GAATCACTCC CCAATGCTG	120
ATGCCTCTGT CAATTNGAC TACAAATCTC CATCCCCATT TGAATGCAGC ACTGATCAAG	180
AAGAGAAAAT TGAAGATGTT GCTAGTCACT GTCTGCCTCA GAAGGACCTG TATACTGCTG	240
AAGAGGAAGC TGCTACCCCTT TTTCTAGGA AAATGACATC CCATAATGGG ATGGAGGACA	300
GTGGAGGAGG AGGTACTGGA GTGAAGAAGA AACGGAAGAA AAAGGAGCCA GGAGACCAAG	360
AGGGTGCAGC AAAGGGAAGC AAGGACAGAG AGCCCAAGCC AAAGAGGAAA CGAGAACCGA	420
AAGAGCCAAA GGAAGAGCTC GAG	443

(2) INFORMATION FOR SEQ ID NO:1032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:

GAATTCGGCC AAAGAGGCCT AATAAAGAGC AAAAAAATGT TAATGTCAAG TCAAATTGCC	60
TGTAAATGAC TTAAGGAATA TGTTAATGAT CTGCTCCAA ATGAATAATT ATAAAGCAGG	120
TGCACTGGAG ATATGATCAT TTAAGTGAAG GAAACAGCT TCTAATGGCT TCAATAACCA	180
AGATAATGGT GATATTGGAG AAGCCTGTGA AACTCATTGT TCATGCCATT CATTTAATAC	240
ACAAGAGAAC TTCAGATGGA ATCTCCCTGT GGAATCATTG CCCTGCTTAT TTAAATAGCA	300
GTTAATTAA ACACACACC AAGTCAAAAC TGCATTATT CTAAACACC TCTTTCTAAT	360
AAACTATGTT CTCAATAAC AGAACCCTG TCTCGAG	397

(2) INFORMATION FOR SEQ ID NO:1033:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 372 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:

GAATTCGGCC AAAGNGGCCT ATTTTAAAAA TCACTTTAAG NATCCAATAG AGAACAACAA	60
AGCCATATTG AGATGCAGGT TTTAGGAATT TGGTAGTAAT CCCTCACAAG GTCAGACTTG	120
ATCTCCTGGA CAATCAGGGC ATGCTAGTCA GCTTTCATGA CTCAGCAAAG CTACAAATTA	180
TGTATTTTGG CTTTTTGTGG AAATGCCAA CCTACAGAT AGCAAACGTC TCCTCGGTTG	240
TCAAAAAGTA AGAGTAGTTT TTAGAATTCT GCCTTTGGGT CTTGTAGAAT GAAATATTTA	300
CAAGATTTGC TATTTGTTAA CATTTTAGCT CCTTCCTTGT TCCTTCAGTC TTGCTGCTGT	360
GCACACCACC AG	372

(2) INFORMATION FOR SEQ ID NO:1034:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:

GAATTCGGCC AAAGAGGCCT AAATATGTTT TTTCTGCTT TTATACTGT AAAATGGAAT	60
GTTCTTCTTA CCTTAACTT TATGATTGAG CTGTCCATAT CAGGTTTTTT TTTCTACTGA	120
CTATTTATTG GGACTAGCTC ACTTTATTAA TTATGCATCC TGATATCTTA TAGAATGGAT	180
AGTGATTTTC AATATTATTA ATTAAGTGGG CCTTTGTTAG ATATAAGCA AGATACCTCC	240
AGTAGGTCCT GTTAGCAGTA AGTTTATAT TGTGGAGGTG AACAAAGGTAT TTTGTGTAA	300
ATCAGTTTAC TAAATTGTAT TATTTTCAAG CTAGATTGTG ACGGTAAGGC TCGAG	355

(2) INFORMATION FOR SEQ ID NO:1035:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:

```

GAATTGCGCC TTCATGGCCT ACGTCTCAGC ATTATGCATT CCAGTTGGTT TTTCCCATG      60
CTTTTCCTGA GCTGTATCCA AGTGAGTCGT ATTAATTTC A GAGGAGTATT T      111

```

(2) INFORMATION FOR SEQ ID NO:1036:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 560 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:

```

GAAATTGCGC CTTTCATGGCC TANATGAACA AAATCCAGA TACCATTGAT AAGAAATTTT      60
GCATCAAGAA GGGCTTCTGA AAAGACCCAC GTGCTCCAGT CCCAGCTCCA AAAGCCACTG      120
ATGACAAGGG CCCCACTGTG GAACCTAAGT CTGGGAGCCC CCTGACTTCT GGCTGGCCAG      180
AGCTGCGGTC CGTCAAGGGC TTGCCTCGCT TCAGAATCAG TAACATAGAT CTTAAGTGCA      240
ATTGATTAAT AAGCAGTGAG TTAGCTGTAGC TTCCTTTAGC TCTACCGAAC TCTTTTAA      300
AACTCAAACT TGAGCAGCCT TAGAAAAGGG GTTGGGGGGT GGAACCACAG GCCATTTCTC      360
TAAGTGGGCT GCTGTGAAGT TTTAAATGAA AGCTCTAGCT TTAGGAGCTT GAGCCATTTC      420
CTGACTGCAC TGGCCTGGCA GTCTGGCTGC TGCAGAAGAG TTTTAAAGA GGGGTCGGAG      480
CCGCCCCGTG AGAGCGGGTC TTCTACCAT GTGGGCTGT ACTACGTGGT GGTCTTGTT      540
TCTCTTCACA GAAATGCTCT

```

(2) INFORMATION FOR SEQ ID NO:1037:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:

```

AAATTGGGCA GTGGTAGCAC CTGACCCAGG GCTGCTGTGA GGCCCCCTG GGCTGAAGCA      60
CATGTGGTGC AGAGGGCCAG GTTGGGGTGT GAGTGCCAGT TCCCACTGGC CTTAGGCCCC      120
ATCCAATGCT GCTCCCAGGG CCATGGGTGA GCCTTTCCAC TTCTTATAAA GTAGAGAAAA      180
GTATTTATAG TATCTTCTTT GGTAATTCCT TTTTCTTGGT GATGTTTCATC TGCAGTTCTG      240
TACATTTTCT CAGATCTTCT GATGAACAAA TTCCTTTAAT TTGTCATGTC AAACCTTGTTA      300
ATATTTTCCT TTGTGACTCG AG

```

(2) INFORMATION FOR SEQ ID NO:1038:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 517 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1038:

GAATTCGGCT	TCATGGCCTA	CACTGTAGCA	AATTGCGTTG	GAAAAGAACT	AGCTCCACAT	60
GTCAGAAGC	ATGGAAGCA	ATTTGTTCCA	GAATCTCTTA	AAAAAGACAA	AGATGGGAAA	120
TTCCTCTGG	ATGGTGCTAA	TGGTTGTAGC	AGCAAGTAGT	GTTCAAGGAT	TTTCAACTGT	180
CTGGCAAGGA	TTGGAATGTG	CAGCTAAATG	CATCGTTAAC	AATGTTTCAG	CAGAAACTGT	240
ACAAACTGTC	AGATACAAAT	ACGGATATAA	TGCAGGAGAA	GCTACCCACC	ATGCGGTGGA	300
TTCTGCGGTC	AATGTTGGCG	TAACTGCCTA	CAATATTAAC	AACATTGGTA	TCAAAGCAAT	360
GGTGAAGAAA	ACTGCAACAC	AAACAGGACA	CACTCTCCTT	GAGGACTATC	AGATAGTTGA	420
TAATTCTCAG	AGGGAAAATC	AAGAAGGAGC	AGCAAATGTC	AACGTGAGAG	GGGAGAAGGA	480
TGAGCAGACG	AAGGAAGTAA	AGGAGGCCAA	ACTCGAG			517

(2) INFORMATION FOR SEQ ID NO:1039:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 548 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039:

GAATTCGGCC	TTCATGGCCT	ACAGAATGAA	GAAAGCAAGC	AGGAGTGTG	GCTCAGTGCC	60
TAAAGTGTCT	GCAATAAGTA	AAACGCAAAAC	AGCAGAAAAA	ATTAAACCTG	AAAACAGCTC	120
TTCAGCATCT	ACGGGAGGCA	AACTTGTGAA	ACCTGGAACA	GCAGCATCAT	TGTCAAAGAC	180
CAAGAGCAGT	GATGACCTTT	TAGCTGGAAT	GGCCGGAGGG	GTAACGGTGA	CTAATGGTGT	240
TAAAGGAAAG	AAAAGCACCT	GCCCATCTGC	AGCACCTTCA	GCACTTGCCC	CTGCCATGAC	300
CACCGTGGAG	AACAAATCCA	AGATTAGCAC	AGGCACAGCT	TCTTCAACCA	AGCGGAGCAC	360
TTCTACAGGT	AATAAAGAAT	CCAGTTCTAC	TAGAGAAAAG	TTACGTGAAC	GTACCCGATT	420
AAACCAGAGC	AAAAAATAC	CTTCTGCAGG	TCAGGGAGCT	AATGACATGG	CATTGGCCAA	480
ACGTTCCCGC	AGTCGAATG	CTACAGAATG	TGACGTTCGT	ATAAGCCTCC	CTATAGTGAG	540
TCGTATTA						548

(2) INFORMATION FOR SEQ ID NO:1040:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:

GAGGAAATGG	CCAAACAGAA	AGCAGCTCCT	GAAGCCAAGA	AACAGAAAGT	GGAAGGCACA	60
GAACCGACTA	CGGCTTTCAA	TCTCTTTGTT	GGAAACCTAA	ACTTTAACAA	ATCTGCTCCT	120
GAATTAAAAA	CTGGTATCAG	CGATGTTTTT	GCTAAAAATG	ATCTTGCTGT	TGTGGATGTC	180
AGAATTGGTA	TGACTAGGAA	ATTGAGTTAT	GTGGATTTTG	AATCTGCTGA	AGACCTGGAG	240
AAAGCGTTGG	AACTCACTGG	TTTGAAAGTC	TTTGGCAATG	AAATTAAACT	AGAGAAACCA	300
AAAGGAAAAG	ACAGTAAGAA	AGAGCAAGAA	CTCGAG			336

(2) INFORMATION FOR SEQ ID NO:1041:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:

```

GAATTCGGCC TTCATGGCCT AGGCTTCCCG AGCAGTCTCC AAACATATAT TACATTGAA      60
GGTCGCGCCC GCCCGCCCC GCTCGCGATT TGGCCCTTCG GGGCCCCCGT CCTCCACCTC      120
CTTCTCTCCC ATGATGCATT GTCATCTGGC TTTTATCACC TGTTCTGCCC TTGAATTTGA      180
ACATGCCAAA GATATAAGTA TTGGATTGCA GTCTTGCACT ATTATTTGGT GAGTTTTTTT      240
TTAATGCATA CAGCTTTTTC ATAAGTGCAT AAATGGGATT ATATAAACAA TGTTTAGAGT      300
AGTTTTCTTT TTACCCTTT TGCCTGGTTT GCTCTTCTTC CCTATCACAT CCCTTCCAAT      360
CCATCTCGAG                                         370

```

(2) INFORMATION FOR SEQ ID NO:1042:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1042:

```

GAATTCGGCC TTCATGGCCT ACGCCATCTT CCAGTAATTC GCCAAAATGA CGAACACAAA      60
GGGAAAGAGG AGAGGCACCC GATATATGTT CTCTAGGCCT TTTAGAAAAC ATGGAGTTGT      120
TCCTTTGGCC ACATATATGC GAATCTATAA GAAAGGTGAT ATGTAGACA TCAAGGGAAT      180
GGGTACTTTC AAAAAGGAAT GCCCCACAAG TGTTACCATG GCAAACTGG AAGAGTCTAC      240
AATGTTACCC AGCATGCTGT TGGCATTGTT GTAAACAAAC AAGTTAAGGG CAAGATTCTT      300
GCCAAGAGAA TTAATGTGCG TATTGAGCAC ATTAAGCACT CTAAGAGCCG AGATAGCTTC      360
CTGAAACGTG TGAAGGAAAA TGATCAGAAA AAGAAAGAAG CCAAAGAGAA AGGTACCTGG      420
GTTCAACTAA AGCGCCAGCC TGCTCCACCC AGAGAAGCAC ACTTTGTGAG AACCAATGGG      480
AAGGAGCCTG AGCTGCTGGA ACCTATTCCC TATGAATTCA TGGCATAATA GGTGTTAAAA      540
AAAAAATAA AGAGACACTC GAG                                         563

```

(2) INFORMATION FOR SEQ ID NO:1043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:

```

GGCTTGATTG TTAGAGAAAT AATGTTGGAA GAAGAACCTT CAATAACATC AGGTGAAAGC      60
CAGACTACCT ACTCTACTTT CAGTGCTCCG TTAAATAAAG CAAATAGAAA AAAGTTAATT      120
GAAAGTCTTT CCCAGATTT TTGTCACCAA AACAAAGGGC TGTTGCTGAC AGTTAATACC      180
AGTAGTCAGA ATGGAAGGCC TGAAGAACA CTTATTAAAG AAATCCAGAG TCCTCTGTCT      240
AGTATCTGTG ATGGCTCCAT AGCTCTAGAT GCTGAGCCTG TTACCCAGCC AGCATCGCTG      300
CCCAGACACA GCAGCACACC AGACCACACC AGCACACTGG AGCCTCCTCG TTGCTCTCAA      360
AGAAAGAACT TACAAAGTGA AAAGGAACT CTCGAG                                         396

```

(2) INFORMATION FOR SEQ ID NO:1044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:

GAATTCGGCC	TTCATGGCCT	AAACTGGA	TCCTCTAAAT	GTCTGTCAAT	GAAGGAATAG	60
ATAAATTGTA	ATATGTTTAT	ATAAATGCT	GCATAAATAA	GTGAAATTTA	TAAATATACT	120
AACGAATGAA	TCTTGAAAAC	AGAGTTGGGA	GATAAAAGCA	AGCTGTTGAA	GAACATGGTC	180
AGTATCCTCT	CACTTATGTA	AGTTAAAAAC	TCCAAAGAAC	ATTATCTATA	TTGGTAATGG	240
CATAGACATG	TGTGGTAAAA	TATAAAAATA	TTAACTAAAA	GTTCTATACG	CTTCAGGATA	300
TTGTTAGTAT	AATAAGGCAG	GAAGTGGATA	GCATTGGGAT	GAGAACTCGA	G	351

(2) INFORMATION FOR SEQ ID NO:1045:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 390 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:

GATTCGGCCT	TCATGGCCTA	AGCAGCTCGG	GGTTCGGCAG	CAGCGGTCCC	ATCGGCTGAA	60
GTTCCGGGGG	GGTGGGGCGC	CGAGCGCGCG	GGGTGGGGGG	GGTCCTGGTC	TTTGGCTTCT	120
CGACTCGGTC	CTGTTTCGAC	AGCGAACATG	TCGCGGCCTG	TCAGAAATAG	GAAGGTTGTT	180
GATTACTCAC	AGTTTCAGGA	ATCTGATGAT	GCAGATGAAG	ATTATGGAAG	AGATTCGGGC	240
CCTCCCACTA	AGAAAATTTC	ATCATCTCCC	CGAGAAGCTA	AAAATAAGAG	GCGATCTGGA	300
AAGRAATTCAC	AGGAAGATAG	TGAGGACTCA	GAAGACAAAG	ATGTGAAGAC	CAAGAAGGAT	360
GATTCTCACT	CAGCAGAGGA	AGCTCTCGAG				390

(2) INFORMATION FOR SEQ ID NO:1046:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 381 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:

GAATTCGGCC	TTCATGGCCT	ATGAAGCATC	TGGATGGGGA	AGAGGATGGC	AGCAGTGATC	60
AGAGTCAGGC	TTCTGGAACC	ACAGGTGGCC	GAAGGGTCTC	AAAGGCTCTA	ATGGCCTCAA	120
TGGCCCGCAG	GGCTTCAAGG	GGTCCCATAG	CCTTTTGGGC	CCGCAGGGCA	TCAAGGACTC	180
GGTTGGCTGC	TTGGGCCCGG	AGAGCCTTGC	TCTCCCTGAG	ATCACCTAAA	GCCCGTAGGG	240
GCAAGGCTCG	CCGTAGAGCT	GCCAAGCTCC	AGTCATCCCA	AGAGCCTGAA	GCACCACCAC	300
CTCGGGATGT	GGCCCTTTTG	CAAGGGAGGG	CAAATGATT	GGTGAAGTAC	CTTTTGGCTA	360
AAGACCAGAC	GAAAACTCGA	G				381

(2) INFORMATION FOR SEQ ID NO:1047:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:

GAATTCGGCC TTCATGGCCT AGGGGTAGCC CTTGACCGCC TCCTGCTGGC ACAGGTCTTG	60
GTTCTTGTCT TTGACGCAGT CAACAGCGGC ACAGGCAATC TTTCGGTCAT CTTTGAAGGC	120
ATCAGCAGTA GCAGTAAAGT GCGGAATGAC CTTCTTACAG TGTGGGAACC AAGGGGCGTA	180
GAACATGACC AAGGTGTGTT TCTTCTTCTT CAGGGTCTCC CGGAAGTTGT CCCCCACCAG	240
GTGCAACACG CTTGTCTGCT GCTCTTCCCA CGTGGGCTCT GGGGGCGGGG GGCCTCAGG	300
GTCTTGCATC CACTCGAG	318

(2) INFORMATION FOR SEQ ID NO:1048:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:

GAATTCGGCC TTCATGGCCT AGCAAATTAT TCTTCAAAAT GATTATAACC AGTTGCACCC	60
TGTATTTCTT TTGCAGCCA GCACAATGTG ACCCAACTTA AAATTGCGG GAAAAAGAAT	120
GCAGGAGTGA AATAACCAAG TCAAAACCAT GTACTATCTC CTGGGGGTT AGGGATGCTA	180
AGAAGAGCCC ACAAAATAGAG GATTACTCTT CCCCTGAATC TCTAACTCA GAAACAATTA	240
CCAAAAATA CATAACTCTT CTTGTAGGG CCCTTTCCTT ATTCATTAG GTAGTGTGAA	300
CATTAAGTAT AAAATAAATT ATGTTCTTAA TGCCTCTTAA ACCACTTACA TTCAAAGGGG	360
AACAGAAATC ATTCTAAGCG GGAAAACTT CCACCTTTT TTTTTTCAA GTATCTCTCT	420
AATAACTAAA TGCCACTTAT TTGCATTCTC CTTGTGGATT TTTGTCAAC TAAGGAAATG	480
CATTTGATGA GTGCTGGAAA CTTCTTAAGT GCTTTACAGT TTGTTTTCAT TGTTCGAGC	540
GGATCACTGG ACATCAAAGA TTCATTGCAC TTATGAACAA GGAACCTCGA G	591

(2) INFORMATION FOR SEQ ID NO:1049:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:

GAATTCGGCC TTCATGGCCT AGGTTTCTTG GTGTTTTTGT TTTCTGGCAG GCAGTGAGAG	60
GAGGGGTGAA GGAGGAGTTT GGTGCCATTT CTCCTTCTGC TTTTCTCTCT TCTGATGTCA	120
AACAAATGAT GAAATCCTG CTATGGGAGC CCGGGAGCCT GGGGCCAGGC TGCTGGGGGG	180
ACGGTAGAGG GTGCTCTGCT GACTTGGGGG GTTAGGGGGG TTCTGGGGCG TTGGAGTCCG	240
ACTGGCCTTG GGCCGAAAGA GGCTGCCCTG CTGGGTGCTG GTGCTGTTGG TGACGGTGGT	300
GTGGTCTGGC TCACCCGAGT CGCTCTCCGT GTAGCTGTAG GCCTGTGCCC TCGAG	355

(2) INFORMATION FOR SEQ ID NO:1050:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 245 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:

GAATTCGGCC TTCATGGCCT AATGTGTTAG AAGACTCCCT CTACCTACCT GTTAAAAAAA	60
AAATGACTTT TTTTGCAATT TTTTGCTGTT TCCTTAAAC TAAAGCTGTG TTCTTCTGTT	120
TTGAAGGGTT TCCGCCCCA ACATATGTTA TCCCCCGCC TGTGGCATT TCTATGGGCT	180
CAGGTTACAC CTTCCAGCT GGTGTTTCTG TCCAGGAAC CTTTCTTCAG CCTACAGCTC	240
TCGAG	245

(2) INFORMATION FOR SEQ ID NO:1051:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 548 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:

AATTCGGCCT TCATGGCCTA GGGAGTTTGA GGGAGTTCTT TGGTATGCCC GCATCCCGGG	60
GTGTTTGCT GGTATTATCT GCCACATTAT CACCTTGTTA CGTTTATGGT ACCGGAGATT	120
GTAGGTAAAG TTTGTTTATG CTTCCACGA CTTCCCTCTG TGGGTCCGG ATGGTTTGTA	180
ATTGGGGTTT GCTTTATAGC AGCGAGGCT GATAGGTAAA GTCTGCTGGC TCACTGTGG	240
CGCCTAGATA AGGCCTTAGA AATGTAAAAA GGCTTGGGGC AGCATGGAGA GGAGTTGCAG	300
AGTGGGGAGG GGCAGGCAGC ACCAAGAAGC TTCTTGAGGC AGTTTGTCCC TAACAGATTT	360
ATTTTCGAA AGGAATTCTG AACTCTGAGA CCAATCAGT ATATTGTGT ATATTTTTC	420
ATATACTTCC AAAGTCTTT AATTCTTAAT TAACCTGATA TTAAAGTGAA AAGGGTTTAC	480
TCATTATCCT AGTTAATTAC ATATTCCATT TGTTAATGAA ACTATCCTTT GCTCACTGCA	540
TACTCGAG	548

(2) INFORMATION FOR SEQ ID NO:1052:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:

GAATTCGGCC TTCATGGCCT ACATAATACT TGCTGCTCTT GGGGTTGAAG CCGTTGTTAT	60
TTTCTTAGGA GTTAAGTTGC TTCCAAAAA GATTGGCGAG CGTGCTATTC TACTGGGAGG	120
ACTCATCGTT GTATGGGTG GCTTCTTTAT CTGTGTACCT TGGGGAATC AATTTCCCAA	180
AATACAGTGG GAAGATTGTC ACAATAATTC AATCCCTAAT ACCACATTG GGGAAATTAT	240
TATTGGTCTT TGAAGTCTC CAATGGAAGA TGACAATGAA AGACCAACTG GTATGCTCGA	300
G	301

(2) INFORMATION FOR SEQ ID NO:1053:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 642 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:

```

CGGAGGCCCT GAATGCCCCA TGCGCACCCC ACAGCTCGCG CTCCTGCAAG TGTTCTTTCT      60
GGTGTTCCCC GATGGCGTCC GGCCTCAGCC CTCTTCCTCC CCATCAGGGG CAGTGCCCCAC      120
GTCTTTGGAG CTGCAGCGAG GGACGGATGG CGGAACCTCC AGTCCCCTTC AGAGGCGACT      180
GCAACTCGCC CGGCCGTGCC TGGACTCCCT ACAGTGGTCC TACTCTCGT GACTCCCTCG      240
GGCCCTGGGA ATAGGACTGT GGACCTCTTC CCAGTCTTAC CGATCTGTGT CTGTGACTTG      300
ACTCCTGGAG CCTGCGATAT AAATTGCTGC TCGACAGGG ACTGCTATCT TCTCCATCCG      360
AGGACAGTTT TCTCCTTCTG CCTTCCAGGC AGCGTAAGGT CTTCAAGCTG GGTTTGTGTA      420
GACAACTCTG TTATCTTCAG GAGTAATTCC CCGTTTCCTT CAAGAGTTTT CATGGATTCT      480
AATGGAATCA GGCAGTTTGT TGTCCATGTG AACAACTCAA ACTTAACTA TTTCCAGAAG      540
CTTCAAAAGG TCAANGCAAC CAACTTCCAG GCCCTGGTTG CAGAGTTTGG AGGCGAATCA      600
TTCATTCAA CATTCCAAAC ACAATCACCA CCACTCCTCG AG                                642

```

(2) INFORMATION FOR SEQ ID NO:1054:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 496 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:

```

GAATTCGGCC TTCATGGCCT ACCTGTGAGT ACCTGGATGA AGCATACCCA GGGAAGAAGC      60
TGTTGCCGGA TGACCCCTAT GAGAAAGCTT GCCAGAAGAT GATCTTAGAG TTGTTTCTA      120
AGGTGCCATC CTTGGTAGGA AGCTTTATTA GAAGCCAAAA TAAAGAAGAC TATGCTGGCC      180
TAAAGAAGA ATTTCTGTA GAATTTACCA AGCTAGAGGA GGTTCTGACT AATAAGAAGA      240
CGACCTTCTT TGGTGGCAAT TCTATCTCTA TGATTGATTA CCTCATCTGG CCCTGTTTGT      300
AACGGCTGGA AGCAATGAAG TTAAATGAGT GTGTAGACCA CACTCCAAAA CTGAAACTGT      360
GGATGGCAGC CATGAAGGAA GATCCACAG TCTCAGCCCT GCTTACTAGT GAGAAAGACT      420
GGCAAGGTTT CCTAGAGCTC TACTTACAGA ACAGCCCTGA GGTCTGTGAC TATGGGCTCT      480
GAAGGGGACA CTCGAG                                496

```

(2) INFORMATION FOR SEQ ID NO:1055:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:

```

GAATTCGGCC TTCATGGCCT AATGTGCTTA ACCCTCAAGA AATTGTCACA ACTGAAAGAC      60
GGGAGCAAGC TGACACTGCA AGGAACACAT GATGCTTTGG AATGGGTGGC CTGCGTATTC      120
AAACACATCA AAGCAGCAGT TACTTGAACA ATCGGAACCTT CTTCAAATAC TGGCCCACTT      180

```

CTTCCTTGGG GTAGGGCCGG AGAGCAATAC AAGTGGCGAT ATTCTCTGGT TGCTCAAGCC	240
ACAGCATGTG GTCAATGTTT TTCTGTTGCA GGGTCTCGGC CAGCTCCTTT AGGGTGGTCT	300
CATCTGGGGC CTCGAG	316

(2) INFORMATION FOR SEQ ID NO:1056:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:

CGGGTTAAGG TAGCATCAGA ACCCTGGACG CGGAGTCAGG GCTGGCAGAT AGCAAGGCAT	60
CTCTCGGAGC GTTCTTGGGA GGCGCCATCT TGCCCGACTC CATGTTATCC AGCCACTCGT	120
CATCCCGCGG AGACAGAGGA GAGAGGAGAG CTCGCGGGGA AGCAGAATTC CCAACCGTTC	180
CATCCAACAA TGGAAATCGT ATCAGGATGT GGTTAGCTCC CTGTACCAGC GAGTGTACAG	240
TCAGAGACTG GCCAGTCCCC TTGTTACAAA CACTGTAGAA GAATGTGACA GCAGCTGCTG	300
TGGCCAGTAG ATTGTCTACC TGTAGTTGCA GAGAAGCCCA AGAGTTTGAT GATGAGGCAG	360
TTCTCTGAG	369

(2) INFORMATION FOR SEQ ID NO:1057:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:

GAATTCGGCC TTCATGGCGT ATCTCATTCT GTCTCCCAGG CTGGAGTGCA GAGAAACAAT	60
CTTGGCTCCT GCAGCCTCAA CCTCCCAGGG TCAAGTGATC TTGTTGCCTC AGCTTCCCCT	120
ACAGCTGAAA GCACAGGTGC ATGCCACCAC ACTTGGCTAA TTTGTATTT TTTGTGGAGA	180
TAGGATCTCT CTATGTTGTC TAGGCTGGTC TTGAACTCC CTGACCCCGT GATCCACCTG	240
CCTCGGCTC CCGAAGTACT GGGATTATAC GCATGAGCCA CCGTGCCAG CCGTCATTCT	300
TATATTATTA TTTCCTAGGT GTCTCTCCTG AAGACTATCT TCTGGTCTCG AAATGGACAT	360
GATGGATCCA CGGATGTACA GCAGAGAGCC TGGAGGTCCA ACCGCCGTAG ACAGGAAGGT	420
ATGGCTCTGT TGGAAATCCG ATAGTGTGGA AATGAGTTG CCCTGGAAAG GGAAAGAACA	480
GCTTCTTGCC CTCAGGTTTC TCACCTTCTC CTCTCCTCAC TCTACCAAG GACCCTCGAG	540

(2) INFORMATION FOR SEQ ID NO:1058:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:

GAATTCGGCC TTTATGCNAN NTTCTTTCA AAAAAAAAAA AGAAAAGAAA TTGCAAAAGT	60
------------------------------------------------------------------	----

TCTTCTAAAG TTAAATCCAA GGTGGTTTGT CTAGCAGAGA GCCAGGAATT CTTTCTAATA	120
GTGGGCAGAG CCCAGAGACA AGGGGAAGAA AGATGACCTT CTCCCCAGTC CTTCCCAGCA	180
CCATTTTGTG TTCACACCAG GCTTGTGGCA TTTTGGTGCT CACAGGGGTT TTGCCTTCTG	240
ACCTCTCCTT GGAGTAGGCC ATTCTCATGC AGGGCTCACC CTGAGGCAGG AGGACCAAGG	300
GCTCCCTGCG TCCACGGACC ACGTATGCCT TGGTGGTCAC TCCCATCGGG GCTATCAGTT	360
CTGCACTGTG CCCTGGTGCG GATTTTAATG CATATTTTTA TATATAAATG TTCCCAAAGG	420
CCGTCTCGAG	430

(2) INFORMATION FOR SEQ ID NO:1059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:

GAATTCGGCC TTCATGGCCT AACATTAAGG AAAAAGCCTT AATGGCCATG AATAACCTGA	60
GTGAGAATTA TGAAAATCAG GGCCGGCTTC AGGTGTACAT GAATAAAGTG ATGGATGATA	120
TCATGGCCTC TAACCTGAAC TCAGCAGTTC AAGTAGTTGG ACTAAAATTT CTAACAAACA	180
TGACTATTAC TAATGACTAC CAACACCTGC TTGTCAATTC CATTGCAAAC TTTTCCGTT	240
TGCTATCTCA GGGAGGTGGA AAAATCAAGG TTGAGATTTT GAAAATCCTT TCGAATTTTG	300
CTGAAAATCC AGATATGTTG AAGAACTTC TCAGTACCCA AGTGCCAGCA TCATTAGTT	360
CCCTCTATAA TTCTTACGTG GAATCAGAAA TCCTTATTAA TGCCCTTACT CTATTTGAGA	420
TTATCTATGA CAATCTCAGA GCAGAAGTGG CCTCGAG	457

(2) INFORMATION FOR SEQ ID NO:1060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:

GAATTCGGCC TTCATGGCCT ACAACCCGCG GATAACCACT GCCGAATGCC TGAAGGCGCT	60
TGAGCACGTG TTTGGGAGCG TTGAGAGCTC TACGGATGCC CCGATCAAAT TTCTGAACAC	120
TTATCAGAAC CCGGGAGAAA AATTGTCTGC TTATGTCATT CGTCTGGAGC CTCTGCTACA	180
GAAGGTGGTA GAGAAGGGGG CCATTGATAA AGATAATGTG AACCAGGCCC GCCTAGAGCA	240
GGTCATTGCC GGGGCCAACC ACAGCGGGGC CATCCGAAGG CAGCTGTGGC TTACCGGGGC	300
TGGGGAAGGG CCAGCCCCAA ACCTCTTTCA GTTGCTGGTG CAGATCCGTG AGGAGGAACC	360
CAAGGAGGAG GAGGAGGAGG CTGAGCCAC CTTCTGCAG TTCGGCCTGG AAGGGCACTT	420
CTGAGTGCCA GGAAAGGCAG CTTTAGTGCA GACCTAGATC ACAGCTACCT CGAG	474

(2) INFORMATION FOR SEQ ID NO:1061:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1061:

GAATTCGGCC TTCATGGCCT ACCAGCCTCT GTTAGATATG TCCAGAGATG GAAACTCACT	60
CCCCTACAAA AGATGGAGCT TAATGGAGAA ATTGCAACTT TCATTAAAAA ACAAAATTCAG	120
ATGAAATATC AGTAACTGTC TTGGACAGTG CTGAAATCAG GTGGTTAAAC GGGTAAACAA	180
AATATACTGT ATTTTGAGAA ATGGCACAAA AACAGGCAGT CATCTTTAAT GGCTATGCCT	240
AGGCCAACTA CTAACATGCA TTGTGAGAAT GCCGTGTATA CCTCACGTAC TGTGTACTTT	300
GTACATATAT TTTACCTTTT ATACCTATGT TCGATTTTGT TTTGTTTTGT CCTGGCGTCC	360
TCGAG	365

(2) INFORMATION FOR SEQ ID NO:1062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:

GAATTCGGCC TTCATGGCCT AGGAGCCGCA GGGCCGTAGG CAGCCATGGC GCCCAGCCGG	60
AATGGCATGG TCTTGAAGCC CCGCGTCGGG TCCCATCCGG CCCATCGTGC GCTGCCCCAC	120
GGTTCGGTAC CACACGAAGG TGGCGCCCGG CCGCGGCTTC AGCCTGGAGG AGCTCAGGGT	180
GGCCGGCATT CACAAGAAGG TGGCCCGGAC CATCGGCATT TCTGTGGATC CGAGGAGCGG	240
GAACAAGTCC ACGGAGTCCC TGCAGGCCAA CGTGCAGCGG CTGAAGGAGT ACCGCTCCAA	300
ACTCATCCTC TTCCCCAGGA AGCCCTCGGC CCCCAAGAAG GGAGACAGTT CTGCTGAAGA	360
ACTGAAACTG GCCACCCAGC TGACCGGACC GGTTCATGCC GTCCGGAACG TCTATAAGAA	420
GGAGAAAGCT CGAG	434

(2) INFORMATION FOR SEQ ID NO:1063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:

GAATTCGGCC TTCATGGCCT ACTTAATTTC AGAGCCGGGT TCGCCGTCGG ATCAACCTCC	60
AGGAGCTAGC AGCGGGCGCG GACCGGGCAG TTTCGCGCT CAGCACAGGC AGCTCGCGGT	120
CATGGGCGGC TCAGCCTCCA GCCAGCTGGA CGAGGGCAAG TCGCCTTACA TCCGAGGGAA	180
AACTGAGGCT GCCATCAAAA ACTTCAGTCC TCACTACAGT CGTCAGTACT CTGTGGCTTT	240
CTGCAATCAC GTGCGCACTG AAGTAGAACA GCAAAGAGAT TTAACGTCAC AGTTTTTGAA	300
GACCAAGCCA CCATTGGCGC CTGGAATAT TTTGTATGAA GCAGAGCTAT CACAATTTTC	360
TGAAGACATA AAGAAGTGGA AGGAGAGATA CGTTGTAGTT AAAAATGATT ATGCTGGGGA	420
GAGCTCGAG	429

(2) INFORMATION FOR SEQ ID NO:1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:

```
GAATTCGGCC TTCATGGCTT AGTCTTGGTC ATGCCTGGGG AGCTCAGAAC GCCCGGGCTT    60
GGGCCCCCAGG CCCATGGACT CCCTTCCCCA TTCTGCCCTC CCATATTCCC CTTTTTGGT    120
CCCAGACACC AGCACAAAGA AAGGAGGGTT CACAGAGGAA GGCCAGGGCA GAGCCTGGCC    180
CCAGGGAGGG GATGAGGACA TTTCCGGTCC AGGTAGCTGC CGGCTGCTCT GGGAGGAAGA    240
GCCATGCGTC TGTAACTGC TGGGGCTGGC GGCCCCCCCC ACTGCAGGGC CCAGCCTTGA    300
CCCCTGCACG TGGCCATCCA GCTGCCCTCT GGCTGCCCCCT GGCCTTGGCA CAGGCATCGA    360
GCCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:1065:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:

```
GAATTCGGCC TTCATGGCCT AAGATGGTTG CCAAGCAAGG AAAACTTATT TTATATTTTT    60
ATACTGTATC CAGGCTATGC CTGGGTGTGG AGGGCTTACT CGAG                      104
```

(2) INFORMATION FOR SEQ ID NO:1066:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 0 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:

(2) INFORMATION FOR SEQ ID NO:1067:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:

```
GAATTCCTGG CCTTTGGGAA CTCATATCCT GACCTCAGAT TGAGAAGACC ATCTGTCAAG    60
GCATATTAGT AATCACCTCC GGTAGAAAAG ATTTACGGG TAACAAGTAG GCCATGAAGG    120
TCGAG
```

(2) INFORMATION FOR SEQ ID NO:1068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:

```

GAATTCGGCC AAAGAGGCCT AAGTTCAAAT AATTCAGAA TGGTGTCTGT TAGGAATGGT      60
CCAGAGGTTG GTTGGGGGAT GAAAGGAGGA CAGGGACTAC AAGGGATATT GCAAATGACT      120
GCCTTAAAT ACCAACATAA AGCAGTGGAT TCCAGAGTC CTCCAATCTG TTATCAGACA      180
CAAAGATTTG AACAAAAATA AATGAAAGAT AGAAATCAAA AGGTTTTCTT TGAAGTCTCA      240
GGGTATTGTT CTTCTGAAAG CAAATGTGTT GTTCTTGCCT CATAGCAAAG TACTTTTCCT      300
ATTGATGCAT CACTTTATTG CTTTCTGTC TTCTCTCGAG      340

```

(2) INFORMATION FOR SEQ ID NO:1069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:

```

GAATTCGGCC AAAGAGGCCT AGACGGGACC TGTTGCAGA CAAGATGCAA GGAACACAGC      60
CTGCAGTGAT TCACAGCTTT GTTCAACCC ACAACCAGA AAATTAGCTC TTGGGTCTGT      120
GGGCCCAAAG TGAACCTTAA AGCAATAAAG ACTGGAAGCA GGTCTGGGAA GGCAATACAA      180
AATGTGGAGA GTTGAAAAGG AGGCAGAGCT GGCAGGAATG GGTAGGGAGA GTGTTTGGTA      240
AATAGCACCT TTGAGTCAAA ATTGAGCAGT TTAGAAATCC AGGAAAGGGG ACTGGCTGTG      300
GGGAGGAGAA CCTGGGGGTA GAGGAAGTGG GGTGAAGATT CCTCACTAAG GGGCAACAGC      360
AGGAGGGTGG CCATCCTGGC CAAATGCCCT AGCCCTGTCC TTCTTAAGGT GATTCGGTTT      420
GGGAAACTCG AG      432

```

(2) INFORMATION FOR SEQ ID NO:1070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:

```

GAATTCGGCC AAAGAGGCCT ATTCTAGACC TGCACAAGCA CGCTGAGGAG AAATTCATTG      60
AATTTGAAGA CTCTCAAGAA CAGGAAAAAA AGGACTTACA GACCCGAGTG GAATCTTTAG      120
AATCTCAAC AAGACAACCT GAGCTGAAAG CGAAAACTA TGCTGACCAG ATTAGCAGAC      180
TTGAAGAAAG AGAAGCAGAA CTGAAGAAGG AATATAATGC ATTACATCAA AGACACACTG      240
AGATGATCCA TAATTATATG GAACATTTAG AAAGAACAAA ACTTCATCAG CTCTCAGGGA      300
GTGATCAACT AGAATCCACA GTCATAGTA GAATTAGAAA AGAAGCCCT CGAG      354

```

(2) INFORMATION FOR SEQ ID NO:1071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1071:

```

GAATTCGGCC AAAGAGGCCT ATTCTGTCTT ATCAAAGGAA GTAAAGAAGT AAAAACAAAA      60
AATGAACGTA TACAAGCACA GATTTTGTAG CTTGATTGT AGAGAAATGG TAGTTATGTG      120
GCTTGCCAAG AAAGTGCATC ACCTACTTCT GCTTCTGGGG ACAGAGGTGA AGGGGTCTGT      180
TCTGGAACCT TCTAAGGAGG CCATCTTCGT TATTACATCA GGGAAAGTTC TAGTCAAAAT      240
GTTATTCCTG TCTACAGGGA AAAACAAAAG CAAAACACAA AAGAACACTG CTTCTAATGG      300
CATCATAGCA AGGAGTTTAT CTAGAAAGAT GATGCCAGCA GTCACCTCTT TTCCAGGAAG      360
ACAGAAACAA AAACCGTTCT CCTCGAG                                     387

```

(2) INFORMATION FOR SEQ ID NO:1072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

```

GAATTCGGCC AAAGAGGCCT AGAAAGTGCC AAGAGGGAAA AAAGGCACTC TGAGAAGTTA      60
CGGCAAAGAA TTGGGAAAGT TOTCAAACA AACAAACAAA AAATAATAGA TTTGTTTTAG      120
CAAACGACTT GGCTAAAAGT TACAAACCTA ATATATGTAA TACACAAGAC TACTTCATCA      180
TCTTCTTTTC TGACAGTCTC ATGTTCTTTT TCAAGCCAAA AAGGGACATA TTCTTATAGC      240
TGGAAGTTTA AGGGAAGAC TTCCAACCTA ACTCTGTGTT GAGGGTCAA ATCATGTGAT      300
GAAGGCTCGA G                                     311

```

(2) INFORMATION FOR SEQ ID NO:1073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:

```

GAATTCGGCC AAAGAGGCCT ACGAAGAAAA AATATTTTGT AGAGAATTTC CCAGATTGAA      60
AGAAGATCTG AAAGGGAACA TTGACAAGCT CCGTGCCCTC GCAGACGATA TTGACAAAAC      120
CCACAAGAAA TTCACCAAGG CTAACATGGT GGCCACCTCT ACTGCTGTCA TCTCTGGAGT      180
GATGAGCCTC CTGGGTTTAG CCCTTGCCCC AGCAACAGGA GGAGGAAGCC TGCTGCTCTC      240
CACCGCTGGT CAAGGTTTGG CAACAGCAGC TGGGGTCACC AGCATCGTGA GTGGTACGTT      300
GGAACGCTCC AAAAATAAAG AAGCCCAAGC ACGGGCGGAA GACATACTGC CCCCCATGAC      360
CCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:

```

GCTTTATCTA TTTCATTTAA TCTAAATGTT TTCTGCAATT GTTTTCCTT TAAACTTTGC      60
TTCAAAAACCT CTTTCATCTAC TTGAGATCTG GGCATTGTGG TTTTGGTCT CGCATTTTCC      120
CTGCCCTTCTG ATGGCTTAGC AGGGGACCCT TTCTTCTTTG GCTGGTGGGG CTCTCTGGA      180
TCAGTAATGT CCACATGCGG CTTCTGCAGC AAGGTTTTCT CTTTGTCTGA TACTGTAACT      240
CGGGGGGCTC TGTTTTCAA GGAATGAGAG GCCTCTGGTT TTCGAAGCCC CCCTCTGCCT      300
TTGCTCACCA CTCGAG                                     316

```

(2) INFORMATION FOR SEQ ID NO:1075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:

```

GAATTCGGCC AAAGAGGCNT AGAACTCGGA GACCAGAAAG TGAACCTCTG GGCAGAGATG      60
GNCCTGCAGA GCCAGGTGTG GTCTCTGGCC ACACCCATGC CCATGGCGGA GAGCTCCNTC      120
TACCGGCAGC GGCTAGAAGT CATCGCTGTA AGTGAAGCCC TCCCGGCGCC CTGGGCACCC      180
CCAAACTTTC CACCATGCTC CTTCTCTGTC TCTCGTCAT CTCTGCGGAG AGCGCCCTCA      240
GCTCCAGCCC CGCCAGGGC TCCCAACACC AATTCTCCAG CCCCCTCTGC CCCCAGTTC      300
CTGTCTGGTC ACTACACCCC TCAGAATGGG GAGCTGTGGC CCCCACACTT CCAGAGCCTG      360
CATCGGCTAT GCCTCATTCC TGAACCCAG CCTCCCAAAA ACCCATGCC TGAGCCGCAT      420
CTCCCGGACC TOGAG                                     435

```

(2) INFORMATION FOR SEQ ID NO:1076:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076:

```

GGAATTGGGC CAAAGAGGCC TAGTGGGAAA AGCTTGGATT ATCAAAACAC ACAACAAATG      60
ATAGAACCAG ATATATAGAT GATACAGTGA AGCACAAGGT CAAAATTTTA AAACGGGTGA      120
GCTCTTCATT AATGCATTAT TTTGTTTATT TAAGAGCTTT TTGTATGGAC TGACTGCAAT      180
AATTTTGAAA TTTCTCTTTA GAAGTTTTAA TGTTCTTTTA CATTTTCAA TTTAGTTTTT      240
CATGAAAGTG AATAGGTTTT TATTAAAAAT TTTTGTGTCG TCTTGGTGAA ATCAGATGGT      300
GACTCTCGAG                                     310

```

(2) INFORMATION FOR SEQ ID NO:1077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:

GAATTGGGCC	AAAGAGGCCT	AGGAAAACAA	ATGGCTTCTT	CAAGTCCTTG	ATTTTGGAT	60
ACACAGGATG	CAGGGCTGTG	TGTAAGGAAA	GGCAGCGTTT	TCCTCTCTTA	GAGCCTCTGA	120
CTGACCTGAG	GCGCAGGTGT	TCCTGGGAGA	CTGGAGGGTG	GGCTCCATGG	GGGTGTCTGG	180
GCCCCACCTG	GCAGGGCTCT	TGGCAGTGAG	CCAGTGGAGG	TTGCCTCCCA	CGTGTGGCTG	240
GCCCTGTAGC	CTGGCTCTGG	AGAACCTGCA	ATTCAGGCTG	GAAGAGACTT	TGGAGCAGCT	300
GGAGTGTGAG	GTCTGCCTGG	GTCTGGTGGG	GAGTGTTTT	ACTTTGCCAG	TGATAGACTG	360
AAATGCCCTC	TTTGAGGACA	AGGTGGCTAT	CTCGAG			396

(2) INFORMATION FOR SEQ ID NO:1078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:

AGTGTTTTCC	TGTATTTTCA	CATATTCCTT	GAAACTCTGC	TGAAAGGAGG	CTGTCAGTCA	60
GGGTTGTATA	AATAGAGTCC	TGGGTAAATC	CTTGAAGCTT	GTCATTCCAC	AGCAAATCCA	120
CATGTTTCTT	CAATGGCTGT	TAGCAGCTTT	TCATATAGCT	TTTCATAGCT	TTCATAGGGT	180
GGAAATGTCTA	TTGATTGAA	GCAAGTGTGG	GCTTTCCGCA	GGTTGTTAGT	GCAGGCATCA	240
ATCTGGTGTA	TGTAAGAG	TCTCGGGCCT	GCAGCACCTT	GCAATGCTTT	GAAGCCCTGC	300
AGAGGCACTC	GAG					313

(2) INFORMATION FOR SEQ ID NO:1079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1079:

GAATTCGGCC	TTCATGGCCT	AAAAATGAAC	TATAATAGTT	CTAATTTACC	TCAAGTTTTT	60
CTAAGATAGC	AAATAAATTG	TAGTGTGACA	TTAGCTTCCT	AAGTAAGGCA	AATTGACCTG	120
CAATAAAGG	TTCTAGTGTG	AGACAAATTA	AACCTTCAAC	TTCCAACCTC	GATTTCTAAT	180
ATAATTCAAA	TTGTCACTGA	AGCTTTTATT	AAGAATAAAA	ATATATTAG	TCTTTATTAT	240
TTTCTGTAAA	TGACTTATTT	TCAGATGCAC	AATCGTGAAA	TAATGAAGAT	TTTGATCAGT	300
TGTTTTTGTC	TTTTTCCTTT	GAAAGGTATT	TTGCAAGAC	CATTAAACT	CGAG	354

(2) INFORMATION FOR SEQ ID NO:1080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 641 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:

GAATTCGGCC	TTCATGGCCT	ACTCCGGTGG	CTCCCCCATC	TCTCAGGCGC	GATGGCTACG	60
GGCGCGGATG	TACGGGACAT	TCTAGAACTC	GGGGGTCCAG	AAGGGGATGC	AGCCTCTGGG	120
ACCATCAGCA	AGAAGGACAT	TATCAACCCG	GACAAGGAAA	AATCCAAGAA	GTCCTCTGAG	180
ACACTGACTT	TCAAGAGGCC	CGAGGGCATG	CACCGGGAAG	TCTATGCCTT	GCTCTACTCT	240
GACAAGAAGG	ATGCACCCCC	ACTGCTACCC	AGTGACACTG	GCCAGGGATA	CCGTACAGTG	300
AAGGCCAAGT	TGGGCTCCAA	GAAGGTGCGG	CCTTGGAAGT	GGATGCCATT	CACCAACCCG	360
GCCCGCAAGG	ACGGAGCAAT	GTCTTCCAC	TGGCGACGTG	CAGCGGAGGA	GGGCAAGGAC	420
TACCCCTTTG	CCAGGTTCAA	TAAGACTGTG	CAGGTGCCTG	TGTACTCGGA	GCAGGAGTAC	480
CAGCTTTATC	TCCACGATGA	TGCTTGGA	ACTGAGCAAAA	CTGACCACCT	CTTTGACCTC	540
AGCCGCGGCT	TTGACCTGCG	TTTGTGTTT	ATCCATGACC	GGTATGACCA	CCAGCAGTTC	600
AAGAAGCGTT	CTGTGGAAGA	CCTGAAGGAG	CACTGCTCGA	G		641

(2) INFORMATION FOR SEQ ID NO:1081:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:

GAATTCGGCC	TTCATGGCCT	AGCCCTTTTT	GGTTTTCTAA	TTAGGAATAT	AGCATCTGCA	60
AATAATGACA	GATTGTTTCT	TCTTTTCTAA	TTCTTACAAC	TTTTGTTACT	TTTTCTTGTC	120
TAATATGCTG	CCTAGAACTG	TAGAGCTTCC	TGCTCTTGTT	CCTCCCTTTT	TTTTATTCTT	180
ATTTTTAGGA	GCAACCCTAT	TAAGTAAGCC	TCACTCTTAA	AGGGGAAGTT	TTCACCACTA	240
AGTACCTTTC	TAATCTAGGT	TTTTTGTGGA	TACCTTTTAT	CAGACTAATG	AAGTTTAATA	300
TTGTTAAATA	CTTTGAATTG	TCTATATTAT	GATGATAGTA	TGCTTTTTTC	TTTTATTAT	360
TAAATGGTC	CCAGGAATTT	GTGAACAGCT	TGGGCAATAC	AGTGTGACGC	TCCGAG	415

(2) INFORMATION FOR SEQ ID NO:1082:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 496 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:

GAATTCGGCC	TTCATGGATC	CTGATACCAA	ACTCATCGGA	AACATGGCAC	TGTTGCCTAT	60
CAGAAGTCAA	TTCAAAGGAC	CTGCCCCCAG	AGAGACAAAA	GATACAGATA	TTGTGGATGA	120
AGCCATCTAT	TACTTCAAGG	CCAATGTCTT	CTTCAAAAAC	TATGAAATTA	AGAATGAAGC	180
TGATAGGACC	TTGATATATA	TAAGCTCTTA	CATTCTGAA	TGTCTGAAGA	AACTGCAAAA	240
GTGCAATTCC	AAAAGCCAAG	GTGAGAAAGA	AATGTATACG	CTGGGAATCA	CTAATTTTCC	300
CATTCTGGA	GAGCCTGGTT	TTCCACTTAA	CGCAATTTAT	GCCAAACCTG	CAACAAACA	360

GGAAGATGAA GTGATGAGAG CCTATTTACA ACAGCTAAGG CAAGAGACTG GACTGAGACT 420
 TTGTGAGAAA GTTTTCGACC CTCAGAATGA TAAACCCAGC AAGTGGTGA CTTGCTTTGT 480
 GAAGAGACTA CTCGAG 496

(2) INFORMATION FOR SEQ ID NO:1083:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:

GAATTCGGCC TTCATGGCCT ATTCACAGGT TTATTGGCTT CTTCTTGAAA TGCCTGTTCA 60
 TGTCTTTTGG CCACTTTTTA TATGGGTCAT TTGTCCCTTA TTGATTATA AGGGTTCTTT 120
 ATTTTTTCC TAGATATTAA TAGTTTGGC CAGATGTTG CAGATGTCTT TTCTCAATAT 180
 GGCTTGCTT TTCAGTTTGG GTGTCTGAT GATCAGAAGA AGTTCTTCAT GTAGTTGATT 240
 TATTGACCTT TTCCATTATG GTTTTCACTC TTTGACTCTA GGAGCTTAAT AAAAGCATGA 300
 AATATTTATT GATTGTCCAT TGCTAATCCG AAAACCTCG AG 342

(2) INFORMATION FOR SEQ ID NO:1084:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:

GAATTCGGCC TTCATGGCCT AACCTACTGA ATGATAAAAC TTGCAGCTAA ATTTGTCTTC 60
 AACACACCTT TCTCAGAGCA TCAATTACAT TATTCATTAA GGAATAAATA GCATCTCTAA 120
 AGCATGTATC AACATCAGAA CTAAGCTTTA TGAATTATAC AGTGCATCTA GTGATTCCTT 180
 ATTCTAAAAG ATCTCTGGTG CCATCTACTG AATGCTTTTT AAAGGAAAAA ACATGAAATC 240
 AAATAATAGA TTTTCACTTA ATTCAATTTT TGTGTTTGT TTAATTTTCA ATTACTAGAC 300
 AGATCTAGGT TTATAAAGA ACTAACAGG AAGTACAGAA TTCCCATATA ATCACTTTTC 360
 CCCCAAGACT CGAG 374

(2) INFORMATION FOR SEQ ID NO:1085:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1085:

GAATTCGGCC TTCATGGCCT ACTGGAACAC CTTCTGCTG CCGCCATACC CTGCTTCTC 60
 CAGCGACAGC CGCCCGTTCA TGAGCTCGC CTCCTTCCTC GGCAGCCAGC CCTGCCCAGA 120
 CACCAGCTAT GCCCCGTGG CCACCGCTC CAGCTTGCCA CCAAAGACCT GCGACTTTGC 180
 TCAGGACTCC TCCTATTTG AGGACTTCTC CAACATCTCC ATCTTCTCCT CGTCGGTGA 240

CTCCCTGTCG GACATCGTGG ACACGCCCGA CTTCTGCGG GCTGACAGCC TCAACCAGGT 300
GTCCACCATC TGGGACGATA ACCCTGCCCC CTCACCTC GAG 343

(2) INFORMATION FOR SEQ ID NO:1086:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 531 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1086:

GAATTCGGCC TTCATGGCCT AGGGCTGACG CGCCACTATG TAGCGGGTTT CGGGCGGGCC 60
 ACGCGTGCGG GACAGGAACC CAACCCAGC CGACCTTGAG CTCCAGGAGT TCGTCTCTTA 120
 CGTCTGCGGA AGTGCAGCTG CCTCAGTTCT TAGCGCAGGT TGACAACTAC AGGCACAAGC 180
 CATTGAAGCT GGAATGTCTT GTTGCTGGTA TTTCAATTGA CTTAAGCCAA CTATCCCTTC 240
 AGTTACAATA GGAAGTGCC TCTAATAAGG CCAATATGC GTACTAACTT GTAGCAACCA 300
 CGTGTCGGT CAGTGCCACA GGAGCTAGAG CAGTGACAAT GCTGGTGGA ACAGGGCAGT 360
 GTAGCAGGTG CTTCATGTTC ACCTTTTCAA CCTTTTCATT TAATTGTAC AACTCGGAGG 420
 TGGATTCTGT TAGGGACAGG CTGCCCCAGG ACCACTCCGC CCCCCTAAC TCAATGCAGC 480
 TGACCCTTAC CCTGAATACT CTGCAGCTGC ATTCTGAA CATATCTCGA G 531

(2) INFORMATION FOR SEQ ID NO:1087:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

GAATTCGGCC TTCATGGCCT ATGACTAGCC ACCAGGAAGG ACATTCCTG CTCAGCTGTC 60
 CCATTAACT CACCTGCTCC TCTCCTCCAC GTTAGTTTTT TTCTAGCCTG TTTATTCCTC 120
 CCTGTAAGAG AAAAAGAGAA AAGCCTATTT CTATCTGATC TTTGAGATGC TTGCAGATCT 180
 TACCTTTGAA GCATTCTCCT TATTGCAATA GTCTCCCTGA CCCTATTGCA ATAGTTCTCT 240
 TCTCCCTGTT TGTATTCACC CATTGAGGCT GCTATATATA GCAAAATACC ATAAGCTGAT 300
 AGCTTATAGA CAATATAAAT TTAATTCCCA CAGTTCTGAA GCCCAGGAAG TCAAAGATCA 360
 AAGTAGGCCA TGAA 374

(2) INFORMATION FOR SEQ ID NO:1088:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 288 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:

GAATTCGGCC TTCATGGCCT AGGAATGTTT CCTTTTGGTT CATTGTAGGC ACATCTGAAA 60
 AAGAAGTTAT GAGTCACTCG TAGTGAGGTT TTAATTGACC TGTGACTTGG GATCTCTGGG 120

GATCATTGGC AGTCTGTCTT ACACTGTTAT TTATAATTCA TGTCTGATCA TCTTCTTAAG	180
GAAGTCTGCA TCGTTTGCTT TATGTAGAGC ATTAACACA AGGATCTGNC ACATTACTTC	240
TGTTGCCATT TTGCTTCTC ATATCCCTGA CCACCCACCA CACTCGAG	288

(2) INFORMATION FOR SEQ ID NO:1089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:

GAATTCGGCC TTCATGGCCT AAGTAGTTAA ACTCATAGAG TTGCAAACTA GAAAGGTGGC	60
CCCCAGGGGT GGGCAAGAGA GAGGAGTGGG GAGCTTGGTG AATGGGTGCC ATTTCCATT	120
TGAAAGATAA AACTGTTCCG GAGACGATGA CGGTGATGGT TGCTAAACAA TGTGAACGTA	180
CTTAATGTCA TGAACTGTA AACTGAAAAA CAGTGGAAAT TGTAATGTT TATACTGGCC	240
ATTCTATATG AACTAATATA TATTATAAT TTTTAATATT TATACATGGT ATATTTTCCC	300
ACAATAAAGA TGAAATTAA AGCAGTTGGT CTCGAG	336

(2) INFORMATION FOR SEQ ID NO:1090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:

GAATTCGGCC TTCATGCCTA CAGAGGGGAA AGGAGAGTCC AGTGAGAAAC CAGCCATTGT	60
CTTCATGTAC AGGTGCGACC CTGCTCAAGG CCAGCTCAGT GTGGATCAGA GCAAGGCTAG	120
GACAGACCAG GCAGCAGTCA TGGAGAAGGG TAGAGCAGAG AATGCATTAC TACAGGACTC	180
AGAGAAGAAG AGGAGTCATT CTCTCCATC ACAGATTCCT AAAAAGATTG TCAGTCACAT	240
GACCCATGAA GTAACAGAGG ATTTTCTCC TCGGGATCCA AGAACTGTTG TTGGGAAGCA	300
AGATGGCAAG GGCTGCACTT CAGTCACAAC AGCATTGTCC CTACCTGAAC TGGAAAGGGA	360
AGATGGAAAA GAAGACATTT CAGATCCTAT GGACCCGAAC CCTTGTTAGT CAACATACAG	420
CAACTTAGGG CAATCTAGAG CAGCCATGAT ACCTCCCAAG CAGCCACGAC AGCCCAAGGG	480
AGCTGTGGAC GATGCCATCG CCTTTGGAGG GAAAACAGAC CAAGAAGCAC CCAATGCTTC	540
CCAACCTACA CCACTCGAG	559

(2) INFORMATION FOR SEQ ID NO:1091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:

GAATTCGGCC TTCATGGCCT ATTCTTATGT GTGTTTCAGG ACGACTGGGT TTGGATTGAG	60
-------------------------------------------------------------------	----

AAGAGGATTA TTATACACCA CAAAAGGTAA AATCAGAAGC AACTTATTTT TAAAACCTAT	120
CTTAAGTCGC ACAGACTCCA TAATATGTCC TCTTTCCTTG GCTCTGTTGT ATCAAGGTGT	180
TTATTTCCGA AGTGTTCCT GTTTGGGAGA CTGACAATTT AGGATTCCTG ATTTAGCACC	240
CTGTGGTCTT GTCAATCTGAC CAAATCAGAG AAAATTGAGA AAGTGGATAC AGCGACTGTG	300
GACATTGTGA AGTCACATCT TACTCAGGGA TGACAGCTAA AATCAGCGTG TACAGCAGAA	360
AAGTCACATA TAGCTACAAA TACCCTGGAA AACTCGAG	398

(2) INFORMATION FOR SEQ ID NO:1092:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:

GAATTCGGCC TTCATGGCCT ACGAGTTTTC TGCAAGTCAG CCATGAAGTC TATGCTCTGC	60
TTCAGGCTCT GAATTCCTTC CTGGCTAAGA ATTTTCATTC CTGAGTGCAA CAGCTTCTTT	120
GCAGCTTTAT AATAAATGGT CTCTGGTTTA TTGTAAATCA TGGCATTAGT ACACATTAGT	180
TTGAAGTTAT CCTTTAGTTC TTCTATGGAC TGATAGTCAT TGTTCTTGAT CTTTCTTTT	240
ATGGTACTAA AATCCATGG GTGTTTAATG ATCATGGAGT AGCCAGGAGC AATAAAATCA	300
GTCACAGGAA ATGAAAAGAA AGCACTTGA TCTTTCTCT GCAATTGTCT CATCAGTTGA	360
TTCAAAGCTT CTGGAAGGGG TGTCTGTTCT ACTTCTTCTT GTTTGGCTAA AGAGCTTGTG	420
AGAGGCTTCG CTCGAG	436

(2) INFORMATION FOR SEQ ID NO:1093:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:

GGGGCAGGGA GCCTGGCCAG GCCTGAGACA CAGAGGCCCA CTGCGAGGGG GACAGTGGCG	60
GTGGGACTGA CCTGCTGACA GTCACCCTCC TTCTGCTGGG ATGAGGTCCA GGAGCCAAC	120
AAAACAATGG CAGAGGAGAC ATCTCTGGTG TTCCCACCAC CCTAGATGAA AATCCACAGC	180
ACAGACCTCT ACOGTGTTTC TCTTCCATCC CTAAACCACT TCCTTAAAT GTTTGGATT	240
GCAAGCCAAT TTGGGGCCTG TGGAGCCTGG GGTGGATAG GGCCATGGCT GGTCCCCAC	300
CATACCTCCC CTCCACATCA CTGACACAGC TGAGCTTGT ATCCATCTCC CCAAACCTTC	360
TCTTCTTTG TACTTCTGT CATCTCGAG	390

(2) INFORMATION FOR SEQ ID NO:1094:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 559 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

AATTCGGCCT TCATGGCCTA GAGGGATTG TTAACCAGTG CCACCATGTA GTTCTGGAAA	60
CGGAGGATGC GGTGGTAGAT GTCCAGTTCT GTCAGCTCAC GTTTGTGGAT GCAGATCTGG	120
TGCTCCTTCT GCGTCTGCAC GATCCGGGCC TGCACTTCTT GCCACGTGCA ATACGGAAGG	180
GCAGACATAG GGATGCGCAG AGCGTGCAGG TAGAAGGAGT GGATCTCCCA GTAGCAGCAA	240
ATGTTATAGA TGAAC TTGAT AAGCCGGTGG ATCCAGAAGA CACCAGCAAT GACCAGGATG	300
GTGATAAGGG AGCCATTTTC CTGAATCCTG GCACTACAGA CTTGAGCAGG CAAAAAGGCG	360
TCTGGCAGAG TGACCTTGAC GGGTTCAGTA GGGTGAAGAC TGTGGTTCAC CATCTTGTG	420
GCAAAATAGGA TGT CATAGTC CACGCAGCTG ACCAGGAAGG TAGTGAAGGC AACCACAAAG	480
AGGAACTGCA TGAGCTCAA GATCTCCCG ATGAGCATAC ATGTGAAGCC ATTCTTCTGG	540
TGCAGATTAT AAAC TCGAG	559

(2) INFORMATION FOR SEQ ID NO:1095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

GAATTCGGCC TTCATGGCCT AGGTTTGAA AGTAAGACAT ACTGGCTTCC TTTATTACAA	60
TTAGCATTTT CCTATTATT TGAACCAAC AATTCATGT TCATTGAATT TCCTTTTTTT	120
TTTTTTTTT AAAGACTGCA AATTTTGCT GGGCACAGTG GCTTGACTCT GTAATCCTAG	180
GTACTTAAGA GGCTAAAGCA TGAGGATCAC TTGAGGGACT CGAG	224

(2) INFORMATION FOR SEQ ID NO:1096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1096:

GAATTCGGCC TTCATGGCCT AGTTCTCTCT GATTGGTTT GTTCTGTCTC AGGCTTCTGT	60
GGCAGGACTG GCCCAGGGAG GAGGAAGCCA GCAGCACACC TGGGGAATGG GGTCCCGGCC	120
GGGAGGCTTG GCCTCTGGGC GACCTCGTCC TGT TTTGTTT GTTTGTTTGT TTGTTTTTTT	180
AAAGGTAAAC CTCCTGGGCC GCAGATGGCA AAGGGAGTGC CTGGGCCTGG TGACCCAGGG	240
CTGGATCCAC CCTGCGGAG CCTGGGCCA GGCAGGTGTC TGCTGCTCAC CTGGCTCTGG	300
AGGGCTGCCC TGCACTGGG CCTGGGACA GGTGGCTGT GGGGCAGCTC AGTACCCTCC	360
CTGAGGCTCA CGGTGGCTCC GAGCATGAGC TCTGCCTCCT GGGCGAGACC CAGCAGTGGA	420
CAGCAAGGTC CTCACACCCA GCTCCCTGCA CACCCAGGCC AGCCACCCCT CCCGCTCGTG	480
CACAGGCAGC CAGATGCGCT CACACGTACA CACACACAAA TGCAACGCCT CGAG	534

(2) INFORMATION FOR SEQ ID NO:1097:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1097:

GAATTCGGCC	TTCATGGCCT	ACTTTATTGG	TGGACATTAA	GAATGGAGGA	ATGTTTCAAC	60
AAAGGAACAA	TCAACAGTAT	CAAAATACTG	CAGAGGGGTC	AATTGGGGA	CTAAGAGGGG	120
AGCCACTGGA	TTTGACAACT	AGGAGATAAA	TTTGTAGTGA	ACGATGAAGG	CAGAATCCAG	180
AGTATAATGA	GCTCAGTGAA	AAAAGGTGAA	NACATGTAGC	TTATTCTCTC	AAGAAACTAG	240
GCTATGATAA	ACTGGCAGAG	GCTCTAAGAG	TGGGAGGTGA	GTTGTTTTCT	CCTTCATGTA	300
AATATATTTA	CCTTTTAAAC	ACTAGGCCCA	ATTTTATATC	CTATTTTCATT	TAACTTTTATG	360
AACATATTTA	TGTATGTATG	CATGTATGTA	TGTATCTCAT	GTGATGTTTT	AGACACTGAA	420
AAATAACTCA	TTTCTATTAT	AAAAGTGATA	TCTTTAGATG	TTTCAGAAGC	AACCTCCTAA	480
AAGGAGGTAG	CAGTAATGGA	GCTATGTCTA	TCATTCTTTC	CCATCAACCC	CCTTGATGGA	540
GATGTAAACA	TGTGTCCATC	AAGCCTTTAA	TTTTTACNTC	TTATCTTCAG	GGCTCTGCCG	600
CTCGAG						606

(2) INFORMATION FOR SEQ ID NO:1098:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:

GAATTCGGCC	TTCATGGCCT	AGCAGAACAT	GGATATTTTT	CCTTTAATAT	TTAGTACTTG	60
GGCTATCATG	AAACAAGGTT	AGCATAACCA	TCCAAAACCC	CAAGTGCTCC	AAAATCCAAA	120
ACTTTTTAAA	CACCAACACG	ATGCCCAAAG	TGGAAGATTC	CATACTTGAC	CTCATGTGAT	180
GGGTCTAAGT	CAAAATGTAG	GCAAACTTT	CACGCACAAA	ATTACTTAAA	ATATTCTACT	240
GAGCCAGGCA	TAGTGGTTCA	TGCCTATAAT	CCCAGCACTT	TGGGAGGCTG	AGATGCCAAT	300
TGCTCGAG						308

(2) INFORMATION FOR SEQ ID NO:1099:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:

GAATTCGGCC	TTCATGGATG	ACCGCAGCAG	GCTGGTCAAG	CAGATGGAGG	ACAAGGTGTC	60
TCAACTGGAG	ATGGAACCTG	AAGAAGAGAG	AAACAACTCA	GATTTGCTGT	CTGAGAGGAT	120
CAGTAGGAGC	AGGGAACAGA	TGGAGCAGTT	GAGGAATGAG	CTACTTCAGG	AGAGAGCTGC	180
GAGACAAGAC	TTGGAGTGCG	ACAAGATTTC	CCTGGAGAGG	CAGAACAAGG	ACTTAAAGAG	240
COGGATTATC	CACCTGGAAG	GTTCTTACAG	GTCCAGCAAA	GAGGGGCTGG	TTGTGCAGAT	300
GGAGGCCAGG	ATCGCGGAGC	TGGAGGACCG	CCTGGAGAGT	GAGGAGAGGG	ATCGGGCCAA	360
TCTTCAGCTC	AGCAACCGGC	GGCTGGAGCG	GAAAGTGAAG	GAGCTGGTGA	TGCAGGTGGA	420
TGATGAGCAC	CTGTCATTGA	CTGATCAGAA	GGACCAGCTG	AGCTTGCGTT	TGAAACCCCT	480
CGAG						484

(2) INFORMATION FOR SEQ ID NO:1100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:

GCAGATTGAG GACCTCCAGA AATCTTTACA GGAACAAGGT TCCAAGTCTG AAGGCGAAAG	60
TTCCAGCAA ATTAAAGCAG AAGTTGGAAG CTCATATGGA AAAACTCACA GAGGTCCATG	120
AAGAATTACA GAAGAAACAA GAACTCATTG AAGATCTTCA GCCAGATATA AATCAAAATG	180
TACAAAAGAT CAATGAACCT GAAGCTGCTC TTCAGAAGAA AGATGAAGAT ATGAAAGCAA	240
TGGAGGAAAG ATATAAAATG TACTTGGAGA AAGCCAGAAA TGTAATAAAA ACTTTGGATC	300
CCAAGTTAAA TCCAGCATCA GCTGAAATAA TGCTACTAAG AAAGCAGTTG GCAGAGAAAG	360
AGAGAAGAAT TGAGATTCTG GAGAGTGAAT GCAAAGTAGC AAAATTCCGT GATTATGAAG	420
AAAACTCGA G	431

(2) INFORMATION FOR SEQ ID NO:1101:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 557 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:

GAATTCGGCC TTCATGGCCT ACTGGGAATC TCTCAGCAGC TTTTGCCAA ACAGATGGGC	60
CAGGAGCCGC GGAACCAGGC TGAGGAATGT TGCCTCAOGA TCTCTCATAT CCATTCCTGG	120
CACCCACCAG CCCAGGGAAT GCCTCTACCA GTTGTCAGCG AGAGGCTTAC ACAGCATCTT	180
AAATAAAAGG GATTATTGAA CCAAGAGGCC AGGGACTGAT GGAAATGCCC ACCTTGCTGG	240
CTCATTGAAA AAGTTTGCA AGGTTGTCAG GAGACATGAA TTAGATGGGC TTGGGTCTTG	300
TGCCCTTTGC TAAACCAAGT GCTGTATTGG GAAAGAGACG GGGAGAGAAG TGTTGGAGAT	360
GCTCTTTAGT CAGGCCTGAG TCACTTGCCC AACCCTGGAG TTGGAGTTGG GGATGGAGCC	420
AGGATCTCCA AACCATATGC CCCTAGAGTT TCAGGGAAAA TATGGATTGT GAATTGAAGA	480
TGGGGGGTGA TGTAAGGCAG ACAAGGACAG AAAATCCCTC TTCCAGCTGT GATTTGCTG	540
TGAGTTTGGC GCTCGAG	557

(2) INFORMATION FOR SEQ ID NO:1102:

(1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 577 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:

GAATTCGGCC TTCATGGCCT AGTTTTTCTA GAGTGAATTA TAGTATTGAC GTGAATCCCA	60
CTGTGGTATA GATTCCATAA TATGCTTGAA TATTATGATA TAGCCATTGA ATAACATTGA	120
TTTCATTCTG TTAAATGAAT TTGGAAATAT GCACTGAAAG AAATGTAAAA CATTTAGAAT	180
AGCTCGTGTT ATGGAAAAAA GTGCACTGAA TTTATTAGAC AAACCTAOGA ATGCTTAACT	240
TCTTTACACA GCATAGGTGA AAATCATATT TGGGCTATTG TATACTATGA ACAATTGTGA	300
AATGTCTTAA TTTGATGTAA ATAACCTCTGA AACAGAGAA AATGTTTTTA ACTTAGAGTA	360
GCCCTAAAAT ATGGATGTGC TTATATAATC GCTTAGTTTT GGAACGTGAT CTGAGTAACA	420

GAGGACAGCT GTTTTTTAAC CCTCTTCTGC AAGTTTGTG ACCTACATGG GCTAATATGG	480
ATACTAAAA TACTACATTG ATCTAAGAAG AAAGTAGCCT TGTGGAGTAT ATAGATGCTT	540
TTCATTATAC ACACAAAAAT CCTGAGTGA CCTCGAG	577

(2) INFORMATION FOR SEQ ID NO:1103:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:

GAATTCGGCC TTCATGGCCT ACATGGACCT CTGACACAAG AACATGAAAC ACCTGTGGTT	60
CTTCCTCCTG CTGGTGGCAG CTCCCAGATG GGCCCTGTCC CAGGTGCAGC TGCAGGAGTC	120
GGGCCCAGGG CTGGTGAAGC CTTCGGAGAC CCTGTCCCTC ACCTGCACTG TCTCTGGTGC	180
CTCCATCAGT AGTGGTGGTT ACTACTGGAG TTGGATTCTG CACCACCCAG GGAAGGGACT	240
GGAGTGGATT GGGCGAATCT CTCACAGCGG GCACACCAAC TACGACCCCT CCCTCGAG	298

(2) INFORMATION FOR SEQ ID NO:1104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:

GAATTCGGCC AAAGAGGCCT AGTCATCTTC AATATCTCTC TCTCTCATCC CTTCAATAAA	60
TCATTCACCA AGTTTGTACA GTTTTCCTTT GCAATGTGTC TCCAAATGGT CATCCTCTTC	120
TCCTTTTCA GATTAGGATT CTGTCTTCT TACTCATTC GTAAAAACAAG TTTGGGAAAT	180
GCTAGTTACG CAGTTAATGG TGTAAGTACC GCAGGACTTG ACAAACCTC TAATGAAAGA	240
ATAAAACATT TGCTATATTT GTTTGATCAG AGAACTTTT TTCCATCTCA GGGGATCATT	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:1105:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 535 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:

GAATTCGGCC AAAGAGGCCT ATAGGCCTCT TTGGCCGTCT AAATGAAATG ATTGCACTGC	60
ACATACTTCT AAAACTGTCC TGCGATTGTA TAGCTTCCAT TTCATGGCGC TTCTTCTGGA	120
TGTCAGGCAC TAAGTCGGGC GCTTTATTCT GTAGTTCTCC TAGCAATCTG GTGAGCTCCA	180
CTCTACAGAT AAGGAAATCG AGGCCAAGGA CAGCTAAAGA AGCGAGGTGC GCAAGGTGCC	240
CAGGTCCGAA GTGTTTCCGC TGCTTTCAGA CTGCAGTCCC AGGGCTCAGG AGTCCATGCT	300
TTCTGCGTAT CTTACGCTG GCCACGGATC ACCTCATCAT TAGATGTGCA AGTTGAACAA	360

GTGGTGTTC	CATTCGGACG	TGTGTTAGGT	AGAAGTGTGT	GTGCACCTGC	GTGTGCGTGT	420
ATGTTCCACA	CGCTGATGCA	GGAGGTATAC	GCACAGATAT	AATTGTCTTT	TAGAAGATTG	480
ACTATCACTA	ATTTTGAAAA	ATTTCTGAA	TGACCTTTCC	GNCCCGGCGC	TCGAG	535

(2) INFORMATION FOR SEQ ID NO:1106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:

GAATTCGGCC	NAAGAGGCCT	AGAAAAAATT	AAAAAGGGAT	ACAGACGAGC	TGCNAGCTAT	60
GGACATAGA	TATTAACCCC	CAAAGAGTCN	TAACCACAGC	TGACTCTTAG	CTTCACAAGC	120
AGNCCTCNGA	ANGTGGTAGC	TTGTTTTAAG	CAGAGGCCAT	GCAGAACCCA	TGAAACCAAA	180
GGACAGAGCC	AGTAGGGCTG	GAGTCTGACC	AGAAAGTTCC	ATGCCCTCTG	CTTTCTGCAT	240
GGAAAATGAC	CTGGTAGGTT	TTAACCTATC	CAAGACTACA	GAGGATTTCA	GAATTTTCAGT	300
TTGAGGTATG	CCTCAAAACA	TTCCAGCCTT	GATCATGAAA	GAAAGAAGTG	ATCAAAATAC	360
CATATGTAC	AATGGAAGAC	CCAAGCGGCC	CCAGAGCTCT	TCTTCAGTAA	TGAGATTTAG	420
TTGATCTGNA	CAGTTATTTA	TGCATTGAGG	TCATATTTTG	GCCAATCTTT	TGCTTACAGC	480
TGTCGCCAAA	TAAAGCCTTC	TGNTTAGCA	TTCTTTTAC	CAAAATCAGG	TTGAGAGATG	540
GTTCTTTGAG	AGGACTGTTT	TGTCAGGGAA	TACAGGGAAT	CTCGAG		586

(2) INFORMATION FOR SEQ ID NO:1107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:

GAATTCGGCC	AAAGAGGCCT	AGGACTTAAA	AGAACAGCTA	GAAAAGATGA	AAGGTGACTT	60
AGAAAGTAAA	AATGAAGAAA	TACTACATCT	GAACCTTAAA	TTGGACATGC	AGAACAGCCA	120
GACTGCTGTC	AGCCTCAGAG	AACCTGAGGA	AGAGAACACG	AGCTTGAAGG	TCATATATAC	180
CAGAAGTTCT	GAGATTGAAG	AGCTGAAAGC	CACTATTGAA	AATCTGCAAG	AGAATCAGAA	240
ACGATTACAA	AAGGAGAAAG	CAGAGGAAAT	TGAACAACTC	CATGAAGTCA	TTGAGAAGCT	300
GCAGCAGGAG	CTGTCCCTCA	TGGGGCCTGT	GGTGACGAA	GTCAGCGACA	GTCAGGCTGG	360
CAGTCTGCAG	AGCGAGCTGC	TCTGCTCCCA	GGCAGGGGGC	CCTCGTGGGC	AGGCCCTACA	420
GGGCGAGCTC	GAG					433

(2) INFORMATION FOR SEQ ID NO:1108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:

GAATTCGGCC	AAAGAGGCCT	ACGTGAATAT	TTTTCCATCT	GTGTTTCATTG	ATGTTAACAA	60
TAAAAATCTT	GTTTATGTGT	ATAAGCCTAA	CATATGCCTG	TGGGTCTTAT	AACAGCCTGT	120
TCAAACCTCA	TGGGATACCA	AAAATGTATC	TGCTTACTTT	GGGGGTCTAA	CTTTAATTCG	180
GTACATATAA	ACATCTCTGG	AAAAAAATGT	AGTTTTTTTC	TTCCCCCTGC	TGTTTTCCCC	240
AGGCTTTCTC	CTTTGACCTG	GCCACGGTTC	CCATAGACTA	CAAGACGACT	TAGAGACATT	300
GCTGTGACAT	CTCGAG					316

(2) INFORMATION FOR SEQ ID NO:1109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:

GAATTCGGCC	AAAGAGGCCT	ACTAACATTT	TCCTAATCTT	ATGTGTTTGG	CTCCTCTCAT	60
TTACTCCCCA	CAGCAGCCAC	ATGAAGTTGG	AATTTGGAAC	TCTTATTTAG	GTATGCAAAA	120
GGGTACCACT	TCTCTTTAAG	GCTTTAGTTC	AGGAGTGGTG	TTAATGTATT	AATGTGTTGG	180
GGCGCGAGAG	GAAGCGGTG	CTTATTTGGA	ATCATGGTAG	GTAAAGATAA	TTTCAACTCT	240
GACACTTCCA	CTAATAAATT	TTCCATCTA	GGGAAAATGA	CGTAAGCTTC	CTAGATCACA	300
GATTTGTTTT	CATCCAAAAC	CCGAAGTCTG	GTTTTGAAAT	CACGCTCTTG	ATACAAAGGT	360
GGCTCGAG						368

(2) INFORMATION FOR SEQ ID NO:1110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:

GAATTCGGCC	AAAGAGGCCT	ATCCGGGGGG	AGTAAGGTGA	GGACAAGGAA	CAGAAAGGCG	60
TGAGGTGATG	GAAGGAAGTC	CGGGAGAACC	ATATGAAGGA	GCAGGAGGAG	AGGAAGAAAC	120
TTTTTTTCCT	TCTTTTCCAG	GAGTAGCTGG	AAATTAAGAT	CGGGTTCCTT	TTCTGCCAGC	180
TTGGAAGGGC	AACCCCATGA	CTGATTGCGA	TTCTGAGGAT	GTCTATGCAA	AGTTGGATTG	240
TTGTTACAGT	GTATCCAATC	TGAAGTATTG	CACATCTGAA	CTGGGACTGT	TAACACTGAT	300
GCCAATACAG	TGTGGGGTGC	CAGAAAGTGT	CTGCTGATAT	TTGTGAAAAA	AAAATCTATT	360
TTGTTTACCT	ACTGTATCAA	AGGGGAGGAA	CTCGAG			396

(2) INFORMATION FOR SEQ ID NO:1111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:

GAATTCGGCC	AAAGAGGCNT	AGATTGTTTT	CATTAGCAAA	CTCATAATTA	TCCTTTTCCT	60
TAACACTTCC	AGTTGAGAAA	ACAAGTATTT	GTTAATGACC	AGTAATAATC	TTGATCCAGG	120
GTAGGCAAAA	TTTTTCTTCC	AGGGCCAGAT	TGATACTTTA	GGCTTTGCAG	GCCACGGGGT	180
CTCTGGCAAC	CCCCAGCTCT	GCTGTTGTAG	CACAAAAGCA	GCCACAGGCA	CAAGTAAACA	240
CATGGGTGTG	TCTCTGTACC	AATAAACTT	TATTTACAGA	AACACAGGGC	AGATGACTGT	300
CTGGCCCCTG	GTCTTGTGAG	CATTTTGTGG	TGGTGAACAA	AAGAACTGT	TCAGATCATT	360
ACATTTACAG	TCATTACCAA	AAATAGAATC	TTCACAGTAG	TTGTACTGTT	GATGAAGCAA	420
GCTCGAG						427

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

GAATTCGGCC	AAAGAGGCCT	AGGTTATAAT	AGCAGCTTAC	TTTTGATAAG	CGTACTAACT	60
GGTACATAGT	AAATACATAC	TGTGCATGCA	TTATGTCATT	TATATCCACA	CAGTCACCTT	120
CAAATTCAGT	ACAATTGTGA	TTCCCGTTTT	ACAGATGAGA	AAGCATATTT	TGGTGAAGTC	180
AACCRAAGTT	ACATGACTAG	TAAATTTTAA	ATGAGATTTA	ATTTCACTAC	TTACTAACCA	240
TTATGCATTG	CTAAATTGTA	ACATTACTTT	AAAATATAAC	TTCTAAAGTG	TTCATATTAG	300
AAACCTATAA	ATATACATAG	ATTGTCTCCT	TCTCTNACGA	AGAACACATG	AAGGAAAGAA	360
AGATATTAAT	TTGGTGGCTT	ATCATATGCC	AGACATAGAT	ATAGATGCTT	GTATGTATGG	420
CATTTAATCC	TTATCTGTGA	GATAGGCTTT	TTTATGCCTT	TCTATAGATT	TAAATTAAG	480
GTTCAGTTTA	GTAACCTGCT	CGAG				504

(2) INFORMATION FOR SEQ ID NO:1113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:

GAATTCGGCC	AAAGAGNNCT	AGAGGGATAT	AGAAACTTAA	CAGCAGTGGC	TGACATTTT	60
GCTTATTTGT	TAGGTATTGG	TGGTGGTGT	AATCGGGTAC	GCATATGCTT	TCCTTAGGAT	120
TTGCATTTGC	TGTTCCCTGT	GTCTAGAACG	CTATTCTTTA	GATAAATCTT	CATTCCTTAC	180
CTCCTTAAAA	TGTTTCTCA	TCTATCACCT	TCCTAAGTCT	GTACTGATCA	CCCTACTTAA	240
AATTATAACT	GCCCCCTTTT	GCTTGCACTT	CTAAGCTTCC	TTACCCTAGT	CTGTTTAGCA	300
GTTACCTCCT	TGAAACATGC	TCTGTAGAAT	TTACTTATTA	TGACTATTGT	CTCTCTTACT	360
ACCCTOGAG						369

(2) INFORMATION FOR SEQ ID NO:1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:

GAATTCGGCC AAAGAGGCCT AGTAAAAAT AGAATTTGAG ATATTTAATT TTCTGCTCTT	60
TTAAGTTAT GAAAACGTAT TTAAGTCGAG	89

(2) INFORMATION FOR SEQ ID NO:1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1115:

GAATTCGCCA AGAGCCTATT AATTTGTAAA CCTTAATATA GTGTAACTG AATAAAAGTA	60
AATAATTATT ATTAGAATGG TAACTAAGTC ATTAAATTTT TTNGCAGAAC TGAAACTTGT	120
ATGTTATTAG TTTATTTTCT TAGACCACTG TAATAATGGA CTGTAAATAG AAAAATAAAT	180
GTCACCTTAC AGTTAGATGT ATCAGAGTCG TTTCAGGAGA ATTTTCCTA TATTGTTACC	240
TTGATTCATT GTTTAAAATT GGTAGGATTT GTATAGATAT AGGATAGTGT TTTATTTATA	300
CTTTATCATA AGCCATAATC ATTTTAAGAA TACTTTATTG GATAGATTTT AGTACTTTTT	360
AAATTCTAAA GTTCTATTTT TCTTTTCACT TCCCCTTCCT TCCCCTTATA AGATCATTTT	420
CATGTCCTTG TTGGTGATCT CAGCCAGAA ATTACAACCTG AAGATATAAA AGCTGCTTTT	480
GCACCAAGTC TCGAG	495

(2) INFORMATION FOR SEQ ID NO:1116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:

GAATTCGGCC AAAGAGGCCT AGGGAAAAGA AGGGCTTTGG GGACCTGCCC ACTTCAAAAA	60
CAGTTTTTCT CATCCTTTGC CTTGGGCTCC AAACCCAGCT TGGTGTTCCT CTAAGGGAGC	120
TACAAATTCT GGAGCATCCC ATGAGGATGA TTTGCTGGCC TCGGTCATTA GGGGGAAGG	180
ATGTTCTCAG AAAACAGCC CTGCAGCTG GTCAGCAGAG ATCTTGAGGT CGTGGCCAG	240
ACTGGACTTG GTGCAGAGCT GAACCCGAGA CTCCAGCTGC TCGCTGAGTT CGTCCAGAGC	300
CCCGGTGCAG GACTCCAGGC TCTCGGCCAG TTTCTGAATC TTGGCCTTCA GCAOGGCCCTG	360
GCTAACCTTG GTGTCCCCCT CCGCCGCTT GGGGATGAGG AAGCCACGTG AGCCAAAGAA	420
GACGATGAAG TAGACAGAAT TGTACAGGGC GATGGAGGCG TTCCTCCGCG ACTGCAGCAG	480
CTGGCGGTCC CCGCAGCCCT GCCAGCGCA GAAAACTCG AG	522

(2) INFORMATION FOR SEQ ID NO:1117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1117:

GAATTCGGCC AAAGAGGCCT AAAAATATTT TACTTGTTC ATCCACAGTT CTCTACAGAA	60
AGAACCAATG AACCCAATAG GAACAAATTC TCTGTGAAA ACAAGCATA GCTGTAGTAG	120
ATACGAATCC AATCACAGAG GAAACAGGAA GAGAAAAACA TCCAAGACTA TAGTGAAAC	180
TGGAAATGGT CTGTTTTGCT GATATTGTA TGATTAAGAT GCAAATTTT TCITAGGAAA	240
ATGTGATTGT TAACTAGCAT TCTGTTTAC ATGTTGACAT TTCTAACACA CACACCACTG	300
ATTTGAACTT CAAAATTAT TTTCTGATTA TATATGCTAG GTCATGCTCG AG	352

(2) INFORMATION FOR SEQ ID NO:1118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:

GAATTCGGCC AAAGAGGCCT AGTGCCCACT CATTTATGTA CTGTCTATAG CTATTTTCAT	60
GCTACAATGG CAAAGCTAAG TAACACTCAA GGCCTAAAT ATTCACTATA TGCCCTTTGA	120
AGAAAAAGTT CACTCAACTC TGCCCTAAAC TACAGACCCT GGCCAAGGTG GGAGGATCAC	180
TTGAGGCTAG TAGTTCAAGA CCAACCTGAC TCTGTCTCTG ACTCTGTCTC TACCAAAAAA	240
AATTAGCTGG GCGTTGGGCT TATCCCTGTA ATCCAGCTA CTCAGGAGTC TGAGGCAAGA	300
GGATCACTTG AGCCCAAGAG TTCAAGGACA CAGTGAGCTA TGATTGCACC ACTATACCCC	360
AGCCTGGGCA ACAGACCAAG ACCCTGTCTC TAAAAACATA AAATAAAAAA TAAAAAATAA	420
AAATAAATAA TAAAGAAAAA AGAAACAGAA TTAAGAAAT TCTTTTGCTC AAAGTCTCGA	480
G	481

(2) INFORMATION FOR SEQ ID NO:1119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:

GAATTCGGCC AAAGAGGCCT AAGTGTGTC AGTGTCTCTC CTAAGGTAGT AAATATAATT	60
GACTTATTCT GAACCAATTC TATTTGAAT CTCCCTTTC CTCTCACAAT ACTTGAACAT	120
TTTAATCTTT TGGAATATTG TCTTCTTTG TTATAACTAT TCATTTTITAG CTTTGTCTC	180
CAGTGCATGA TCTCATATTT TTGCTTTTAT TTTTAGTATA AGAACATTTA TAAATCATA	240
TTTTTGTTAC TGCAATTGTT TTATTGTTG TGTGGCAAT GAGAAATCCT TTATTTATTG	300
TGCTGTATCT CGAG	314

(2) INFORMATION FOR SEQ ID NO:1120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:

GAATTCGGCC TTCATGGCCT ACCAGATACT GTTTTTTTAA TACATATTCA AAAGAAAGCT	60
ATTAACCCTG ACAGACATT CTCAGTCTGT GCTTTTTTCT ATTTTATCAT TTAAAGTAC	120
TTAAGATAGA AAGATGAAAA AGCATTGTGT GGCTACTTGG TTAGCTTCAC AAATTTTCCC	180
CCTTCCTACG CAGCTCGAG	199

(2) INFORMATION FOR SEQ ID NO:1121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:

GAATTCGGCC TTCATGGCCT AGTAGCATAT TAACAGTGTA ATAAAAATA AAAACAACT	60
CTAGTATCCA GAGGATCACA TGCTGACCAG ACCCTGTGTA GAAAGTGCCG AAGAGCATCA	120
AGGAAATGGA AACGTTGGAA TTCCATCCGT GCTTGTGGCT TTCCTTAAAC TTTTGTATG	180
GAAATTTCA AATATACCCC GAAGTGGAGA TTGGCTTAAA TCAGCCCCAC GTGCCCATCA	240
CTCGGCTCCA GTCATTATCC AGTGTGGTTC CTCGATCTT CACCACCCCC TCGAG	295

(2) INFORMATION FOR SEQ ID NO:1122:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 410 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:

GAATTCGGCC TTCATGGCCT AACGGAAGCG TCTCCTCATT GATGGAGATG GTGCTGGAGA	60
TGATCGGAGA ATTAATCTGC TAGTGAAGAG TTTCATTAAA TGGTGCAACT CTGGGTCCCA	120
GGAAGAGGGA TATAGCCAGT ACCAAGTAT GCTGAGCAG CTGTCTCAAT GTGAATTTTC	180
AATGGGCAA ACCTTACTAG TATATGATAT GAATCTCAGA GAAATGGAAA ATTATGAAAA	240
AATTTACAAG GAAATAGAAT GTAGCATAGC TGGAGCACAT GAAAAAATTG CTGAGTGCAA	300
AAAGCAAATT CTTCAAGCAA AACGAATACG AAAAAATCGC CAAGAATATG ATGCTTTGGC	360
AAAAGTGATT CAGCACCATC CAGACAGGCA TGAGACACAG GGAACGAG	410

(2) INFORMATION FOR SEQ ID NO:1123:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 308 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:

GAATTCGGCC AAAGAGGCCT ACCTTTCTTT CCTCCCTTCC TCCTCCCATG TCCCTCTCTC	60
-------------------------------------------------------------------	----


```

CTCCCTCCCA CCTCTCACCC TTCTCCATCC CTCTCCCTC TTTTCTTTG TACTTTCCAG      120
CTGGAGCAGC AGCAGCAGCT GGGCCTGAAT CAATGATTGA CTTCGCCAGC ACCTCCCCTT      180
CTCTTTTGCC AATGATATCT CTTTGCCCTT CCAGTCATCT TTTAATTTA TCGTGATGG      240
TTTGTCTTCT CCTTCCTCCT CTCTCTCTCT TCCTCTTTC TCCCCCTCT CCCCACCGA      300
CAGTCGAG                                     308

```

(2) INFORMATION FOR SEQ ID NO:1124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

```

GAATTCGGCC TTCATGGCCT ACAATTTTGC CATGGTTCTG CTCATTTTTC CTGCAATTCT      60
CAGCATGGAT TTATATCGAC GCGAGGACAG GAGACTGGAT ATTTTCTGCT GTTTTACAAG      120
CCCCTGCGTC AGCAGAGTGA TTCAGTTTGA ACCTCAGGCC TACACCGACA CACACGACAA      180
TACCGGCTAC AGCCCCCAC CTCCCTACAG CAGCCACAGC TTTGCCCATG AAACGCAGAT      240
TACCATGCAG TCCACTGTCC AGCTCCGCAC GGAGTAGGAC CCCCACAGC ACGTGTACTA      300
CACCACCGCT GAGCCGCGCT CCGAGATCTC TGTGCAGCCC GTCACCGTGA CACAGGACAC      360
CCTCAGCTGC CAGAGCCCAG AGAGCACCAG CTCCACAAGG GACCTGCTCT CCCAGTTCTC      420
CGACTCCAGC CTCCACTGCC TCGAG                                     445

```

(2) INFORMATION FOR SEQ ID NO:1125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:

```

GAATTGCCTT CATGGCCTAC ACCAGCCTAT TCTCTGCTTC TGTGAGTTTG ACTCTTTTTT      60
TTTTTATGAG ACAGAGTCTC ACTCTATCTC CCAGGCTGGA GTGCAGTGGC ACAATCTCGG      120
CTCACTGCAA CCACCACCTC CCAGGTTCAA GCAGTTCTCC TGCCCTCAGCC TCCCAAGTAG      180
CTGGAAATAT AGGTGTGCCC CACCACGACT GGCTAATTTT TGTATTTTGA GTAGAGACAG      240
GGTTTCACCA TGTGCGCCAG GCTGGTCTCG AACTCCAGGC CTCATGTAAT CCGCCACCT      300
TGGCCACACT CGAG                                     314

```

(2) INFORMATION FOR SEQ ID NO:1126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:

```

GAATTGGGCC TTCATGGCCT ACACGCCCCC GCCCCGCCTG CTGCCCAGGA ATACTTTCTC      60

```

CAGGAAGGCT	TTCAAGCTGA	AGAAGCCCTC	CAAATACTGC	AGCTGGAAAT	GTGCTGCCCT	120
CTCGCCATT	GCGCGGCC	TCCTCTTGGC	TATTTTGCTG	GCGTATTTC	TAGCAATGCA	180
TCTGCTCGGA	CTCAATTGGC	AACTCCAGCC	TGCAGATGGG	CACACCTTTA	ACAATGGGAT	240
AAGGACCGGC	TTACCAGGAA	ACGATGATGT	GGCAACAATG	CCATCTGGAG	GCAAAGTGCC	300
CTGGTCGTTG	AAAAACAGGC	AACTCGAG				328

(2) INFORMATION FOR SEQ ID NO:1127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

GAATTCGGCC	TTCATGGCCT	AGTGAGGCTC	CATTATTTTC	ATTTTAAACA	AGTTTCAAAA	60
TGTGGCTGCT	GCTGTTGCTG	GTGGTCCGGA	GCCTGCAGAC	AGGGGGATT	GCCTGGGAAG	120
GAGAAGTAGA	AAACAACGTG	TACAGCCAGG	CTACAGGGGT	GGTCCCCCAG	CACAAGTATC	180
ACCCCAACAGC	AGGCAGCTAT	CAGCTTCAAT	TTGCCCTGCA	GCAACTTGAA	CAACAAAAAC	240
TTCAGTCCCG	GCAGCTCCTG	GACCAGAGTC	GAGCCCGGCA	CCAGGCAATC	TTTGGCAGCC	300
AGACACTACC	TAACTCCAAT	TTATGGACAA	TGAATAATGG	TGCAGGTTGT	AGAATTTC	360
GTGCCACAGC	TAGTGCCAG	AAGCCAACCA	CTCTGCCACA	AAAAGTGGA	CCACCTCCAA	420
GTTCTTGC	CTCCCTGGTT	CCCAAACCCC	CACCGCTCGA	G		461

(2) INFORMATION FOR SEQ ID NO:1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:

GAATTCGGCC	TTCATGGCCT	AGAATTATCA	TGGCATCTGT	AACACACATG	CCTGTGCTAT	60
ATTCTCACAA	TTTTGTTCAG	GTTGTGCATA	TTAAATATG	GAGCTCCATA	TTTTTCACT	120
TCCTAGTTGA	TCACAGTTGA	CTGGGTTGTC	TTTTCTGTCA	CCTGTTAGTT	TTGAAGAGAT	180
GTCTCATATG	TAGTGATGTT	AGGTATGATG	CATTACAGCA	TAGTAAATAC	CTGGTACTGT	240
CTCTCAAAA	AAGCCTTTAG	CTTTTGTGTA	AAGAGGACAA	CAGAAAACAC	ACCAAAAAAG	300
CAGAAAAATA	TGTGTGGGTG	ATAGTGGGAG	AAACTTATAA	ATCATGGTCA	TATGTTACCC	360
CAGAGAAGGC	TTACACAAGG	TCAGCTACAG	TTTACCCAAT	AACGCTGTGA	TTGTCTGGTT	420
CCTTGGCTTA	GAAAGCTTAG	TCTCTGCCAA	GCGGCCTCGA	G		461

(2) INFORMATION FOR SEQ ID NO:1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:

```

GAATTCGGCC TTCATGGCCT ACAAGAATGA AGCACTGAAA AGCGAAGAAG GCTGCATTCC      60
GAATATCGCC CCAGACATCT GCATAGCATA CAAACTGCAC CTAGAGTGTA GCAGGCTCAT      120
CAACCTCGTG GACTGGTCAG AGGCTTTTGC AACAGTTGTG ACAGCTGCTG AAAAAATGGA      180
TGCAAATTCT GCAACCTCAG AAGAAATGAA TGAAATTATC CATGCTCGGT TTATTAGAGC      240
TGTTTCTGAA CTAGAACTTT TAGGATTAT AAAACCTACC AAACAGAAGA CTGACCATGT      300
GGCAAGACTA ACATGGGGAG GCTGCTAGAA AGCAAATAAG CAAAGCCAGA ACTATCACAT      360
TTAGCTTAAG AGAAAAAGGT GACCAGTCAT ATTTACATAT ATTAGAGGAG CCTGTTTTGT      420
TGAGAAGATA AATGTGTAAC CCCCATTGAT GTTTAACCAG AAAAGTACAT TGCTAACCCC      480
AAGAGCTCGA G

```

(2) INFORMATION FOR SEQ ID NO:1130:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:

```

GAATTCGGCC TTCATGGCCT AGGGCAACAG GAAACTCTTT ATTATGGTGA TGAGATCGAC      60
AATCTCCCCT ACTGTTAACC TTCGCTCCTG CACACTTCAG TGTCTCACT CTGTAGGGCT      120
CGCTGGCCTG GGCTTCTGCG ACCCGGATC GTCCAGGAGA GGGCACTCGG CGCCCTTCCT      180
GGGGCGCTTC TGGGGCGGAA TTTGCTAGGC CGCGTAGCA GCGGTGCCAG GTCAGAAGCC      240
GAGCCGGCCC GCTTTTCGTT CTTTAATTGG ACTCTGGCT AAGACGCTAC CGACACCCCG      300
TCAGGTGGTG GAGGAAGAAG GACAACAGG AGAGGTCGAG GGCCGAGACG GCCTCGAG      358

```

(2) INFORMATION FOR SEQ ID NO:1131:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:

```

GAATTCGGCC TTCATGGCCT AAACATCCTC CTGCCACTTA GGAGGAAACA CCTCCCTATG      60
GTACCATTTA TGTTTCTCAG AACCAGCAGA ATCAGTGCCT AGCCTGTGCC CAGCAAATAG      120
TTGGCACTCA ATAAAGATT GCAGAAATTA ATACAGATCT TTTCAGCTGT TCTTAGGGCA      180
TTATAAATGG AAATCATAAC GTGGTTCTAG GTTATCAAAC CATGGAGTGA TGTGGAGCTA      240
GGATTGTGAG TGACCTGCAG GCCATTATCA GTGCCTCATC TGTGCAGACC TCGAG      295

```

(2) INFORMATION FOR SEQ ID NO:1132:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:

GAATTCGGCC	TTCATGGCCT	AATGAAAAAC	AAAACAAAGA	TGATGAAGCA	GAGTGGCAAG	60
AATTACAACA	AAGCATACAG	CGAAAAGAGA	GAGCTCTATT	GGAAACCAAA	TCAAAAATAA	120
CACATCCTGT	GTATAGCCTT	TACTTTCCTG	AGGTAGAGCT	GAAGTTTCCT	GCACCAGGCA	180
AGCCTGGAAA	TTATCAGTAT	ACTGTGTTTC	TGAGATCAGA	CTCCTATATG	GGTTTGGATC	240
AGATTAAACC	ATTGAAGTTG	GAAGTTCATG	AGGCTAAGCC	TGTGCCAGAA	AATCACCAC	300
AGTGGGATAC	AGCAATAGAG	GGGGATGAAG	ACCAGGAGGA	CAGTGAGGGC	TTTGAAGATA	360
GCTTTGAGGA	AGAAGAGGAG	GAAGAAGAAG	ATGATGACTA	AGCAGTACTC	TGAATGGACC	420
ACAGTGTTTG	CACATATTTG	CAATTTTTTG	CTGTTTTGGA	AGTGTATCAT	AAACCAGAAA	480
CAGTACATAA	CAATCTCGAG					500

(2) INFORMATION FOR SEQ ID NO:1133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:

GAATTCGGCC	TTCATGGCCT	AGATTATATT	GCATATATTT	TATAGAACAA	GGCAAGCAAA	60
ATATTTTAGT	ATTGCAAAAT	CATGTTACTA	TAATTATTAG	ATCATAGTAC	CATTTATATA	120
AAGTATTAGG	TTGGTGCAAA	AGTAATTGCG	GTTTTGGACC	GTGAATTTTA	AATCATTATA	180
AGTCGGCTCA	GACAOGTCTT	TATTAATCAG	AGCAGGAAGC	ATTATAATCA	ACACATTTTT	240
GCCAATGAGA	AATAAGTTTG	TTCAATCCTG	TAGCTTAAAA	ATTCATGCTT	TGGGATTTGG	300
AAAGCATTTT	CTGCTTTCCA	AAAACCTGCT	GGTTTTGGAA	GCATTTTCCT	TTCAAATAGT	360
TGTCGAGATG	CTTGAAGAAG	TGGTGGTTGA	CAAGAGGTCA	GGTGAATACG	GCGGCTCGAG	420

(2) INFORMATION FOR SEQ ID NO:1134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:

GAATTCGGCC	TTCATGGCCT	AACTAGTCCT	GACTGCTTAG	ACAAAGTCAT	AGATTATGTT	60
CCAGGCATTT	TCCNAGAAAA	CAGTTTTTACA	ATCCAATACA	TTCTGGACAC	CAGTGATAAG	120
CTGAGTACTG	AGCTCTTTCA	GGACAAAAGT	GAAGAGGCTT	CCCTTGACCT	CGTGTTTGAG	180
CTGGTGAACC	AGTTGCAGTA	CCCACTCAC	CAAGAGAACG	GAATTGAAAT	TTGCATGGAC	240
TTCTGCAAG	GCACTTGAT	TTATGGCAGG	GATTGTTTGA	AGCACCACAC	TGTCTTGCCA	300
TATCATTGGC	AGATCAAAAG	AACAACCTAGC	TCGAG			335

(2) INFORMATION FOR SEQ ID NO:1135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:

GAATTCGGCC	TTCATGGCCT	AGCAATTTT	CCCTCAGGGG	GGCTCCCATC	TTCTTACACA	60
GAGAGGCAGC	TGAGGCAGGA	CAGTGGGGCT	AACTGTAGAC	CAGGCGAGGG	CACGGGCTGC	120
TGGGGTGGCC	CTGCTTCCCC	AGTGACATA	TTGTATCTGT	GTAACATTTT	GTATATTCCA	180
GGGGTAGGGC	CGCCCCCTGT	ATCATACCTA	GCAGAGGTTG	GAGCTGGCAC	ATGGGGAGGA	240
GGTTCTAATA	ATTATTGGG	GCTGGGAAAC	TTATTATTG	ATAGCATAGG	ACAGAGCCCA	300
CTCTCGAG						308

(2) INFORMATION FOR SEQ ID NO:1136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:

GAATTCGGCC	TTCATGGCCT	ACCGAGGCTT	CAGCGGGTGC	CGCCCGCCTA	GAGGGAGTGG	60
AGCGGCTAGA	CAGCTTTAGG	AACTGAAAGG	TTCACGAGGC	TGTAACGAAG	AGTCGAGTTG	120
CTCCAGAGAG	CCTACGACTA	GATTTCATC	TTTACGTCCT	GCGCGGAGGC	TGCTACACAC	180
ATGCAGAAGT	CATGCTGGTG	GCCTGGACAG	TGAAGGGAGA	GAAGTGGATT	TGGGAGACAT	240
TTAGGAGGAA	CAGTAAGAGG	ACCTTGTCGA	TGAATAATT	GTTTCCACAC	TACAGAGTGG	300
GTAATAAGCA	GATTAGTAAA	AACAATTCTG	CTTCACTTCA	ATAACAGCCT	CCTCCAATC	360
ATTTTCTCTC	AACAACTTA	TTTTCCAGCA	GAAGAATCCC	AGACTTCTTA	GAGAACCCAG	420
TGACTTTTGT	CACCTTAAAT	CTGTGAAATC	CTCATGTTTT	CTTCTGCCGT	ATCCATAGTT	480
CAACAAGAA	CCTCGAG					497

(2) INFORMATION FOR SEQ ID NO:1137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:

GAATTCGGCC	TTCATGGCCT	ACAATTGTAT	GCTGAAAAAT	GGGAGTAACT	ACATGAAATG	60
AGCAAATGCC	TAGAAACAAA	AAACCTACGA	AGATTGTATC	ATGAAGAAAT	AGAAAATATG	120
AATAGACGTG	TGTATTAGTC	TGTTCTCACA	CTGCTAATAA	AGACGTACCC	AAGACTGGGT	180
AATTTTTTTG	TTTTTAAGAA	AAAAGAGGTT	TAATGGACTC	ACAGTTCCAC	GTGGATGGGG	240
AGGCCTTATA	ATCATGGCAG	AAGGCAAACA	GCACGTCTTA	CATGGCAGCA	GGCAAGAGAG	300
AATACTCGAG						310

(2) INFORMATION FOR SEQ ID NO:1138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:

GAATTCGGCC	TTCATGGCCT	AAGCAAATCA	CTTTTCCCGA	TGAAAATAC	ACTTTACAAA	60
AGTGTTCAT	GCTTTTGCAT	TGTTTAGGAC	TATACGGTAT	CTTTACAGAC	GGCTACAGCG	120
GATGTTAGGT	TTAAGAAGAG	GCTCTGAGAA	TGAAGACCTC	TGGGCAGAGA	GTGAAGGAAC	180
TGTGGCATGC	CTTGGTGCTG	AGGACCGAGC	AGCTACCTCA	GCAAAATCTT	GGCCAATATT	240
CTTGTTCTTG	GCTGTTATCC	TTGGTGGTCC	TTACCTCATT	TGGAAACTAT	TGTCTACTCA	300
CAGTGATGAA	GTAACAGACA	GCATCAACTG	GGCAAGTGGT	GAGGATGACC	ATGTAGTTGC	360
CAGAGCAGAA	TATGATTTTG	CTGCCGTATC	TGAAGAAGAA	ATTTCTTTCC	GGGCTGGTGA	420
TATGCTGAAC	TTAGCTCTCA	AAGAACAACA	ACCCAAAGCA	CTCGAG		466

(2) INFORMATION FOR SEQ ID NO:1139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:

GAATTCGGCC	TTCATGGCCT	AATTTTTTTT	AATAGAGACG	AGGTCTTGCT	ATGTTGCCCA	60
GGCTGGTCCC	AAACTCCTGG	CCTCAAGCAG	TCCTTCCACC	TTGGCCTCCC	AAAGTGCTGG	120
GATTATCAAT	ATGAGCCACC	ATGCCAGATT	TGTTTCATTTT	TAAATATTTT	TATCTCTTCA	180
AGTCATCTTT	TGATCTTTTA	AAAAGCACCT	TCAAACAGCT	GCACCTTCCA	TTTGCACTAG	240
GAAATGAAGG	TAGTGATGGG	ATTGGCAATG	TTCTTGGCAG	ATGTTTCAGC	CCAAAAGCTC	300
TTCTACAGAC	CGGTTTAGAG	CTGGTGCCCT	ATGAGAAATAT	TAGGGAGCTT	TTATTTTAAA	360
TTGAACTTTA	CCCTTGTTCA	TGCAAGGCAT	TCCTCCTGAA	TGCATCCATG	AATTTGTTTA	420
CTTTTGGCTC	AAACATATGA	GCCATTGTCA	TGCTCAGCAT	GTGCCACCTC	GAG	473

(2) INFORMATION FOR SEQ ID NO:1140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:

GAATTCGGCC	TTCATGGCCT	AAATGAAGAT	CAGCTTCGTG	CAAAGGGTTA	TGACAAAACA	60
CCAGACTTCA	TTTTACAAGT	ACCAGTTGCT	GTAGAAGGGC	ACATAATTCA	CTGGATTGAA	120
AGCAAAGCCT	CATTTGGTGA	TGAATGTAGC	CACCACGCCT	ACCTGCATGA	CCAGTTCTGG	180
AGCTACTGGA	ATAGGGTCCC	AATATAACAG	ACAAATGGTG	AAACAGAGGG	ATACTCACTA	240
GGAAACAGAT	TTGGGCCAGG	CTTAGTCATC	TATTGGTATG	GATTTATCCA	GGAGCTGGAC	300
TGCAACCGGG	AAAGGGGCAT	CCTGCTCAAA	GCCTGTTTCC	CCACGTCCTC	GAG	353

(2) INFORMATION FOR SEQ ID NO:1141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:

GAATTCGGCC	TTCATGGNCT	ACCAATTCT	CATGGTTCCC	TAGGACCTTC	CTAGCTCCCC	60
AGGGAAAGCC	TNTGCTGTTT	CCCTTGNTTT	CTTTTCACTT	GACAACTCC	TACTCAAAC	120
TCAAAACCCA	ACTCAGGAAA	CATCTCCCT	AGGAAGCTCT	CCTTAACTTT	TTCTGCTGGG	180
TCCCGCTGCC	TCTGCTAAAG	TCCACGTGAG	GGACTGCCAA	GANGTTTGCT	CTGTCTCACA	240
GATTGAGTGC	CAAGAGGGCA	GGGACNTCTC	TTTGAGAGAG	TTTAACCTCT	GTAACATAAG	300
CAAGTTTACT	TAATCACTGA	TAAACCACT	TTGTGCCTCA	GTTTCCCAT	TTGTTAAGCA	360
TGAATTATCA	CTGTCACTAT	CTGCCAGGAC	TGTGAAGGGG	GTGTAAATGC	ATGAACATCA	420
TAAAGTGCTT	AGAAGCATGC	CTGGTACAAA	GAAAGTTCTC	TAGGNAAACA	ANAAACAAAC	480
AAAAAAAAC	AAACAGAAA	TGTATCTAGA	GGTCAGATAC	CAGTCCACA	TCGAGTGCAG	540
ATAATGGGCT	AAGTAACCA	TGAGTCTCGA	G			571

(2) INFORMATION FOR SEQ ID NO:1142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:

GAATTCGGCC	TTCATGGCCT	AGTAAGGAGA	GCCTCTATCA	AAGGGTGGCC	TGGAGCAGAA	60
TATCAGGCTA	TGTGTATTAG	TTGGTTTTCA	CACGCTATGA	AGAACTACCT	GAGACTGGGT	120
AATTTATAAA	GAAAAGAGGT	TTGATTAACT	CAGAGTCCC	ATGCTGGGG	AGGCCTCAGG	180
AACTTACAA	TCATGGTGGA	AGGCATGATA	GCAGGAGGGG	TGGAAGAGG	GGAGTGTAC	240
ACTTTAAAC	CATCAGATCT	TGTGAGAACT	CACTCACTAT	CATGAGAATA	GCAAGGGAGA	300
AATCCACCA	CTCGAG					316

(2) INFORMATION FOR SEQ ID NO:1143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1143:

GAATTCGGCC	TTCATGGCCT	ACTCAAGCGT	TTCAGTGTGC	GATATCTGCG	ACTGCTCGCA	60
GTCTTGCTT	CCTTGGTTCT	CCCCTGGGG	CTCAGGATTA	CGAGGCCTGA	AGCTCCTAGA	120
GGCTAAATGC	CAGGGGGATG	GAGTGAGCTA	CGAGGAAACC	ACTATTCCCC	GACCCAGCGC	180
CTACCACAAT	CTGTTGGAT	TACCACTGAT	TAATCGTCNA	GATGCTGAGG	TGGTACTGAC	240
GAGTCGTGAG	CTTGACAGCC	TGGCCTTGAA	CCAGTCCACG	GGGCTGCCTA	CCCTTACTCT	300
ACCCOGAGGA	ACGACCTGCT	TACCCCTGTC	CTTACTCCCT	TACCTGGAAC	AGTTCCGGCG	360
GATTGTATTC	TGGTTGGGG	ATGACCTTCG	GTCCTGGGAA	GCCGCCAAGT	TGTTTGACG	420
AAAACCTGAGC	CCCAAACCTG	AG				442

(2) INFORMATION FOR SEQ ID NO:1144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1144:

GAATTCGGCC TTCATGGCCT ACCATCTACA GCTGTATTCT TGTCCCTTG ATGGCACAAT	60
TAAACTGTGG GACTATATAG ATGGCATCTT AATAAAGACT TTCATAGTTG GATGTAAACT	120
TCATGCCCTC TTTACTCTTG CCCAAGCTGA GGATTCTGTC TTTGTTATAG TGAATAAAGA	180
AAAACCAGAT ATATTTCAGC TGGTTTCAGT GAAACTGCCA AAATCCTCAA GCCAGGAAGT	240
AGAAGCCAAG GAGCTGTCCT TTGTTTGGGA TTACATAAAC CAGTCACCCA AGTGCATTGC	300
CTTTGGAAAC GAGGGAGTAT ATGTTGCGCA GTACTCGAG	339

(2) INFORMATION FOR SEQ ID NO:1145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:

GAATTCGGCC TTCATGGCCT AGGCCAGGGG ACCCGGCCTC AGGTCTGTGG AGGTGCTTCA	60
ACAGCAGGAT GCTCATTCTC TGTCGGTAGT GTCTCCATAT ACTTTCTCAT CTTCTCCACC	120
ATCCAGGAGG GTAGGACAAA GGATTTCAT TCCTCTAGCT TCAGATCCAG GCATCCTCTG	180
TAATCATCAC TGGCCGCAAG GTCCCGGATG TCCTCCTCGA TGAGGAGGTA GGCCATCTTG	240
CCCCCTGTTG CCGCATGTG ATGCTGCTCA GCCAGCCAGT GCTTATCCTG GGGGTCAGCT	300
GCATACTTAA AGAGGTGTGG GTGCTTGATG TAGATTCTTC CTCTGGTGCC CCCCATCCCC	360
AGGGCTTTGT TGGCTCGAG	379

(2) INFORMATION FOR SEQ ID NO:1146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:

GAATTCGGCC TTCATGGCCT AGGAAAGCTG GGGCAAGGA AGAGCCTTGA ATCTTGAGGT	60
GGGAGTTGA CTCTAAGATG TCCTTGAGCA GTGGAGCCTC CGGAGGGAAA GGAGTGGATG	120
CAAAACCCGGT TGAGACATAC GACAGTGGGG ATGAATGGGA CATTGAGTA GGGAAATCTCA	180
TCATTGACCT GGACGCGAT CTGGAAAAGG ACCAGCAGAA ACTGGAAATG TCAGGCTCAA	240
AGGAGGTGGG GATACCGGCT CCCAATGCTG TGGCCACACT ACCAGACAAC ATCAAGTTTG	300
TGACCCCACT GCCAGGTCCT CAAGGAAAGG AAGGGCTCGA G	341

(2) INFORMATION FOR SEQ ID NO:1147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1147:

GAATTCGGCC	TTCATGGCCT	AGGGGGGGCC	ATCTTTAATT	CTGTAAGTTC	ATGGTAAAGG	60
TATCTCCCC	CACACTGGG	CAGGCGGCG	AATAAGCTCC	AGCGTTCATG	CGCCACTCAC	120
AGGACTGCTT	ACCCCACTG	CACCTACAAT	GCAGTCACAG	AGTTACGGCA	TGTTACCCGG	180
TGTCCATGAC	AAGCAACACC	AAGTATAAAT	AACAGAACTA	CAGCAGAGCA	AACTAAGATA	240
AATATGTTTT	TGCATCGTCC	TCCACATAGT	TTCTTTTAA	AAAGAAGAGT	CACATCCAGG	300
GGTCTATCCC	TCGAG					315

(2) INFORMATION FOR SEQ ID NO:1148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:

GAATTCGGCC	TTCATGGCCT	AGCTCTTTGG	GGAGCTGTTT	CAGAGGGAAA	GTGGATGAAG	60
GCTGAAGTGG	AGGCCAAATT	AGGTGCTCTA	GTACCCTCTC	TTGGATCTCT	TTCAGCTTTT	120
ACCTGTTTTA	TATGCTGGGA	TTTTATATAC	AACATTTTGC	AGAACTCAAC	TGCTAAAGTA	180
AAACGGTGGG	GAGGACTATT	GGATTGGGAG	ATCTCTAAAA	TCCCATTGGG	ATTGATGAAA	240
AAGAGAACTA	TCAGCAGAAA	AGAGGAAGGG	AACAAATGAG	TTGTTAGTAC	CTTAGTTCCT	300
AATTATGTT	CCTTTATTGT	AGATTCTTTT	CTTGCCACT	ACACTCCTTA	GAAATATAAT	360
TCACACTGT	TTCTTTTACC	ATTTTGTATG	ATATGCAAAG	TCCAGCTTTA	CTCAGCCACA	420
TTTGTCCAC	TGGCTTATAT	TTAATTTATA	TTTAGGATA	CAGATAACTC	GAG	473

(2) INFORMATION FOR SEQ ID NO:1149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:

GAATTCGGTC	TTCATGGCCT	ACTCTGGGTT	GCCTGTGGTC	ACTTCTGGTT	GCCTAGGACT	60
AGAAGGCTCA	GATTTTCAGT	GTCGGGACAC	TCCCATTCCT	CATCAAAGAA	GATCAATTGA	120
ATGCTGCACA	GAAAGGAACG	AATGTAATAA	AGACCTACAC	CCTACACTGC	CTCCATTGAA	180
AAACAGAGAT	TTTGTTGATG	GACCTATACA	CCACAGGGCT	TTACTTATAT	CTGTGACTGT	240
CTGTAGTTTG	CTCTTGGTCC	TTATCATATT	ATTTTGTTAC	TTCCGGTATA	AAAGACAAGA	300
AACCAGACAA	CTCGAG					316

(2) INFORMATION FOR SEQ ID NO:1150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:

GCCACGAAAG GTACCCCTGA ATTCTGGACT CATAAAATCT CTTAGATAAT ACATATTTGT	60
TGTTTAAACC CACTCAGTTT TGCATTGGTT ACACAGCAAT AGAAAATAAA GGAGGCAGAT	120
GAAATTGATG GAGAACAATT GCAACGAAAA CAGAATACAC AATGCACGAG CCTGTGTCAG	180
GAATGACAGT GCATTCCACG GAAGAGTTGC ACAGAGAGAG ACGCCGCTCG AG	232

(2) INFORMATION FOR SEQ ID NO:1151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:

GAATTCGGCC TTCATGGCCT AGCCTTTAAC ACTTGATATA AAATCCAAGC ATTTTTCAGA	60
CCTCAACCCA GAATAGTAGA TACCTGAAAT TAAGATTCCT ATTGGTGAGA AACAGATCT	120
GTATATTTCC CTATCCCTAT CCCCAATGC CAGTGGGTCA TTTCCCAT GCCTAGCTCC	180
ATTCACAGCT AATATGTGGA TTGAGGCTTT ATTCCAAAC ATTTAGGTTT TATATTCTTC	240
CCTAGCCCTG ATTAGCAGTG CTCATCTTTG AAGATCATTG TGACTTTCA GACTATTGTA	300
GTGATGGCTC AACCTGACCC CTCTCTCTCC TTTCAGGATT TGGCAGAGAG AACGGCCGCT	360
TCTCGAG	367

(2) INFORMATION FOR SEQ ID NO:1152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:

GAATTCGGCC TTCATGGACA GCACAGTGGC CAAAGAAGGC ACTAATGTAC CATTAGTTGC	60
TGCTGGTCTT TGTGATGATG AAGGCATTGT GACTAGCACA GGCGCNAAAG AGGAAGACGA	120
GGAAGGGGAG GATGTTGTGA CTAGTACTGG AAGAGGAAAT GAAATTGGGC ATGCTTCAAC	180
TTGTACAGGG TTAGGAGAAG AAAGTGAAGG GGTCTTGATT TGTGAAAGTG CAGAAGGGGA	240
CAGTCAGATT GGTACTGTGG TAGAGCATGT GGAAGCTGAG GCTGGAGCTG CCATCATGAA	300
TGCAAATGAA AATAATGTTG ACAGCATGAG TGGCACAGAG AAAGGAAGTA AAGACACAGA	360
TATCTGCTCC AGTGCNAAAG GGAGTCTCGA G	391

(2) INFORMATION FOR SEQ ID NO:1153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1153:

GAATTCGGCC	AAAGAGGCCT	AGCACTTGTC	TCATTTTAAT	GTAAAGATT	GCTTCCATT	60
TCCTACAGGC	AGTCTCTCTC	TTCCTCACAG	TCCCAGTGTG	CAGGTGCTAT	TGTTACTCTT	120
ACGAATATTT	TCAGTAATGT	TATTTTCTTC	TAAGTGAAAT	TTCTAGCCTG	CACTTTGATG	180
TCATGTGTTT	CCTTTGTCTT	TCAAACCTCA	AGGTTCCTCT	GTGGNCCTCT	CCCTTACCCT	240
GGGAAGGCCT	CTTGGAGACC	TTACCCCTTG	CTGTTTGGAC	TTTGTATACT	TTAAATAATT	300
TAACCTACCCT	TAATTACTTA	AAAAAAAAAA	AAAAAGCTT	TATGATTTTC	ATAACTTATT	360
GCTGATTTTA	ATGGATTGTT	AATTTTCAGT	CTGTAGTTT	ATTTTATGTT	TAGATAGGGC	420
TGGCAAGGA	AAAAGAAAT	AAAGACAACC	ATACTCGAG			459

(2) INFORMATION FOR SEQ ID NO:1154:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1154:

GAATTCGGCC	AAAGAGGCCT	ACTCCTTCAG	ACTACAAGCT	CCACAGAGCC	GCGGGAGGAC	60
GGTTGCCTGG	TATTATTAGC	AAGCAGCAAA	TATGGCGGTG	GCGCGCGTGG	ACGCGGCTTT	120
GCCTCCCGGA	GAAGGATCAG	TGGTCAATTG	GTCAGGACAG	GGACTACAGA	AATTAGGTCC	180
AAATTTACCC	TGTGAAGCTG	ATATTCACAC	TTTGATTCTG	GATAAAATC	AGATTATTAA	240
ATTGGAATAT	CTGGAGAAAT	GCAACGATT	AATACAGTTA	TCAGTAGCTA	ATAATCGGCT	300
GGTTCCGATG	ATGGGTGTGG	CCAAGCTGAC	GTGCTTCGT	GTATTAAATT	TGCCTCATAA	360
TAGCATTGGC	TGTGTGGAAG	GGCTCTOGAG				390

(2) INFORMATION FOR SEQ ID NO:1155:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1155:

GAATTCGGCC	AAAGAGGCCT	ACGAATGTGG	CCGGGTGGGA	CCCGGACATA	CGAGAGATTG	60
TCCTCATCGT	GGCCATGATG	ACATTGTCAA	CTTCGAGAGG	CAGGAGCAGG	AGGGAGAGCA	120
GTACCGTTCC	CAGAGGGACC	CACTGGAGGG	CAAGCGGGAC	CGGAGCAAGG	CCAGGTCTCC	180
GTACTCGCCA	GCCGAGGAGG	ATGCCTTGTT	TATGGATTTA	CCCACTGGCC	CAAGAGGCCA	240
GCAGGCACAG	CCCCAACGGG	CAGAGAAGAA	TGGAATGCTG	CCTGCCTCAT	ATGGCCCAGG	300
AGAACAGAAT	GGGACTGGTG	GGTACCAGCG	GGCCTTTCCT	CCCAGGACCA	ACCCTGAAAA	360
ACACAGCCAA	AGGAAGAGCA	ATCTGGCCCA	GGTGGAGCAC	TGGGCAAGGG	CCCAGAAAGG	420
GGATAGCAGG	AGTCTTCCTT	TGGACCAGAC	GCTTCCTCGC	CAGGGTCCTG	GCCAATCCCT	480
GTCTTCCCA	GAAACTACC	AGACTCTTCC	CAAGAGCACC	CGAAACGCCT	CGAG	534

(2) INFORMATION FOR SEQ ID NO:1156:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 505 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1156:

```

GAATTCGGCC AAAGAGGCCT AATGGATCTA GTCACCTTCA GATTTC AATT TGAGGTTAAG      60
TATATAAAGC ACATCCCAAT TTTATATGCT GCCTTGAGAA AATTACAGGA TGCACGGCAA      120
TTTGTAGGAA TTCAAATGG GATCATTAA ACATTTGAAA AATTATTTTA AAAACCATCT      180
AGTTTGCTTT TGGATTTTAG ACATTAAAGC CTATGTTGTC TGTTTAACAG GGGTGGAAATG      240
TATAACCATC AGATTCAGCA TGTGATTTC CCTTTGAATC TGAGTATTTT TCCCTATCT      300
TCTTTGAGTC ATTTTGGAG CAGACTGTCA CCAGTATTGA TAACTAAGCA TTAAGGGGAA      360
AAGTTGCATT GCAACTATGC ATTGGTTTCC TGAAGAAGT TTTCTTTGT TTTAGTGAAT      420
GAAGAGGCTT GATGGGATCA CTTACTGTAA CTCCTTCTAC ATAAGGACCC CTTCTGCAAG      480
CAGAACACAA AAGAACACGC TCGAG                                         505

```

(2) INFORMATION FOR SEQ ID NO:1157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1157:

```

GAATTCGGCC AAAGAGGCCT ATGTTATTGG GAAGGACCCA GAGAACAAAA AGTTGAATAC      60
GGAAAAGAAA ATAGGATTTG CAAGAAGCAC NTTTTTTTTT TTTTTTTTTT TTTNGAGACA      120
AANTCTCGNT TTGCANTCCA GCCTGGGTGA CAAGAGCAAA ACCTNGTNTC CAAGNAAAAA      180
AAAATACAGT TTTGGTGATA ATACAGTTTG AAAGTAATTA GCATGTGGAT AGTCATAGAA      240
ACCACAGGCA TCAATGAAAC TGGCTAGGAG AAAGGACACC AAGAGGAAAT GGCCAGAGGT      300
AACAGGAAAA TCAGGGGAGT GTGGTTCACA GAAGCCTGGG AAGTGCTATT TCAAGAAGAG      360
AGTGGGTGGA AATTGTTAAG TGTCTAATGC TGCTCAGAAG CCAAGCAAGA TAAAGACAGA      420
AGAATCTAGT GGGAACTCGA G                                         441

```

(2) INFORMATION FOR SEQ ID NO:1158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1158:

```

GAATTCGGCC AAAGAGGCCT AGCAGAACCC GACCAGGGGA GCCTTGCCTG TGTGTTTCAG      60
GTGCTCTGCG ACCACTTCTA TAAACCTAA AAAAGGAGAT TGCTCTGATT GCAACAGGTG      120
TGGGGGACCA GTATCCCATC CCATTGGCCC TGCCCTCCCA CCTGTAAGGC AGAATATGGT      180
TGGGAAATCA TTGCCATATG CAGAAGGGGT CACTGAGGGG TTTTAAACAA CAGTGACATG      240
CTCAGTTCTC TGGGTTGAGG CATCATCACC CTGGTGGCCA TGTGGAGGAT GGAAGGAAA      300
AGGCATTGAG TTAGAAGACC TCTGCAGGAG TCCAAGGAAG AAACAGGCAA ATCTGCAGGA      360
GGCAGGCATA TCCAAGCTCG AG                                         382

```

(2) INFORMATION FOR SEQ ID NO:1159:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1159:

```
GAATTCGGCC AAAGAGGCCT AGCCTCGGTG ATTTCCAGTG GAAGAATGTA GGTCCCAATA    60
CCACAAGCAC AGTCATTAGC ACAGATGCTT TTAGGCCAGG AGTTCGATAT GACTTCAGAA    120
TTTATGGGTT ATCTACAAAA AGGATTGCTT GTTTATTAGA GAAAAAAAC AGGATACTCT    180
CAGGAACCTG CTCCTTCAGA CAACCCTCAC GTGCTGGTGG ATACATTGAC ATCCCACTCC    240
TTCACTCTGA GTTGAAAGA TTACTCTACT GAATCTCAAC CTGGTTTAT ACAAGGGTAC    300
CATGTCTATC TGAAATCCAA GGCGAGGCAG TGCCACACCG ATCTCGAG    348
```

(2) INFORMATION FOR SEQ ID NO:1160:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1160:

```
GAATTCGGCC AAAGAGGCCT AGAAAACTG AAAAAATAAG AAAC TTAGA GAAAAAGAGG    60
AATCAGTGCA GGCTAGGGGA ATGAAC TTGG TAATCCAGTA GTCTTCCCT GCCAGCATT    120
TGATTGATAA GCTAAGTGC TGCTTTTCT CATCCCTTAT TTTTGGCAG GAAACCAGTA    180
TTTTGATACT TGAATGCCTT CTTTCTATCT TAAGGGAGAA GCCTTCTTA ACTTCAAGTG    240
TGAAGTAGAT CCTTTAGGTA TAGGATGAAA AATTAAGTGG GACTATTTGT GAATTACTAA    300
ATCGCAACTC GAG    313
```

(2) INFORMATION FOR SEQ ID NO:1161:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1161:

```
GAATTCGGCC AAAGAGGCCT AGGAGCCTAG AAAAGAAGAA AGGTCTATTT TTATAAAAC    60
TGATGAAATA CTTGTGGCAG GGAGTCCTCG AG    92
```

(2) INFORMATION FOR SEQ ID NO:1162:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1162:

GAATTCGGCA AAAGAGGCCT AGTGCATAAG GAATCACTGT GTACAAACTG GCCAAGTGCT	60
TCTGTAGATA ACGTCAGTGG AGTAAATATT CGACAGGCCA TAACTTGAGT CTATTGCCTT	120
GCCTTTATTA CATGTACATT TTGAATTCTG TGACCAGTGA TTTGGGTTTT ATTTTGATT	180
TGCAGGGTTT GTCATTAATA ATTAATGCCC CTCTCTTACA GAACACTCCT ATTTGTACCT	240
CAACAAATGC AAATTTTCCC CGTTTGCCCT ACGCCCTTT TGATACACCA CTCGAG	296

(2) INFORMATION FOR SEQ ID NO:1163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1163:

GAATTCGGCC AAAGAGGCCT ATTAAAAATA AGTGTCTAAT ACTGTGTATT CATATAGCCT	60
TTATATCTCA ATACGTGCTT ATCTGTTGGT ATACCTTAGA GAAATAACCC ACCATCAATG	120
AGAAGAAGGA AAGGCAGGAG GAAAAAAGTT TATATAACAC TTTAAATGG TAGATTATTT	180
GTTGCCATTT GAATTTACTG ATTTGAAGTT CTTAAAGATG CTGAGCCATG CCTTACATAG	240
TTATTTTAGA ATCTAAAGTT GTTCTGTATT TGCATAACGT TTCTGTTCTT TTTCTTCTTT	300
AAACCCTGAA AGTGATAGAT GGGGAAGGAGG AACCAGATAT TTGGCATGGT CTGACAAAAA	360
TAACTTGTG AACTCGAG	378

(2) INFORMATION FOR SEQ ID NO:1164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1164:

GAATTCGGCC AAAGAGGCCT ACTCCAGGCT ACTTTTCCCC TAGGCCTGAC CTTTGTAGTGT	60
CTTTTGTGCC ANACATATTT AAGACCAGAG GAAAAAAGCA ATTGCTTTAG TTTCTATGTT	120
TGGGTAACAA AATCTACCCA CAGACAAGAG AATAACAAAA ACCAAACAGT ACAGTGGGAA	180
ATATACCAGA AAGGAAAAAA AAGATCATCA CATTAAATGT AAATGAGGTA AATTTTATA	240
ATAAAGAATC TTTTATGAAG AATGTCTCAA ACCAAATATT GTACTTTCCA ATTTCTTGGG	300
CACTGGGGAT GCTGAAGTGT AGTTAGATGA GTATATAACC CTATAGGGCT CTCGAG	356

(2) INFORMATION FOR SEQ ID NO:1165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1165:

GAATTCGGCC	AAAGAGGCCT	AGTCTTCTGC	CCCCCTATGA	AGTTTGAGTT	TCAGCCCCAC	60
ATGGGGGATA	TGGCTTCCCA	GCTCTGTGCC	CAGCAGCCTG	TCCAGAGTGA	GCTGGTACAG	120
AGATGCCAAC	AACTGCAGTC	TCGCTTATCC	ACTCTAAAGA	TTGAAAACGA	AGAGGTAAAG	180
AAGACAATGG	AGGCCACCCT	GCAAACCATC	CAGGACATTG	TGACTGTGCA	GGACTTTGAT	240
GTGTCTGACT	GCTTCCAGTA	CAGCAACTCC	ATGGAGTCCG	TCAAGTCCAC	GGTCTCTGAA	300
ACCTTCATGA	GCAAGCCCAG	CATTGCTAAG	AGGAGAGCCA	ACCAGCAAAT	CCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:1166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1166:

GAATTCGGCC	TTCATGGCCT	AGACAGGCGG	ACCCAGAGAG	ACTTGCACTA	CGTGGAGAAG	60
ATGGAGAACC	AAATGAAAGG	ACTGGAGTCC	AAGTTCAAAC	AGGTGGAGGA	GAGTCATAAG	120
CAACACCTGG	CCAGGCAGTT	TAAGGGCTAA	CTTAAAGAG	TTTTTTCAAT	GCTGCAGTGA	180
CTGAAGAAGC	AGTCCACTCC	CATGTAACCA	TGAAAGAGAG	CCAGAGAGCT	TTTTGCACCA	240
TGCATTTTGA	CTATTATTTT	CCAATACTTA	GCACCATTTT	ACTAAGGAAC	CTTGAATACA	300
ACGAGGATCC	TCCTTTGCAT	GCGACTGTAG	CTGCATTTC	TGAATAGTTT	GAACCCTTGT	360
CAATGCAATC	TCGAG					375

(2) INFORMATION FOR SEQ ID NO:1167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1167:

GGCTTATTGA	TGACTCTTAT	TTTAATTATG	TTTTTAGCAA	TGATAAGTTA	CAATATAATA	60
GCTGGAGATA	CTTTGAGCAA	AGTTTTTCAA	AGAATCCCAG	GAGTTGATCC	TGAAAACGTG	120
TTTATTGGTC	GCCACTTCAT	TATTGGACTT	TCCACAGTTA	CCTTTACTCT	GCCTTTATCC	180
TTGTACCGAA	ATATAGCAAA	GCTTGGAAAG	GTCTCCCTCA	TCTCTACAGG	TTTAACAAC	240
CTGATTCTTG	GAATTGTAAT	GGCAAGGGCA	ATTTCACTGG	GTCCACACAT	ACCAAAAACA	300
GAAGACGCTT	GGGTATTTGC	AAAGCCCAAT	GCCATTCAAG	CGGTCGGGGT	TATGTCTTTT	360
GGGGACGTTT	TCGAG					375

(2) INFORMATION FOR SEQ ID NO:1168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1168:

```

GAATTCGGCC TTCATGTCTC TGCAATCTGA AAATAGTGCC TTTTACCAAG AAGAGGACAG      60
AATTGGCGTT TGGAAAGGCTG AGGGTCATGG TGTAAGGGCT TTTGAGTCAA AATCTTGGTG      120
TCAAGCAGAT GAGGCTGCAA CACAGACCTG TGACCAAAC TGTGTGGAGC GTGTGGTGGA      180
CACGCAGGGG ACTGTGCAGA GGACAGATGG CCTAAAGCTT AGCATGGCAC AAGGAGTGCC      240
CCCCGATGGC AAGTCTCCCA GTCAACTCCA GATCTCTTCA CAGTAACTGT GTTTCCTCCG      300
CATTTATTTT CAACCTGCAC AGAGGAAGAA GAGAGGGAAA CAAGCCCAGG TGACAAAACA      360
GAGGGTGAAA TATGTGTGAA GAGTTCAGTC AGTGTGTAC GAGACCAGCT GAGTGACCTT      420
CAAAGGTTAG AAGGTAGTGA AAAAGAATCA CTGCAAGCAA AGTATAGTGA GACAAGTGAA      480
GATGACATAG AGACTGTCAA GTCAGATTCT AAAACAACCT ATGAGTGGGA AACAGGNACA      540
CAAAAACCTG AG                                     552

```

(2) INFORMATION FOR SEQ ID NO:1169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1169:

```

GAATTCGGCC TTCATGGCCT AGAGCGGAGT AAATTCTCCA CAAGCTGGGA ACAAACCTCG      60
TCCCAACTCC CACCCACCGG CGTTTCTCCA GCTCGATCTG GAGGCTGCTT CGCCAGTGTG      120
GGACGCAGCT GACGCCCGCT TATTAGCTCT CGCTGCGTCG CCCCGGCTCA GAAGCTCCGT      180
GGCGGCGGCG ACCGTGACGA GAAGCCACG GCCAGCTCAG TTTTCTTCTA CTTTGGGAGA      240
GAGAGAAAGT CAGATGCCCC TTTTAACTC CCTCTTCAA ACTCATCTCC TGGGTGACTG      300
AGTTAATAGA GTGGATACAA CCTTGCTGAA GATGAAGAAT ATACCATATT GAGGATATTT      360
TTTTTCTTTT TTTTTCAG TCTTGATTG TGGCTTACCT CAAGTTACCA TTTTTCAGTC      420
AAGTCTGTTT GTTTGCTTCT TCAGAAATGT TTTTACAAT CTCAGAAAAA AATATGTCCC      480
AGAAATTGAG TTTACTGTTG CTTGTATTG GACTCATTG GGGATTGATG TTACTGCACT      540
ATACTTTTCA ACAACCAGAA CTCGAG                                     566

```

(2) INFORMATION FOR SEQ ID NO:1170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1170:

```

GAATTCGGCC AAAGAGGCCT AGGGAGTCAA TCATGATCNT TTCATATATG CTGGCNATAG      60
AAAATGGTCT CGGTGAAGTA ATGGTCTGTC TGTCAAGCAT GACATCCTTG CCTGTGTTAA      120
GTTTTTGTG CTCTTCTGGG ATGTTGATCG TGACGTCTTG TCCGGGATTG AGAAGCTTCT      180
GTTGCTCTTC TGGGATGTCA TTCATGATCT CTTCATATAT GCTGGCTATA GAAATTGGGC      240
TCTGTGAAGA AATAGTGTGT CCAAAACCTT GGTACAGGCC CCCTGGGGAG GGTACCTTTG      300
AAGAACCAGA AGTTAGATCT TGTGAAGAAG AAGAAAGTAG GCTCGAG                                     347

```

(2) INFORMATION FOR SEQ ID NO:1171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1171:

GAATTCGGCC TTCATGGCCT ACTTTTGGG GACTGGTACT GGAGAAAAAT CTGAGAGCAA	60
AAGTGCTTGG CTAAATTCCC TTTTITTTCT TTTAGTTTTT GAAATCATGA ATCCTGTTTA	120
TAGTCCTGGA TCTTCTGGGG TTCCCTATGC AAATGCCAAA GGAATTGGTT ATCCAGCTGG	180
TTTTCCCATG GGCTATGCAG CAGCAGCTCC CTGCCTATTC TCCTAACATG TATCCTGGAG	240
CGAATCCTAC CTTCCAAACA GGTTACACTC CTGGCACACC TTACAAAGTG TCCTGTTCCC	300
CCACCAGCGG GGCTGTGCCA CCGTACGTCC CCCTCGAG	338

(2) INFORMATION FOR SEQ ID NO:1172:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1172:

GAATTCGGCC TTCATAATCT CCTGCTCTTG AGAATGTGCC GATATGTCAA AATATCTACT	60
GAAACTGAAG AAACTGAAGG ATCCCTACAC TGCTGTAAGG ACCAAAATAT TAATGGGAAT	120
GGCCCAAATG GCATACATGA AGAAGGCTCA CCAAGTGAAA TGGAAACAGA TGAGCCAGAT	180
GATGAATCCA GCCAGGATCA AGAACTTCCC TCAGAGAATG AAAACAGTCA GTCTGAAGAT	240
TCAGTTGGAG GAGATAATGA TTCTGAAAAT GGATTATGTA CCGGGATACT CGAG	294

(2) INFORMATION FOR SEQ ID NO:1173:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1173:

GAATTCGGCC TTCATGGCCT ACATAAAAGA ACGAAAAGGA AGGAACTTCA GTCAACATAT	60
TTTCATTGAC TCCTTAGTAC AAGGGAACCT TAATGACCAA CAGATCCTAG AAGACAGTAT	120
GATATTTTCT CTGGCCAGTT GCATAATAAC TGCAAAATTG TGTACCTGGG CAATCTGTTT	180
TTTAACCACC TCTGAAGAAG TTCAAAAAAA ATTATATGAA GAGATAAACC AAGTTTTTGG	240
AAATGGTCCT GTTACTCCAG AGAAAATTGA GCAGCTCAGA CTCGAG	286

(2) INFORMATION FOR SEQ ID NO:1174:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1174:

GAATTCGGCC	TTCATGGCCT	AAATATGAAA	AGACTAGACA	TACAGAGATA	TTTATCATAG	60
CAAAAAGTTG	CAAGTACTGG	GGATTGACAA	AATTATCACA	ATGGTTATAT	TATTATTATT	120
ATTATTATTA	TTATTTAATC	AATCAGTGTC	TTGCTTTGTT	GCCCAGACTG	GTTTCAAATC	180
CCTGGCCTCA	CGTGATCCTC	CCGCCTCAGC	TTCCCAAATT	GCTGGGATTA	CAGGCATGAA	240
CCACCGCGCC	TGGCCTATTG	TTCTGCCACA	TCTTTCTTTT	ATTTTGTAGA	GAGAGTCTTG	300
CTTAGTCCAG	GCTGGAGTAG	AGTTGTGCCG	TCATAGCTCA	CTGCAGTCTC	AATTCTTTGG	360
GCTCAAGCAA	TCCTCCTGCC	TCAGCCTCTT	GAGTAGCTGG	GAATACAGGC	ACACTCTCGA	420
G						421

(2) INFORMATION FOR SEQ ID NO:1175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1175:

GAATTCGGCC	TCATGGCCTA	GTGCTTAAAA	GCTGTTCTCA	TAAGAATTCT	ACTGGCCTGT	60
ATCTACCCAA	CCACTTTCTA	TACCTCTCTT	CCAACCAAAA	GTCTTAATAT	GGGAATATCC	120
CTCACCACGA	TCCTAATACT	GTCAGTAGCT	GTCCTGCTGT	CCACAGCAGC	CCCTCCGAGC	180
TGCCGTGAGT	GTTATCAGTC	TTTGCACTAC	AGAGGGGAGA	TGCAACAATA	CTTTACTTAC	240
CATACTCATA	TAGAAAGATC	CTGTTATGGA	AACTTAATCG	AGGAATGTGT	TGAATCAGGA	300
AAGAGTTATT	ATAAAGTAAA	GAATCCAGGT	GCACTCGAG			339

(2) INFORMATION FOR SEQ ID NO:1176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1176:

GAATTCGGCC	TTCATGGCCT	AGGGTCACCG	GGTTCCGGGC	TAAAGAAGCC	CCCGCGCTCC	60
CTAGAATCCA	GGAACGGGGA	CTGGCAGAGG	CCTGGGTAGG	AGTCCATTGG	GCTGCTGGAG	120
GGCAGATTGC	CCAAAGGGAG	TCCACCTTGA	AGAAAGGGCC	TCTGCAGTGG	CGTACGGCTG	180
CCTTNTAGGC	CAGGGGTTCC	ACAACCCAGA	TGCTGTTCTC	GTTTCAGAGCC	CAGAACATCC	240
TTGAAGAGCT	GCTGCAGGTC	CTTGGATTCC	ATCTTGGGCA	GTTCTCTGTG	GAAATCCTGT	300
CTAAGTCAGA	GCTAAGCATC	CCITCACCTG	GGGTGCCTGG	CTTCTCAGGG	TCACTGGGCA	360
CTGGGGATGC	CTTCACGCCC	CCATCCTCAG	GTCCTGGTGT	ATCGGCTTTG	CCCTCGAG	418

(2) INFORMATION FOR SEQ ID NO:1177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1177:

```

GAATTCGGCC TTCATGGCCT AAAGAACCCC GTGGTGATGG TGGACGAGAT TATGAGCTCC      60
AGCCCTCCCA AGTTCACCTT CCCTGAAGCA GGCTTACGAA TCATGATCAC CAATAAGTTT      120
GGACCTAGGA CCCGACTACG GATGGCCAGC AGGATCATCA TTAATGAGCG GCAGAGACTG      180
ATCAACTCGG CCAATGGTGT GAGCAGTAAG CCGCTTCAAA ACGGGAGGCA CGAGAACATT      240
GAGAACGGGA ATGTTCTCTG GAAAAACCCC GAAGACCCTC AGCAGAATCA GGAGCAGCAG      300
CCGCCGCCAC AGCCACCACC GCCAGAGCCA GAGCGGTGG AGGCTGACTT CCTGTCCCCC      360
TTCTCGTGC CGGGCTGGAG TGTAGTGGCA TGATCTCCGC TGA CTGCAAC CTCGCTTCC      420
CGGGACTCTC GAG                                     433

```

(2) INFORMATION FOR SEQ ID NO:1178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1178:

```

GAATTCGGCC TTCATGGCCT AGTTGTTGTA AGCATATTTA TGGTAATTTG TTACTGCACC      60
CTTGGGAAAC TAACACACCA AGGTTTCATGG ACAGCATGAA AAAGAAAAAC CATAGGCCAA      120
TATTGTGTTAG GAAAAGACAC AAAAGATCTA AACAAATATT AGCTCCTACC CCTCCAAAAA      180
AGCAAATTCA ATCCAGTAAG GCATTTGAAA AATATGTCAT GACTAATGAA CTTATTTAAG      240
TTTACCCAC AATACAAGGA TGGTTTAAAT TTTACAAAAA GTATTCATTT AATTCATCAT      300
ATTGATAAAG GAGGAAATTT AATTAAGATA ATCTCTTGAT TGTCTCTCA TATCTTTGA      360
TTATCTCGAG                                     370

```

(2) INFORMATION FOR SEQ ID NO:1179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1179:

```

GAATTCGGCC TTCATGGCCT AAAAAATACA AAAAAAAAC NNNANNGAAG AAAAAAGAAA      60
AAACTACCAAG CCTGAAAATG CATAGTGTTT GCTACCTTAT TGCTTTTAGC ACATCTAGAA      120
AGACACTAAA CCCAGTGAGA TTGCAAGTTT CAAAATATTG TGTGTATAT GGCTTTGCTT      180
AAACGGATAT ATTTGTTTCT GAGTGAAAAC TTTTACGTA GAGGTTTATT TGTAGAGGCT      240
TGTAACCTTA AGTGTAAGTT TTAGTGTTG TGTTAAGTTG TTCTTACCCC GCATTAGCAC      300
TCGAG                                     305

```

(2) INFORMATION FOR SEQ ID NO:1180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1180:

GAATTCGGCC TTCATGGCCT AGCTGGGAGG TGTAGGTTGT AGCGAGCCGA GATCACGCCA	60
CTGCACTCCA GCCTGGGCAC TATTGAGCAC TGAGTGAACG AGACTCCGTC TGCAATCCTG	120
GCACCTCGGG AGGCTGAGGC TGGCGGATCA CTCGCGGTTA AGGGCTGGAG ACCGGCCCCG	180
CCAACACAGC GAAACCCCGT CTCCACCAAA ACCAGTCAGG CGTGGTGGCG CGTGCCTGCA	240
ATCGCAGGCA CTCGGCAGGC TGAGGCAGGA GAATCAGGCA GGGAGGTTGC AGTGAGCCGA	300
GATGGCAGCA GTACAGTCCA GCTTCGGGCT CCGCATGAGA GGGAGACCGT GGAAGAGAG	360
GGAAACCGTG GGGAGAGGGA GAGGGAGAGG GAGAGGGGAG CGATTCTGGT GTATCTTAAC	420
TTGGATTTC ATCCTGTTTG GGTTCGCTCA GCTGAATCTA TAGGTTTGTG TATAATACCA	480
AAGTATTTTG TATTAGTGGT TACAACGCAA AGTTGGATCG TGAAGTCAAT TTTGTGGCTT	540
ATGACTAGTA TTATGATTGG TTTTAATAG AATAGAAAAT GAAAATATAT CCCAGGTATC	600
TCGAG	605

(2) INFORMATION FOR SEQ ID NO:1181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1181:

GAATTCGGCC TTCATGGCCT AGGAGAGTGG TGATGGTGGC ACAACAATGT GAATGTAATT	60
AATGCTACTG AGTTGTATGC TTAATAATGA AAAATTTTAT GTTATACACA TTTTATGACA	120
AAAATTAATA GATGTATTAA TAAGATTAAA TGGGTTGTTT TAATGTTCTG TTAATAATCA	180
ACGCTGAGGG CATTAAATGA GATTCTTATT TACCCACATG TCCTTTTAAA ACAAGAACCC	240
TCTTTAATAT GTGTTTCTT CTGGTTTATA GAACATATTT TAAAACGGGC TTAATATTCA	300
ATAATATCAA TTGATTATTG AGGAATACAA GTTAATTAAA TTGTGCAAGT CAGTTGTTTG	360
GCCTTACTTC ATGCTTTTGG TGAACACTGA TGCAGTACTA GAATTACTCT TTTTGATAAA	420
TTGCCAAAAG CAGGCCACCT CGAG	444

(2) INFORMATION FOR SEQ ID NO:1182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1182:

GAATTCGGCC TTCATGGCCT ACTGTTTCAA AAAAAAAAAA AGGAATCCAA AGAAAAAAAAAT	60
ACATCACCTG CAAAAGGTGA AGAGAGAAAG GAAGCTTTTT CTCTAAAAAT GGTGCAGCTA	120
TCCTCTGAAC CAATTCCTT CGGTTTAATG TACCTGTATC TTGGGGTTTT TTCCACTTA	180
ATTTATCCTG GAGCTCTTC CATAACAACA CTTGGAAAGC ACTCTCATCC TTTTTCAC	240
GCTGAACAGA ATTCCACTGT GCGGATGGAA CTCGAG	276

(2) INFORMATION FOR SEQ ID NO:1183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1183:

GAATTCGGCC	TTCATGGCCT	AGCATGTTGA	GATAACTTCT	GGGATTAAAA	TAGTCTTTTG	60
CTTTACTTTT	TTGGTTTCCT	AAAACAACTT	TATTGACTTT	TAGTCCATAC	TGTTATATTT	120
TTGTCTTAAA	GAAAATTTAA	ACTACAAATA	CCAAAAGAAA	ACATTTTAAA	TTTAGGGATG	180
AGACTTTGGT	GTATCGTGGG	TCTAGGTTTA	ATGAACACAT	CTGGGGTTAA	GTTGGCATT	240
CTTCACATCT	CCACACCCAC	ACCAACCATC	ACAGCCCCC	AAAATCTCGA	G	291

(2) INFORMATION FOR SEQ ID NO:1184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 364 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1184:

GAATTCGGCC	TTCATGGCCT	AAGGGGAGGC	AGAGGCTGTA	GTGAGCCGAG	ATCGCGCCAC	60
TGTACTCCAG	CCTGGGCAAC	AACAGTGAAA	CTCCGTCTCC	AAAAAAAAAA	AAAAAAAAAA	120
AAAACCTGTT	TTCCCTTTGT	AATTTGGTTT	TCCTAAAAAT	TTTAGTATTT	CTAGAGAACA	180
TTTTTTTCCC	AGGCTGTAA	CTGGTTCTGA	AAACAATCTT	ACAGTAAGTA	TAATTTAAAA	240
CATACCTCCT	TTTCCAAAAG	CTCATGTGT	ACCAAGCAAG	CACGTCTGTA	GTTAAAAATT	300
GTTACTGAGG	TTGGTTCAAG	GTAAGAAGAA	TGGAGAATAT	TTACAACATC	TTCAAATTCT	360
CGAG						364

(2) INFORMATION FOR SEQ ID NO:1185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1185:

GAATTCGGCC	TTCATGGCCT	AGAGTAAAGG	TGGGATTACA	GGTGTGTGCC	ACCACGCCTG	60
GCTAATTTTT	TTGTATTTTT	AGTAGAGACA	GGTTTCACC	ATGTTGGCCA	GGCTGGTCTT	120
AAACTCCCGA	CTTCAAGTGA	TCTGTCCACC	TTGGCCTCCC	CAAGTGTGGG	ATTACAGSTA	180
TGAGTCACCA	AGCCCGGCCT	GTATCCTTTA	TTAAAAGAAA	CAAACAAACA	AACAAAAAAC	240
CCTTTTCTTG	ACTGACATCC	CTTTTCAGCT	GCAGCCCTGT	TTCTTTGCTA	CCTTTGTAGC	300
AAAATTCACT	AGGTTGTTCC	TACTTGCTGT	TTCCAGTTTT	TTGGTTTTTT	TCCTTTCCTA	360
GGAAATGAGA	GGCCCATGCT	CGAG				384

(2) INFORMATION FOR SEQ ID NO:1186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1186:

CTCGAGGGGG TCAATTCCTG GGGGCTCTTG ATATTGCTCA GAGCTCTGGA GAAGTGTTCA	60
TCCACTACGC TGCTGATGTC CCCTTGGAAG TAGGTGAAAA GGACACACCG GGAATTCCAT	120
TCCGTCTTTA TAGGCTTCTG TTTGCCTTTG GGCAGCCGGA TGGCAGTCTT CTTCAATTTCT	180
TCCATTGTGA GTGAATGACA CAGGTGACAG CTCTTAATTC TGGACCATCA CTTGATTCTG	240
TGGCTGGGAA AAGATGGCCA GAGCTGCCTG GCTCACTTCA GAGCAGGTTA GTGCTTGCGG	300
AAGCAGGAGC TGAGGATTG TACTAGGCCA TGAAGGCCGA ATTC	344

(2) INFORMATION FOR SEQ ID NO:1187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 0 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1187:

(2) INFORMATION FOR SEQ ID NO:1188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1188:

GAATTCGGCC TTCATGGCCT AGCGATGGCT CACATCAGCA CTTTGGGAGG CTGGGGCAAG	60
AGCATCACCT GAAGCCAGGA GTTCAAGCCC AGCCTCGGCA ACACAGTGAG ATCTCATCTC	120
TACAAAAAAT TTA AAAATGA GTTTGGCGTG GTGGTACATA ATCGTGTAGT CCCTGCTACT	180
TGGGAAGCTG AGGCGGAAGG ATCACCTGGG CTCAGAAGTT CAAGGCTGCA GTGAGCTATG	240
ACTGCACCAC TGCACACCAG CGTGGGTGAC ACAGTGAGAG CCTATTAAAA AAAAAACAA	300
AACCAATAAA CCAACAAAAC AAAACCTAAA ATACAAAAAA TTAGCTGGGC GCAGAGGCAC	360
GGGCTGTAG TCCCAGCTAC AAAGAACCT. CGAG	394

(2) INFORMATION FOR SEQ ID NO:1189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1189:

GAATTCGGCC	TTCATGGCCT	AGGAGATGTA	CCTGATAGCA	ANTTACTGCN	TCTCAGCTCA	60
AAATTCACCC	TTCAAAACCT	TTTCTACACC	AATGGATAGA	ATTCTGTCA	GCATTCTCT	120
TNNAACGTTG	AACACAATGT	TAAGCTTCCT	CAGTGAAGGA	CCCTAGATGG	ACATTGCAGG	180
AAGAAGGGAC	TTCCCCTGTT	GGACCTAGAG	GTTGTACCAG	CATTGTAGGT	GGGAGGACAT	240
CCACTGGCTC	TTTGCAATAG	CCATGTGTCC	ATAAAGTATA	GTTTCTCAGC	AATCTCATTG	300
CCCAGTCTAG	GCNTGGCAAT	CACCCTCTG	CAGCCTTATC	AACACATTGC	TCGAG	355

(2) INFORMATION FOR SEQ ID NO:1190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1190:

GAATTCGGCC	TTCATGGCCT	ACTTGGAGAG	CCTCATGCCG	TCTCTACCTT	CGCACACTGG	60
TCAAGTATCT	GCTGAGCTTC	TTGGCGCAA	GGATGCAGAA	ATAGGCTGAG	GGTCCATGGG	120
AAGAAGACA	CAATGAGGCA	GTAGGAGGTG	GGAAGAAAAG	AAGACAGACT	TTCAAAATGG	180
AATTAGGCAC	TGGGGAGAGA	TCAGTTTCCC	CACATCAGGG	AGAAGAAGGT	ATAGGTGGGG	240
AAGGGGGTGG	CCAGGAGCAG	AAGGAAGAAG	ACTCAAGATG	GAAAGGGAGC	CGCTGTGCCT	300
GTGGCAATAC	CACTTGGAGA	GGTCGACTTC	ATACCTTCAA	GCCTTTTCCC	CTGGGCTTTT	360
GATTGTGTCT	GTGCCCCCTT	TCTTGTCTCT	TCTGCAGATG	CCCAGTAGGG	GCTACCTCAT	420
CCTCGTGTCT	TTCTTGTGTA	GCATTCTCGA	G			451

(2) INFORMATION FOR SEQ ID NO:1191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1191:

GAATTCGGCC	TTCATGGCCT	AACAGAGATG	GCTTAGACTT	CAAGACTTGA	TTTGTAGCTA	60
TGTTCTACCA	GCCTCCAGCT	GTCTATGCGT	TGGCCTCACG	CATGTCCCAA	ACGTGGTCCC	120
ACACATGTTT	ACACATTGGT	CCCACATATG	CTGAGAGTAA	TTACTTTCTA	TTCATCAGAG	180
GTCAGAATAG	AATAAAGAAT	GTTTATGTCA	TAGTATGACT	TTTTAGGTGA	TTTTGAAAAG	240
CAAGAATATG	AATTCTATGA	AAAAAATCTA	TTAGGAAATT	ATGGAAATGA	CAGAATGCAG	300
AGGTATTGG	AAATAGAAAA	AAAACGGGTG	ATCTCGAG			338

(2) INFORMATION FOR SEQ ID NO:1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1192:

GAATTCGGCC TTCATGGCCT ACCGACCACA TTCTACTCTC ACCGCTGTAG GAATCCAGAT	60
GCAGGCCAAG TACAGCAGCA CGAGGGACAT GCTGGATGAT GATGGGGACA CCACCATGAG	120
CCTGCATTCT CAAGCCTCTG CCACAACCTCG GCATCCAGAG CCCCAGCGCA CAGAGCACAG	180
GGCTCCCTCT TCAACGTGGC GACCACTGGC CCTGACCCTG CTGACTTTGT GCTTGGTGCT	240
GCTGATAGGG CTGGCAGCCC TGGGGCTTTT GTTTTTCAG TACTACCAGC TCTCCAATAC	300
TGGTCAAGAC ACCGCACTCG AG	322

(2) INFORMATION FOR SEQ ID NO:1193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1193:

CTCGAGGGGT GCTGAGCATT TTTTCATGA ACCTGTGGTC ATTCATATGT CTTCTTTTGA	60
GATGTGTCTA TTCAGGTCCT TTGCTTATAT TTTAATCAAG TTATTGTTT ACTATTGAGT	120
GAAAGAGTTC TTTATGTATT TTGTTATTA GCCCCTTAAC AGATATATGT ATAGCTTGCA	180
AAATATTTT CCCAGTCTGT GGGTTGTCTC TTCAATTGT TAATCTTTT TTTTTTTTT	240
GTGCTGGGC AGAACGTTT TAGTTTGATG CAATCCCATC TGTCTATTT TGCTTTTGT	300
GCCTGAGCTT TTGGGGTCAT AGCCAAAAA TCCTTGCCCA AACAGCAGTG TTATGGAGCT	360
TTTCCCTAA GTTTTtaggc CATGAAGGCC GAATTC	396

(2) INFORMATION FOR SEQ ID NO:1194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1194:

GAATTCGGCC AAAGAGGCCT AGGTAGGGAA TGCAAGCAGG CACTGGGGAG AAATNGGGCN	60
GGAAAGTAGT CTCATGGAAT AAGCCTTTTT TACTTTAATT CAGCATTAT TGCTTTGATT	120
AAAAAATAAT TTCAAAAATC TTTCTGCTTA CTGAATAAAG AATGCNTTGG AAAGAACAAG	180
AATGGATAAA GGAGAGTGCT TAGGAGGCTC CTGGAGCAGG AAGAGGTGGT GGCGAATAGA	240
CTACCGGAGC AGTGGAGGGT GGAGATGGAG AGACGTGGAA AGACTGAAGA CATATCCTCG	300
AG	302

(2) INFORMATION FOR SEQ ID NO:1195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1195:

GAATTCGGCC AAAGAGGCCT ACTCAGAAAC ACAAGGGAAA GGACAGAAGA GGGACCGGGG	60
-------------------------------------------------------------------	----

AGGAAGAGAG	TGAGGAGAGA	GGTATGTAAG	GTGTTTAGTA	CACAGTAAGT	GCTCAAAATG	120
TGTCCACTCC	CTCTGCCAGG	AGAGAGCAGA	AAGTCAGAAA	GGAGAGGACA	CCAATAGAGA	180
GGAAAGAAAG	GGGCCAGGCG	CCGTGGCTCA	TGTCTGTAAT	CCTAGCACTT	TGAGAGGCAG	240
AGGTGGGAGG	ATCGCTTGAG	CCCGAGAGTT	CGAGACCAGC	CTGGCCAACG	TAGAGAGACC	300
CTGTCTCTAC	AAAAAATACA	AAAATTAGGC	TGGGTGCGGT	GGCTCATTCC	TGTAATTCCA	360
GCACTAGGGA	GCTCGAG					377

(2) INFORMATION FOR SEQ ID NO:1196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1196:

GAATTCGGCC	AAAGAGGCCT	AGTGTTACAC	AGCACTCACA	CTAAAGATGA	AAAATTCCAT	60
TAGCTCATCC	TGGTTCTTCT	GCTTACTTAC	CTAATCATCT	GTTTATGATT	TAAAAAATA	120
GGGTACTGT	GAAGAGAGTG	CTTGTGTGTG	AGACAGAGAG	GGAGGGTTGT	TTTTCAAATG	180
TATAGAATAT	ACCAATGTAG	TTTTTGGTTG	GGTATTTTTT	TAAATCATGA	CTTTATTAAA	240
TTTACTTAAT	TAATATTCAT	TTTTATCCTT	TTTTTATGTT	TTTAAAGTTT	TTATTATTTA	300
TTAATTTATT	TGAGATAAGG	TCTTGCTCTG	TCACCCCGA	G		341

(2) INFORMATION FOR SEQ ID NO:1197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1197:

GAATTCGGCC	AAAGAGGCCT	ACAGAAATTT	AAATTAATCT	CTCATCCATT	GGCTTTTGCT	60
ACTTTAGGTT	AATATTAAAA	TATAACATAC	ATTTTTGGGG	TTTATGCTGT	TAGCTCCAAA	120
CCAAAGATT	TTGGAATTT	ATTTTGGAAA	TTTTGTGTTT	AGAATATGAA	TAAATCTGCT	180
TATTCAGAAA	AATTAAACCT	TGATAACTTG	GGACCTCCTA	TCCTGTATG	TTCTCTGACA	240
TACATTGAGG	GATTTGGCTC	TCTTTTGTTT	ATTTGTTTTA	CTAGTCAGAC	ATTCCTTTGG	300
CTGCCCATAC	TTAATTCTGT	TGGGTGTTTC	CGCCCCCGCC	CTCAGCTTCT	GAAGCTACTC	360
GAG						363

(2) INFORMATION FOR SEQ ID NO:1198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1198:

GAATTCGGCC	AAAGAGGCCT	ACCTGACAAG	TGTTAAGCAG	ACACATAGAG	AAAGTTAAAA	60
------------	------------	------------	------------	------------	------------	----

TTTGTTTTGA GTCCTTAAGA GTGAAGTTAA GGAATAAGAC CTATAAATGG ACACCATGTG 120
 ATGAGTGCTG TCATCAAAGC ATGGACAATG GGCTTTGAGA GTACTCGAG 169

(2) INFORMATION FOR SEQ ID NO:1199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1199:

GAATTCGGCC AAAGAGGCCT ATAAAAACGT TATGTTATTT TTGGAAGTTT TTCTCATATC 60
 TCTGTTGCCA GGGTCACTCG AG 82

(2) INFORMATION FOR SEQ ID NO:1200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1200:

GAATTCGGCC AAAGAGGCCT AAGGTGGTGC AGTGGGGACA GCACCTCCGA CCCTATGGGG 60
 TGTACCTTCA AGTAGCAAGG CTGACAATGA TGTCTAGAAA GGTCTCCACT TCTGCCTGAG 120
 TTTTGCCAAA CCCAGTGGTC TATAGGGATG TGGCAAAAGA ATGACCTACC GCAGTGTGAT 180
 TATCAGTGTT TTTTAAAATA AAGAGCACAG TTTTGCCTTT AAAATAATTC ACATCAACGG 240
 TATTTGGGAG AACATGGAGC TGGCATAACA TTGGCGTAGA AAGCAGGGCC AGGCCACCC 300
 ACGGGGCCCT CGTGTGGGGA CGGGTGCCTG AGCCCTGAG CCCCTCGAG 349

(2) INFORMATION FOR SEQ ID NO:1201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1201:

GAATTCGGCC AAAGAGGCCT AGGGGAAGAG GTTCAAATGT GGGGCTGGAC GTGGCCTTGG 60
 GGTGCGGATC CCTCACAAN ANTTCGTCTT CATAATCCTN ATGAGGTNGC GGGGAGTCCC 120
 GCAGGACAGA CTCAGATATT CGGAGGGAGA TCCTCCCTGG AGTGCTCGGG GCCCCAAGAG 180
 GTGTGTCTGG GTCAGAAGTG CTGCATAAAC TTGGAAGACT CTGCTGTTTT TGATAGTGCT 240
 TCAGGTTTGC AAAATCAGGG GCTGAGGATT CCTCAGGAAG GNTGTCTCT CTGGCTGCT 300
 GGGCCCACTT TGCTCGAG 318

(2) INFORMATION FOR SEQ ID NO:1202:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1202:

GAATTCGGCC AAAGAGGCCT ACTACAAGAT AACTTCCCAG TACTTTAAAA AAGTCTCAAA	60
GTCATAAACA AGAAAGAACT GAGGGACTAT TGCATATTGG AGCGATCTAA AGAAGTATTA	120
CAATTTGTGG AATTCTTGAT TAAATCCTGG ACCAGCAAAA GGACATTAGT GGGAAAATTG	180
ATGAAATTCA AATGAGATCT TATATTGAAG TTAATTGTGT CAGTGTACAT TTCCTGGTTT	240
TCATAATTGC AAGTGATTAT GTAAGGTTTG TTAATATTGG GAGCAACCTC GAG	293

(2) INFORMATION FOR SEQ ID NO:1203:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1203:

GAATTCGGCC AAAGAGGCCT AGTTTTGAGA AATAAATGGG ATAGCACGTG TAAATCACAT	60
AGAACAGTGC CTGGCACATA AACACTCAAT AAATGTTAAT TGATACTATA ATTTATCTAA	120
TTTATCTTTA TTCCTCCTGC AAAGATTCCCT TGGACTATTT AGAATCTCTG GTCACCTCTAA	180
TGAGATGGTG GTGTTTTTTT TTGGTTTTTT TTTTTTTTGC TTAAAGAAC TTCTGTAGAT	240
CAGCTGTAAT TTACTGCTAA ATAATCTCTT GTAGTTATTA TTTTCAGTCT ACTTGGGATC	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:1204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 598 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1204:

GAATTCGGCC TTCATGGCCT ACGAGATAAT ACTGGAGTCA ACTGTACATT AACTTGCTTG	60
GAGGGCTATG ATTTCACAGA AGGGTCTACT GACAAGTATT ATTGTGCTTA TGAAGATGGC	120
GTCTGGAAC CAACATATAC CACTGAATGG CCAGACTGTG CCATTTCTAG AAAAACGTTT	180
TGCAAACCAC GGGTTCAAGT CCTTTGAGAT GTTCTACAAA GCAGCTCGTT GTGATGACAC	240
AGATCTGATG AAGAAGTTTT CTGAAGCATT TGAGACGACC CTGGGAAAAA TGGTCCCATC	300
ATTTTGTAGT GATGCAGAGG ACATTGACTG CAGACTGGAG GAGAACCTGA CCAAAAAATA	360
TTGCCTAGAA TATAATTATG ACTATGAAAA TGGCTTTGCA ATTGGACCAG GTGGCTGGGG	420
TGCAGCTAAT AGGCTGGATT ACTCTTACGA TGACTTCCTG GACACTGTGC AAGAAACAGC	480
CACAAGCATC GGCAATGCCA AGTCCTCAGG GATTAAAAGA AGTGCCCAT TATCTGACTA	540
TAAAATTAAG TTAATTTTAA ACATCACAGC TAGTGTGCCA TTACCGATG ATCTCGAG	598

(2) INFORMATION FOR SEQ ID NO:1205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1205:

GAATTCGGCC TTCATGGCCT AGTCTAACCA TTATGGAAAG AGAACAGTCC CTTCAATATC	60
CCACTATCTG TAGGGCATGA CACAGCCAAA TCCAAGTCAG ACCATCCCTT TGATCAATTT	120
CTACCAATAA CTGTTTCATTG CACACCCTGT ACAGAGCACT GCGACCAAGC TGTTCCTTGA	180
CCTTCTCCTT TCCTAGTGTT TGGTCACAAC ACTCCCTAAA GCCCTAACTC AAGTTCTTGG	240
GATGATACCA CCAGAAGAGG GAAAAAAGGA GCCGTCTTCC TGAAGTCACC TGGGTAGAGC	300
AGCTGGGGAT TTTTCCTCC TCGAG	325

(2) INFORMATION FOR SEQ ID NO:1206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1206:

GAATTCGGCC TTCATGGCCT ACCCACTGCA ATGATGTTTA CCAGCACTAT TAACTTACTG	60
CAGACTCTTT GTCTGTCTGC TGGAGTTCAT GCTGAGATCA TGCAGAGCGA AGCCACCAGA	120
CTCGAG	126

(2) INFORMATION FOR SEQ ID NO:1207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1207:

GAATTCGGCC TTCATGGCCT ACTAATGTGG TTTTGTGAAG TTGCTGTCAA ATTTACGAGC	60
ATAAAATTGT TTGTAATATT CCCTTATATT CTTTAAAC TGCTATAGGA TCTGTACTGA	120
TGTTCTGTTT CATACCTGAT GTTTGTGTC TTCTGTTTGT CTTTTTNGT TGTGTGTT	180
GTTGTGTTA GTTTTGATAG AGGCTTACAA ATTTTTTGCT TAATTGATTT TCTCTATTTT	240
CCTCTTTTAT TTCTTCTTT AATAATTCCT TCCTTCTTGC TTTGGCTTCA TTTTGCTCNT	300
TTTGTAGTTT TTTTGGTAAT TCAATTACTG GTTCGACATC TTTCTCGAG	349

(2) INFORMATION FOR SEQ ID NO:1208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1208:

GAATTCGGCC TTCATGGCCT AGAGTGATTG TGGGTATATA TAGAGCAGAT TGTTTTAAAA	60
AGAGACTTGT GAGCCAAGAC TAAATCCTGG TTTTACTATT TATTAATCTG TATAGCTATA	120
GCCAAGCTAT TAAACTCCC TTATTTCTCA GTTTTTCGT TCATGAAGTG GGTACAGTAC	180
CTAAAGGTTT ATGTTGAG	198

(2) INFORMATION FOR SEQ ID NO:1209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1209:

GAATTCGGCC TTCATGGCCT ACAGGGGATG ATTCAGTCCG ATACAGTCAG GGAACCGTAC	60
ATAGAATAGA ATGACTAGAG TATAATCTGC AAAGGATGGA ATGGCAGAAG TAGTCAGAAG	120
AGGTATGCAA TGGTTGGATC AAAAAGAGCT TTGTATCCAG CGTCACAGGG CCTCAAATTG	180
TACTGTAATC ATATGTCTTT TACCTGTTCT CTGGCATTTA AATATTCTTG TAAAGAGCTA	240
AGCCATTACT GATAAAATGT CTGTTGTGTA CAGTTGTACA AATTAAATTC AGTCACAAAA	300
CTGAAAGAAC AGCAGTGGGA CATCTATCCT AGTGAAAGTT AGAATACT TTTGTGGTCT	360
TTAATAACAG AGTTGATTGT TTACCTTCTC CTTTGGTTAG AAGACTGGTA TGGGGATTGT	420
TTGGAATGAA GAGGTAGGAG AGAGAAATAA TTCAATTCTG TATTCTCCA TCATCTTTAT	480
ATTTGAACCTG AGAAATGTGT GTTCTATCA TTCATTCAA TTATTAAACA AAAACAGAGA	540
CTCGAG	546

(2) INFORMATION FOR SEQ ID NO:1210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1210:

GAATTCGGCC TTCATGGCCT AAAGATATTT TAGCTAACAG GAGAACGGCC CAAGGGGGCA	60
TTCTCATGTT AATTACCAA TGTGGGCTTG TCAAAATCAA ATAGCTCCAG GAATAATGCA	120
AGTAGCTCTG CATCATTATA TTGTTTGGCC CTCAACCCAA TATTAGCTAC TTTTAAAAAT	180
CTGGGTTTCA TAGGCTTTTA AATTAAAAG AGGAATCACT ATTGGGAGCC TTCAGAAGAA	240
TGTAAAGCAC AGCCAGCAGT GCCAGAGTTT AATGTAAATG ACATTAAAAA ATAGTTTCAT	300
ATCACACACT CGAG	314

(2) INFORMATION FOR SEQ ID NO:1211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1211:

GAATTCGGCC	TTCATGGCCT	ACGCATGAAA	ATTACTTAAA	CGTTGCACAC	AACGTTTCAC	60
AAAATCTTTT	GTGAAAGAAG	AAAAGGAAAT	TCAGTGTGTG	AGTCTCAGCA	GGAGTTAAGC	120
TAATGCAGCT	TAAAATAATG	CCGAAAAAGA	AGCGCTTATC	TGCGGGCAGA	GTGCCCTTGA	180
TTCTCTTCCT	GTGCCAGATG	ATTAGTGCAC	TGGAAGTACC	TCTTGATCTG	GTACAGCCTC	240
CAACCATCAC	CCAACAGTCT	CCAAAAGATT	ACATTATTGA	CCCTCGGGAG	AATATTGTAA	300
TCCAGTGTGA	AGCCAAAGGG	AAACCGCCCC	CAAGCTTTTC	CTGGACCCGT	AATGGGACTC	360
ATTTTGACAT	CGATAAAGAC	CCTCTGGTCA	CCATGAAGCC	TGGCACAGGG	CTCGAG	416

(2) INFORMATION FOR SEQ ID NO:1212:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 328 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1212:

GAATTCGGCC	TTCATGGCCT	AAGGGAAGCC	TGAGCAGGCC	AGTGGGCTGG	GCGCAGAGCG	60
GGGTGTGGGG	GCCAGGCTGT	GTGACCATGA	CAGAAAGAAC	CCCAGCTAGC	CCAGCTTGCT	120
CCCTGGGGCA	GGACTCACCA	ACCCCGTGAG	GGCCTGGGGT	AACAGTGGTC	CAGTGGCCAA	180
GACCAGCAGT	CGCCAGGTAC	CCACTGGCCA	CAAACCAACC	AGAATACTTG	CCGCTGGAGG	240
CCCAGCCCA	GGGTCAACCC	AGCCGCCGCC	CTGTCTTTGT	GTGTGGGTGG	GTCAGCCCCA	300
TCCTGCGCTT	TCGGACTAAA	AACTCGAG				328

(2) INFORMATION FOR SEQ ID NO:1213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 471 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1213:

GAATTCGGCC	TTCATGGCCT	AGAGGCATTA	ATATATTTTA	CATTACTGGG	ACCATAGTAC	60
AGAAATTTCT	AAATGGTTTG	TAAAATAACT	TGTTATTGTG	GTGTGTGTAA	AAGCAGTTAA	120
TACAATGGAA	AAACTCGTAA	TAAGAAGATA	CAGTTTAAAC	TCAAAAAGTT	TACCCAAGGT	180
AATTATGAGT	ACTACCTGGC	AAAACCTCAC	GGAAGCTGTG	GTATCACTTT	TATGATGGAA	240
GAATGGTGTG	TGCATTTTGT	GTAAAAGTAC	TTGCGGCTGG	GCGTGGTGGC	TCATGTCCCA	300
GTGCTTTTGGG	AGGCGAAGGC	AGGTGGATCA	TCTGAGCCCA	GGAGTTCGAG	ACCAGCCTAG	360
GCAACGTGGC	AAGAGCCTGT	CTCTCCAAAA	CCTACAAAAT	TTAGCCAAGC	TTGGTGGTGT	420
GAGCCTGTAG	TCCAGCTAC	TTGGGAGACT	CACGCTGGAG	GATCTCTCGA	G	471

(2) INFORMATION FOR SEQ ID NO:1214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 585 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1214:

GAATTCGGNC	TTCATGGCCT	AGTCAATGAA	AGAATTCCTG	CAGTTTCATT	ACCTATGAAN	60
ATTGTGGGGT	CCTCTTGTGG	GACATGAAAG	GGGGACAGAT	AGATGAATAT	TGTTTGGATT	120
TTTGGTCCTC	AGTGCCATCC	ACAGACTCCA	GAAGGGATCA	GCTATTTGCT	GAACAATCTT	180
TCAGTTCTCA	TAGAGCCCTG	ATATGTTTTC	AGGGTCCACA	AATGCCTGTG	ACGGTGGCCT	240
CAAGAACCCA	GTGTCCCTT	GTAGGTGGGA	TAGCATACCT	CTTAAAGGTC	AGCATGAGAT	300
TCCACCCATG	TCATCCCCAG	CATTGGTGGG	GTCAGCAGAT	CCTCTCTCTG	GGGTTTCTNTT	360
TTCTGCTCAA	CCTCCCTGCT	TTGATGGACT	GCACAGACAA	GCCCCATCTT	GGTGGGAAGGG	420
TCTCCCCATG	GGCTGTCTG	GAGGGTCACT	CCCACAGATA	TGCCCCATCC	TGGTGGGAAGG	480
GTCTCCCTGG	GGGCTGTCTG	GGAGGGTCAG	TCCCACAGAC	AAGCCCCATC	CTGTGGGAGG	540
GTCTCCCGT	GGGCCATCT	GGAGGGTCAG	TCCCACAAAC	TCGAG		585

(2) INFORMATION FOR SEQ ID NO:1215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1215:

GCGATTGAAT	TCTAGACCTA	CCTCGATAAC	CCAAGAGACT	ATGAGCAGAC	ATGACATCAT	60
TGCGATGGGT	AATGACATAG	TATCTTTAAA	CTACACAAAA	GTGGAACAGC	TTTGTTCAGG	120
AGCGGCCTAT	TGCCAATTCA	TGGACATGCT	CTTCCCTGGC	TGCATTAGTT	TGAAGAAAGT	180
AAAATTTCAA	GCAAAGCTGG	AACATGAATA	TATTCACAAT	TTTAAACTTC	TGCAAGCATC	240
ATTTAAGCGA	ATGAACGTTG	ATAAGGTAAT	TCCAGTGGAG	AAGCTAGTGA	AAGGACGTTT	300
CCAGGACAAAC	CTGGATTTTA	TTCAATGGTT	TAAGAAATTC	TATGATGCTA	ACTACGATGG	360
GAAGGAGTAT	GATCCTGTAG	AGGCAACGACA	AGGGCAAGAT	GCAATTCCTC	CTCCTGACCC	420
TGGTGAACAG	ATCTTCAACC	TGCCAAAAAA	GTCTCACCAT	GCAAACCTCC	CCACAGCAGG	480
TGCAGCTAAA	TCAAGTCCAG	CAGCTAAACC	AGGATCCACA	CTTCTCGAG		529

(2) INFORMATION FOR SEQ ID NO:1216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1216:

GAATTCGGCC	TTCATGGCCT	ATCGGCCCCG	CGGCGGAGGG	ANANGATCCT	CCACAGTGCT	60
CTCTTCAGTN	CCCCTTCAAA	TGCTGTTTTA	TCTCAGCGGA	ANGTACTACG	CCCTGTATTT	120
CCTCGCCACG	CTCCTGATGA	TCAGGTATAA	AAGTCAGGTG	TTGAGCTATC	CTCACCGGTA	180
CCTGGTCCTC	GATCTTGCTC	TGCTGTTTCT	GATGGGGATT	CTAGAAGCAG	TTGGGTTAAA	240
CCTGGATACA	CCCCTGATGC	CCGATGTCCA	GTGAGGAACC	AAGGCTGCGG	GGAAGGGTGG	300
CCCCACCCCT	TCCTCTTGTT	ATCAGGCCTC	AGACACACTA	GGAGGATGGA	GGCGAGTTCT	360
CTCAGCTGCC	CATCCACTG	AGGGGTGCCC	GGCCGTCACT	GTCTTGTTG	CACTCACGTC	420
CCAGAACCTC	TAGAGCTTGC	CCCCCAGGGC	GGGCACTGCT	GGGAGGGTGC	GAGCACCGCT	480
GCGGCACAGA	GGCCCGGTTT	TTGGNTGATC	TTCTGGGGCC	TGGCCTGCC	CTGAGGTGGT	540
GGGGACAGGG	TGTGGCCTGG	CCCTGCTGGG	GGCTGCTAGG	CCAACGGGAC	CCTCCCCAAG	600

CGCGCCGCAC ACTGCAGGTG CCTCGAG

627

(2) INFORMATION FOR SEQ ID NO:1217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1217:

GCAAATATTG AACATAATCT AAAATCTGAG GAAGAAAAGG ATCAGGAAAA GCAACAGATG	60
TTTGAAAATA AGCTTATAAA ATCTGAAGAA ATTAAAGATA CTATTTTGCA AACAGTAGAT	120
TTAGTTTCTC AAGAGACTGG AGAAAAAGAG GCAAATATTC AGGCAGTTGA TAGTGAAGTT	180
GGGCTTACAA AGGAAGACAC CCAAGAGAAA TTGGGGGAAG ACGACAAAAC TCAAAAAGAT	240
GTGATCAGCA ATACAAGTGA TGTGATAGGA ACATGTGAGG CAGCAGATGT GGCTCAGAAA	300
GTGGATGAAG ACAGTGCTGA GGATACGCAG AGTAATGATG GGAAAGAAGT GGTCGAAGTA	360
GGCCAGAAAT TAATTAATAA GCCCATGGTG GGTCTGAGG CTGGTGGTAC TAAGGAAGTT	420
CCTATTAAAG AAATAGTTGA AATGAATGAA ATAGAAGAAG GTAAAAATAA GGAACAAGCA	480
CTCGAG	486

(2) INFORMATION FOR SEQ ID NO:1218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1218:

GAATTCGGCC TTCATGGCCT ATGAATTCTA GACCTGCCTC GAGATCTGAG CAGGAATTAC	60
TCTCAGATGA CGCTTCATCT GTTTCACAAA TTCAGTCTCA AACTCAGTCA CCGCAAAATG	120
TCCCTGAAAA ATTAGAAGAA AACCATGAGC TGTTTTCCTA GAGCTTCATC TCCATGGAAG	180
TGCCTGTCAT GGTAGTAAAT GGCAAGGATG ATATGCATGA TGTTGAAGAT GAGCTTGCTA	240
AGCGAGTGAG TAGGTTAAGC ACAAGTACAA CCATAGAAAA CATCGAGATT ACTATTAAGT	300
CTCCAGAGAA AATCGAAGAA GTCCTGTCAC CTGAAGGCTC CCCTTCAAAA TCGCCATCCA	360
AGAAAAAGAA GAAATTCGC ACTCCTTCTT TTCTGAAAAA GAACAAAAAA AAGGAGAAAG	420
TTGAGGCTTA AATAAGTCT TTTTATAATT ATTATTATAA CAATGTGACA TTGCACATCT	480
AAATACCACA TCTCGAG	497

(2) INFORMATION FOR SEQ ID NO:1219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1219:

GAATTCGGCC TTCATGGCCT AAAAGATGGC GGAGGTGCAG GTCCTGGTGC TTGATGGTCG	60
-------------------------------------------------------------------	----

AGGCCATCTC	CTGGGCCGCC	TGGCGGCCAT	CGTGGCTAAA	CAGGTACTGC	TGGGCCGGAA	120
GGTGGTGGTC	GTACGCTGTG	AAGGCATCAA	CATTTCTGGC	AATTTCTACA	GAAACAAGTT	180
GAAGTACCTG	GCTTTCTCTC	GCAAGCGGAT	GAACACCAAC	CCTTCCCGAG	GCCCCTACCA	240
CTTCCGGGCC	CCCAGCCGCA	TCTTCTGGCG	GACCGTGCGA	GGTATGCTGC	CCCACAAAAC	300
CAAGCGAGGC	CAGGCCGCTC	TGGACCGTCT	CAAGGTGTTT	GACGGCATCC	CACCACCCTA	360
CGACAAGAAA	AAGCGGATGG	TGGTTCCTGC	TGCCCTCAAG	GTCGTGCGTC	TGAAGCCTAC	420
AAGAAAGTTT	GCCTATCTGG	GGCGCTGGC	TCACGAGGTT	GGCTGGAAGT	ACCAGGCAGT	480
GACAGCCACC	CTGGAGGAGA	AGAGGAAAGA	GAGAGCCACT	CGAG		524

(2) INFORMATION FOR SEQ ID NO:1220:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1220:

GAATTCGGC	CTTCATGGCC	TATGATAAGT	TCATTCTGGC	TGGAGTATGG	TGGAGAGCCA	60
TGGAGTACTG	GTAGGTGAGG	GGCTGGAGGA	GGGATAGGTT	GGAGATGTTG	AGAAAGGCTT	120
TAAAGATCGT	GGTGAGTTGT	TTGGGTTTGT	GTGGCTGTG	AGGAGTCATC	AGAGGTTTTA	180
ATGCAGGAAA	GTGTTTGTGA	CTCTATACTC	CAGCAGCAGA	GGTTGGTTGA	GTGGTGCTCA	240
AACTTTGTG	TGTATTGGAA	TCATCTGAAG	AGCTTATAAA	AATACCAGTA	CCCAGGCTAC	300
AAACAGTAAA	ATCAGATTTT	CTGAAGGAGA	GGCCAGATA	TTGGATTTT	GATAATTTCC	360
CAGGTGATT	CAGTGCAT	CTGAGTTTGA	GAAGTACTCT	TTAGAGGGG	TCTGATGGAG	420
TAAGGAATTC	AGAGGCCACT	CGAG				444

(2) INFORMATION FOR SEQ ID NO:1221:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 354 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1221:

GCTTGAACAA	CACAGGTTTG	AACTGTGCAG	GTCCACTTAT	CCATGAGTAT	TTTCAACCAA	60
ACTAGTATCA	AATATACAGT	ATACGCGGGA	CTTGAAACCC	ACGTGTAAGG	AGGACGAAGT	120
TTTCGTGTAA	GTCAGCTCCG	AAGCACTGAC	TTTGGGACTT	GAATTTGCAC	AGATTTTGAT	180
ATGAAGTGGG	GAAGGGGGTA	ACTTGGTACA	AATCCCCTGC	ATATACTGTG	GGATGACTCT	240
AGTTTGATT	TGGAGTGATA	TATGGAAGAC	ATAATTCTTC	CCATAAAAAA	TCATAATCTT	300
GGTAGTCTAT	CATAGTCTAG	CATTAAGAGC	ATGAACTTTG	GAGCCGTCCT	CGAG	354

(2) INFORMATION FOR SEQ ID NO:1222:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1222:

GAATTCGGCC	TTCATGGCCT	AGCTAGTTCA	TGCTTGCGTT	GAAAGAGTGG	TCGTTGCGC	60
TGGGTCATCA	CTGTGTAGTA	TTGGGGATAC	TTAGGTGAGA	AAAAAACTTA	ACGCTAGAGA	120
CGTTCACGCA	CTAGTGGAGA	AGCCAGGATT	GTTGCCCTAG	AGTTACAGTA	GATAAAAGTA	180
CCTCAGAGAA	CTGCGGGGGC	TCCCAACCTG	GACGCTTGCA	CCGGAGTATT	AAATCCAGCT	240
AGAGAAATGGC	ATGTGCAAAG	ATACAGAGCT	TTTAGAAGTT	GCCTGCATTG	CTTGGCCCCA	300
TCCTCACTCG	AG					312

(2) INFORMATION FOR SEQ ID NO:1223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1223:

GAATTCGGCC	TTCATGGCCT	AATAAAAACT	GGCTGGGCGT	GGTGGCGGCA	CCTGTAATTG	60
CAGCTATTTG	AGAGGCTGAG	CCAGGAGAAT	CGCTTGAACC	TGGGAGATGG	GGGTGTCAGT	120
GAGCCGAGAC	CGCCCCATCG	CACTCCAGCC	TGGGCAACAA	TAGTGAAACT	CCGTCTCAA	180
AAGAAAAAAA	GTTTCCTTAG	AATGGAAAAT	ATTCAATTCAT	GAGCTCTTTT	GGCAATCCGT	240
CATCAGTATA	TTCTGAAAAC	CAATAAGATG	TTGCCAAGTT	GGGGGCGAGA	GCTATGTAAT	300
GCAAGGCATA	TGCCTGATGA	AGTATACAAA	TACACCTGAC	CAGAACTTTT	GTCTCCCAA	360
TAAGTCTCGA	G					371

(2) INFORMATION FOR SEQ ID NO:1224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1224:

GAATTCGGGC	TTCATGGNCT	AAAGAAAAGT	GCTGTAAATG	AGGATGTGGC	TTGCTGGGCA	60
ATAATCATTG	TAGAGTGGTA	CACCCAGTGC	CTTCACAGGA	TGCTTGAATA	CTGCCTGCAA	120
GCCTCGTGTC	ATTAGCCCAG	TAGGCATATG	ATAAGCCTCT	GGTCATCATT	TCCACTGTTA	180
AGAGTTAGTG	TCAGATATGG	AGCACCAATA	GGCTTGTAAG	TGAGAGCATC	CCTCAAAGTT	240
GTCACCTTAG	GAGACTCTGA	TGACCATGAT	GCTGCCATTG	TCCAAATGTG	CACTCATCTG	300
TCTTTTGGGG	AGTGATTCCC	GACAAATTTAT	AGATTACAAG	AGAAAAGCAG	TCTGTATTTT	360
CATCAAATGA	TAGTTTAAAT	GGAAATGAA	TCAGAAGTCT	CGAG		404

(2) INFORMATION FOR SEQ ID NO:1225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1225:

GAATTCGGCC	TTCATGGCCT	AGTTGGGGTT	AATTATGGCA	CCTAACTTAT	AGAAGAGGAA	60
ACCAATTAG	AGACATTAAA	ATACTGTTC	AAGGTTACAC	GGCAGGAAA	AGGCAGAGTC	120
AGGATCTGTA	TTCTGTAGTC	TGAATCCAAA	GCGAATCCAA	AACTCTGAGG	TGCTNTGCTC	180
TGCTACCTGC	TGATGGTTCT	GCTGGGGGAT	GCTCAACCAC	CAGATGTCTT	ACTTGGGAAC	240
TGCACCTGGAG	GTCGAGGGTC	TGCATTCTCC	TTCTGTGTA	AAATCACAAC	GTCCCCATCT	300
TTCAAGCCAT	AAGAAGCCAA	TGATCTGTGG	TTGTCTGTGA	GAGGTCTTTC	CGCATAGACG	360
ATCTGGCTCT	CGGCTGCGGG	GATGCCAGAC	TCGAG			395

(2) INFORMATION FOR SEQ ID NO:1226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1226:

TCAAAGGTCC	TTTTGTGGAA	GCGGAGGTGC	CCGATGTTGA	TCTGGAGTGT	CCTGATGCAA	60
AGTTGAAAGG	GCCCAAGTTT	AAGATGCCTG	AGATGCACTT	CAAGGCCCCC	AAGATCTCCA	120
TGCCTGATGT	GGACTTACAC	CTGAAAGGCC	CCAAAGTCAA	AGGGGATGCG	GATGTGTCGG	180
TGCCAAATT	GGAGGGAGAT	TTAACAGGCC	CCAGTGTGGG	TGTGGAGGTG	CCTGATGTTG	240
AGCTGGAGTG	TCCTGATGCA	AAGTTGAAAG	GCCCTTGTCT	CGAG		284

(2) INFORMATION FOR SEQ ID NO:1227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1227:

GAATTCGGCC	TTCATGGCCT	AAGCAGACGG	GCAGTAGGTC	CCAGAGTTAT	ACTTCGGAGC	60
ACATGTTCAA	GAGGGAAATG	ACGACCGGCC	CCCAACGGTCC	TGGGATGCAG	GTGTGAGGAC	120
TGAGAATGCT	GGACGGGGTG	TGGTCGAGGC	ATGGTCAGGG	TGGCCCCGAG	CTGTGCCCCA	180
CCCCAGGGAT	GCAGCAAGGG	TGCTCTGTGC	AGGACCCOGA	ACTTGGGCTC	TGCCCACTTT	240
CAGTGTCTGT	TGCATGTCAC	GCTGGCATCT	TCGGCATGTC	CACAGTTTGT	CACCCCCCAT	300
TTGGAGAAGC	TGCAGCGGAA	GATGGTTTCC	TCTGTGCCCT	GCAGGCAACG	TCATCCATCC	360
AGATCCTCCC	AGTGCCTTGC	CCGAATCGAN	CTGTGCGGTA	CATCCTCCA	NACCGCGGAA	420
GCCGAGCATG	CGGCACACCA	CGTCTCCGTC	CTTCTGTGCC	CAGCCGTCGT	CACACACAGT	480
GCCCCAGCGC	CGGTGCTGGT	ACACTTCCAC	GCGGCCCTCG	TGCGGACCTG	AGCCATTAC	540
CAGGCGGATC	ATCATCGGGG	CCTCCACGCC	ACTGGCATCC	CCAGCTCTGT	CTCCTTTCTC	600
TCCTTTCTCT	CCTTTTGGGC	CTCGGTCACC	TAAAACAGAG	GAGGAAACTG	GCATTAGAAA	660
TGAAAAGAAA	TCCTAATTGT	GAATAAAATA	TTACCTGCAG	GAGATTGATG	AACTCGAG	718

(2) INFORMATION FOR SEQ ID NO:1228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1228:

```

GAATTCGGCC TTCATGGCCT AGCTGGGTTG ACCCTGCAGA GGCCAGAGAG CCGAGGGGCC      60
ATGTGTGCTG GCATGGGGCT CCTGCCCCT TTCTGAGGCT CAGCACGGAG GGGAGAAACC      120
CACATTTTCA GAGGGAACCA GCAGCAGAGC AGAACCAGTA ACCAAGATCC CGGCAACCCC      180
TTGTGCTGAC CCCACACACG CTTCCCTCT TCCTGGCCAG GCCACTCCAA AGCTCTGTGC      240
ACACAGACAA TAGACATCAG GACTTTCATC TTCACTGTC ATCTGGCAGC AGAGAGCCTG      300
CAGGGCTGGG CTGCAGGGAG AAGAGTTCCT TTCCTCACGC ATCCAGGCAA GGGGAGAGCA      360
GCTCTGTGCC TGCCACTGGC CCACTCGAG                                     389

```

(2) INFORMATION FOR SEQ ID NO:1229:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 289 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1229:

```

GAATTCGGCC TTCATGGCCT ACACAAACAT GATTTTATTT TATTATTTTA TTTTATTTT      60
TTATTTTATT TTGAGATGGA GTCTCGCTCT ATCGCCCAGG CTGGAGTGTA GTGGCATGAT      120
CTCGGCTCAC TGCAAGCTCC GCCTCCTGAG GCGGGAGAAT TCCTTGGGCC TGGGAGGCGG      180
AGGTGCGGT GAGCTGAGAT TGCCCCATTG CACTCCAGCC GAGGCAACAA GAGCGAAACT      240
CCTTCTCAA AACAACAAA CAAACAACAA CAACAACAA ACTCTCGAG                                     289

```

(2) INFORMATION FOR SEQ ID NO:1230:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 600 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1230:

```

GAATTCGGCC TTCATGGCCT AATGTGTTTT ATGAACGATA GATCACATCA GAACTCCTGT      60
GGGGAGGAAA CCTTATAAAT TAAACACATG GCCCCCTTAG AGACCACAGG TGATGTCTGT      120
CTCCATCCTT CCCTCTCCTT TTCTGTCACC TTTCCCCTA GCTGGCTCCT TTGGACCTAC      180
CCCTGTCCTT GCTGACTTGT GTTGCAATTG ATTCCAAACG TGTTTACAGG TTCTCTTAAG      240
CAATGTTGTA TTTGCAGGCT TTTCTGAATA CCAAATCTGC TTTTGTAAA GCGTAAAAAC      300
ATCACAAAGT AGGTCATTCC ATCACCACCC TTGTCTCTCT ACACATTTTG CCTTTGGGGA      360
TCTGTTGGG GTTTTGGGTT TTTTGTGTT GTTGTATTAT TGTTATTTTA AAGGTAAATT      420
GCACTTTAA AAAAATAATT GGTGACTTA ATATATTTGC TTTTCTCTC ACCTGCACTT      480
AGAGGAAATT TGAACAAGTT GGAAAAAAC AATTTTTGT TCAATTCTAA GAAACACTTG      540
CAGCTCTAGT ATTCACTTGA GTCTCCTGT TTTTCTGTA CCGGTTATC CTGCCTCGAG      600

```

(2) INFORMATION FOR SEQ ID NO:1231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1231:

```

GAATTCGGCC TTCATGGCCT AGGAGGGCCA CATCTGCCAN AGCCTGGAGT CTGCGAAGGC      60
CGGGACCCGG TTCCTCGGCC CACAGTGGGG GTGTGCAAAC CCGAGAGAAC TGGGTTGCAA      120
ATTCGTGAAG AATCAGCATC ATGTTTGGCA GCTGAGTATT GGAGCCAGGA GCCTGCCATG      180
AGGTTTTGAG AACAGAGTGC TGTTTTAGAG CTGGCAGCAG CATCTCAGCC CAAGAGAAGG      240
TTATATTCCC AGAGGATGTC AGTCCCAAG ACCAGTAGCT GCCATCAGTT TGGATTCTGA      300
AAACTAACTG GCATCAACAC TGGGTGTAGA AACATGCTTG CCTTATGTAT CAGAGGACAT      360
GCTCAGCAGA TCCAAGAGAT ATATTTGGCA ACTTTTCTA GAAAAGGCAC CTGCCTCGAG      420

```

(2) INFORMATION FOR SEQ ID NO:1232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1232:

```

GAATTCGGCC TTCATGGCCT ACCACCCGGG ACAGTTTCCC AGCAGGGCTC ACAGCAGCGT      60
TCCGCGTCAT GGGGATTGCG CAGCGTCTGC TGCTTTTGGG TGGGGTGTGG CTCGGGGCTG      120
GTGGCGGGGC CACTGCCCGG CTTGGGGGAA GCCGAGCGAT GGTTTGTGGG CGCCAGTTGT      180
CTGGCGCCGG GAGTGAGACC CTAAACAAA GAAGAACACA AATCATGTCC CGAGGACTTC      240
CAAAGCAGAA ACCGATAGAA GGTGTTAAAC AAGTTATAGT TGTGGCTTCT GGAAAGGGTG      300
GAGTCGGAAA ATCTACTACA GCAGTGAATC TTGCACTTGC ACTAGCAGCG AACGATTCTG      360
CCAAGGCCAT TGGTTTGCTA GATGTGGATG TGTATGGACC TTCAGTTCCA AAGATGATGA      420
ATCTGAAAGG AAATCCGGAA TTATCACAGA GCAACCTAAT GAGGCCTCTC TTGAATTATG      480
GTATTGCTTG TATGTCTATG GGCTTTCTGG TTGAAGAAAG TGAACAGTA GTTTGGAGAG      540
GCCTTATGGT AATGTCGGCC ATTGAGAAAT TGTGAGGCA GGTAGATTGG GTTCCACTCG      600
AG                                                                                   602

```

(2) INFORMATION FOR SEQ ID NO:1233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1233:

```

GAATTCGGCC TTCATGGCCT ACTANACCTG CCTCGTAGTC CAGAAAGATC CCCACGCGCC      60
TGGGTGGGTC CCGGAGTGGA GCCAAGGCCG GTTCCGAGGA NTTGTAATAG CTCCCAGGA      120
AGACCAGGAT CCAGAAGCCG TTGCCCGCGN ANAGCTCGCC CTTCTCCTTC CTGTTACGT      180
TCTCCCTGCA CACCCCCAGG GCCCAGCTGG TCGGTCCCC AACCTCCACC TCCAGTAGT      240
GGCGGCTGAG GTGAAGCGCT CCTGGCCAG CACGCAGGGG CCGGGGTCAA AGCGCTCTGG      300
GCTGTCCGGC ANGGCCTGCC GTANGTCCCC CGCTGCAGG CGTCCGCTTG TCTTCAGACA      360
GGATCAGCTC AGGGTTGGCG GTGTCCGGGT CCAAGGTACG GTCCCCCGA AACCTCCGCA      420
GTGTTTNTAC CAGTCCCGGG ACCCTGCACA CGGTCCTCAG CTCCATAGGC ACAACTTNTG      480
GGGCTGCAG CTTACATCC TGGACCCTGC NCAGGCGTC CTTGATGTCC TGCAGCAGCC      540
CCAGAGCAGG CAGCTGGCAG CGGCCCTCGA G                                                                                   571

```

(2) INFORMATION FOR SEQ ID NO:1234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 631 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1234:

```

GAATTCGGCC TTCATGGCCT ACTTAATTTA TAGTCTTTTT CTGTGAAAT GATCATTGAA    60
GTAGTTACTA ACAGGTAATG AAATAAAATA CCAATTTTGC TAGTGAAAAA TAGTTTTCAG    120
CTGAGAAAAG CACTTGGCAG AAGACCTACA AACATGCAGG CTAATGCTAC ACTCTATTGC    180
AGCTTCAAAT AAGTTGTTTT TGATGCCTTT TGAGAAGAAC AAAGTAAGAT GAAAATAATT    240
CCTTGAACAT TTATCAGCAT TGCTGTTTAG GTACCCATTA GAAAGTGATT AACATTGAT    300
ACCTACCTTT TCCAAAACAC AAAATCACTG GCAAGCATCA TCACACACTC CTAAACCAGC    360
AACATCTGAG AAGCACAAAA CACCTTCCCT TTTGTCTAAT AACCTGTTGG TTAGTTATTG    420
GAACTGCAAG GCTTACAAAC TCCTCCCTG TCCTTTATCC TTATGTAAGC TTGCACATTC    480
TCCAGGAATA GCTATTTTCA AAGGTAATTT CAAAAGAATT AATACAATGA ATTCTACTGG    540
GCAGTTTGGG GGAAAATATT GACGATATTA AAATTTAAAA AATGCCTGCC TGACACATAT    600
AAGGCCTCCC CAGTCCCTCA TACAACCTGA G                                     631

```

(2) INFORMATION FOR SEQ ID NO:1235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1235:

```

GAATTCGGCC TTCGTGGCCT AAGGACAGTG TATAAAAAGG CAGCGTCACA CAGGTGGGCT    60
CTGGGGTCTT TGGTCCATTA GGAGATGGCC TTGTCCTCAG GAAGGAAGGC TTCCCAGTAC    120
TTTGCCAGCT GCTGCTGTGA GTAAAGGAGT GTCTCAAGGT ACTTGATGAC GTGGTCTTGG    180
AAGTCCTTGG ATTTCTCTTT CTCAAAACCGT ATCACTTCTT TTCGGACCAC TGTTGAAATC    240
CTCTCGAAGT CCCTTTCATA TTGAGTCACC CGAGAGTCCC ACTCGAG                                     287

```

(2) INFORMATION FOR SEQ ID NO:1236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1236:

```

GAATTCGGCC TTCATGGCCT AGGCTGGCGG GGTAGGGGTT GGTGGTAAG GCTTGAGCAG    60
AAGGTTCTAG ATGCATTGAG GAGATAAAGA TGCATTGGG GTTATTGCAC TTCTCCTAGA    120
AACATAAACA TTGACTTCCT TTGTGGAAG AAAAATGTTA TGTTAGCTAT TTGACGTTTC    180
AGGAAGGGTG GCTTCAGCTT GGNATTTGGG GATGTTTGTG TACANGTGGC CAGGCTGCTT    240
TCTGCTTGG AAGACTATTG TTTCTTGGGA ATTGTCTGTA TCAGACATCA TGGGAGCAGA    300

```

TCCAGGGCGA	CATCAAAGGG	AACATGATTN	NCNNAGGACC	AGAGGGGCTT	GGATGCAGAT	360
GATCATCATC	TGGGCACTGN	TGGATACTGA	GTAAGCCCCA	GCTGCACCCC	ACCTCTGCGC	420
TCTGAGCATG	GGAGGCAGCC	TGTGCAGCTA	TAATCAGCC	TGACTTTTTC	CTTCCCTGCA	480
TACTCTTGAA	ATACACTGGA	GATGAGTAGG	GGCGAGTGAG	CTGCACACCA	GAATAAG	537

(2) INFORMATION FOR SEQ ID NO:1237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1237:

GAATTCGGCC	TTCATGGCCT	ATCTCCANAT	AATTNGATC	ATAGGCCGGA	GTGAGTCATT	60
CCACCTGCAC	CTTCTGTAC	AAATACTAAT	TCAATTTTAA	GTCTTAAGTC	ACTTTTTTAA	120
TATATATGAT	CTTCTGCTCT	TCCCACTTCC	TCCCNNTCT	ACTGCTCTCC	CATTTTCCT	180
TGCTGGGAGT	AGCCACATGC	TTTTTGCCCC	CAAACCTTG	TATATGGGGA	CAGTGGGGTC	240
AGTGCAGCTA	CCCTTTCTTT	CCCTCTGCG	GAACAGCGGA	CCCAGCAAGA	GCATCCACAT	300
CTCGAG						306

(2) INFORMATION FOR SEQ ID NO:1238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1238:

GAATTCGCCT	TCATGGCCTA	ATTTTCATGCC	CCATATTTGG	CATATAGTGG	AAGGAGAAAG	60
GTAGTATTTT	TGCAGTATTT	AATAACATTG	AGCCTTGAAG	CTGTTTGGCA	AAAGGTAAGT	120
TTCTTTTGTG	GCTTTGCTGA	AAAACAAGGC	ATAGATTTAC	ATAGATACGT	GTTTAATCT	180
CTGCTTCACT	AAAGAAAGCA	AATGCCTATT	AAGCCACTTC	AGTTGGGATA	ATCCCTGATT	240
ATTGTGAGAT	TGAAATTACT	TTGTCAATT	TACAAATAGT	TTTATCTTT	CCATTTACAT	300
ATTTACCATG	ACAACTCGAG					320

(2) INFORMATION FOR SEQ ID NO:1239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1239:

GAATTCGGCC	TTCATGCCTA	CAGCGATGAG	TGCACGAGTG	AGATCAAGAT	CCAGAGGAAG	60
AGGAGATGGT	CAGGAGGCTC	CCGATGTGGT	TGCATTCTGT	GCTCCCGGTG	AATCTCAGCA	120
AGAGGAACCA	CCAACTGACA	ATCAGGATAT	TGAACCTGGA	CAAGAGAGAG	AAGGAACACC	180
TCCGATCGAA	GAACGTAAAG	TAGAAGGTGA	TTGCCAGGAA	ATGGATCTGG	AAAAGACTCG	240

GAGTGAGCGT GGAGATGGCT CTGATGTAAA AGAGAAGACT CCACCTAATC CTAAGCATGC 300
TAAGACTAAA GAAGCAGGAA GACTCGAG 328

(2) INFORMATION FOR SEQ ID NO:1240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1240:

GGGGATCCTT TTATTTTAAAT CACAAAAATG CTGAAAATTT TGGGTTGCAA TTTCAATCCA 60
 CAGTAAAGCA TGGGCATTTT TTTTTTTTTT TTAAATCAGA GTGAAGTCCC TCGCGTCTTT 120
 CTTTTTAAGG GTTACACTGT ATGTGTTCTG TGTTTTATTT AACTGTTCCC CTCCTGAGGG 180
 GCATTCCGCT TGTTCGAGCT TTTCTCCCTC TTGCTGACAG TGCTGCAGTA ATCATTCTTG 240
 TCCATTTTAA TCCCTATGTA TTACACGGT ATTCTCGAG 279

(2) INFORMATION FOR SEQ ID NO:1241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 445 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1241:

GAATTCGGCC TTCATGGCCT ACGGAAAAGG AAACCTTGGT GGGATTGCTG TGGATGACAT 60
 TAGTATTAAT AACCACATTT CACAAGAAGA TTGTGCAAAA CCAGCAGACC TGGATAAAAA 120
 GAACCCAGAA ATTAATAATTG ATGAAACAGG GAGCAGCCA GGATACGAAG GTGAAGGAGA 180
 AGGTGACAAG AACATCTCCA GGAAGCCAGG CAATGTGTTG AAGACCTTAG ACCCCATCCT 240
 CATCACCATC ATAGCCATGA GTGCCCTGGG GGTCTCTCTG GGGGCTGTCT GTGGGGTCGT 300
 GCTGTACTGT GCCTGTTGGC ATAATGGGAT GTCAGAAAGA AACTTGTCTG CCCTGGAGAA 360
 CTATAACTTT GAACTTGTGG ATGGTGTGAA GTTGAAAAA GACAACTGA ATACACAGAG 420
 TACTTATTCG GAGAGCATTC TCGAG 445

(2) INFORMATION FOR SEQ ID NO:1242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1242:

GAATTCGGCC TTCATGGCCT AATCATGCCT CCTGCTTTTG TCACCTAATA CGTGACAGAC 60
 TTCTTGCCAT ATGTGGAAAT AGATAACTCT TTCACTATTC TTAATAATGG ATATTTAGAT 120
 GGCTTCATT TGTCCCTGTT ATTGTTGTAA CATATATTCT TGCATACATT TCCTTTCATA 180
 CTTACTCAAT TATTAGCTGA ACTTTGGAGT AAAATCACTA AGTAAATACG TTTTAGGCTT 240
 TTGCTATGTG TTACAAGATT TCCTGTCAGC AATTTAAGAT ACTTTTATTG CTCCTCACAG 300

CCTTGCCAGA ACTCATTGGG ACACTCGAG

329

(2) INFORMATION FOR SEQ ID NO:1243:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1243:

GAATTCGGCC	TTCATGGCCT	AAAAATAGTA	AATTCCCAGA	AATTCAGTGT	TTAGACGAGG	60
GAATTTAATT	CCTATTTTGT	CCATGTTGGT	GATGTACTGT	ACTTCCCTTC	CTTTTCTCTG	120
CATCCCCCAT	CACCTCATAG	AAGACTCTTT	GTTGATCATT	GTATGTTAAT	AATGTATAAA	180
ATGGCTATCT	TGTAAGCGTG	CTGTCCTGGT	ACTAGTGTAG	CGACTTTTTT	TCTCCTCTTT	240
CTTCTAGTAC	ATATTGATAG	GTATAACATA	ATTAAGGTTT	AAAAAAAATT	AGACATAGTT	300
ATTCAGATTT	AGGACCAGTA	AGGATAGAAC	TTTCTCTTAT	TTATGAAAAA	AAATGCTAAT	360
AATTTTGGGG	CAGTTTTTTC	CTTTAATTAT	TTTTTTCAAT	TTCAAGTTTA	ATTTTATTTT	420
AGCTGATCTC	GAG					433

(2) INFORMATION FOR SEQ ID NO:1244:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1244:

GAATTCGGCC	TTCATGGCCT	ACATGACTGA	GTATATTACC	TCTGTTTGAG	AGAGAACCAT	60
TTTCTTCAGA	AATTCATATC	CTACCGTTCT	GCTGTTTTTC	ATGATAATTG	TTTTTCTCCT	120
AACATTATAT	TTCTGTCTTT	TAGATTTTAG	TATTTACCTT	TTAGAATAC	ATTTTGGATG	180
ATGAAGTTGT	TTTTCTTATT	TCTCCTACCC	CCTTTCCTTC	ATCTCAGACA	TTATTTCCCA	240
GCTTTCITTG	TTTCAGCTTT	TTATTATGAA	AAATGTCAAA	TGTGCAGAAA	AATGGAAAGA	300
ACAGTACAAC	ACACCCCCAA	TCTCGAG				327

(2) INFORMATION FOR SEQ ID NO:1245:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 397 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1245:

GAATTCGGCC	TTCATGGCCT	ACTGAGAATC	TTCACCATTA	AACTTAGGAG	TGTTCTACAA	60
AATAGTGCTT	AGAACAGCTA	TTGATACTCA	AGAGGGCTGT	TTAAGTAGCT	AGAAAAGTCT	120
AACCTAAAAT	CCCATTGTG	ATTAGATTAT	GCACTGATGA	AAAAATGTTT	AATGCCGTTA	180
AAAAGAACT	ATTACATTAT	ATTCTTTCAG	GCCATGGTAA	AGTTACAAAT	TTGAACTCAA	240
TAGGCTGTGT	GTGTATTGT	ATGTGTGTAT	TTTTCTTCT	TTTATTGGCA	GTCTCAATAA	300

TTGTTAAGCC ACACACTGCA CAGTATACAC ACACACTGCA CACCACACAC ACACCACAGA 360
 NTGCACACCA CACACAGCAC AACCACCCAC ACTCGAG 397

(2) INFORMATION FOR SEQ ID NO:1246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1246:

GAATTCGGCC TTCATGGCCT AGTGGGCAGA TCACCTGAAG TCAGGAGTTT GAGAACAACC 60
 TGGCCAACAT GGTGAAACCC TGTCTTACA AAAAATAAAA AAATTAGCCA GGGGTGAGGG 120
 CAGGTGCCTG TAGTCTTAGC TACTTAGGAG GCTGAGGCGG GAGAATCACT GGAACCCACG 180
 GGGCGGAGGT TGCAGTGAGC CGAGATCACA CCAGTGCACT CCACCCTGGG CGATAGAATG 240
 GGACTTTTAA AAAAAAAAAA AAACGCCTCA CACGGTTTTA GGTGCTATTA ATACAGTAAG 300
 AAACAAATAA ACAAAGCTCA TTGCCCTTGA TGGACTTTAA AAAATGATCC AAGTATATGC 360
 TGTCTGTAAA AGATACACCC TAGACTCAAA GACACAAATA AGCAAATCAA AGGATGAAAA 420
 AGATACACTA TATGCTCGAG 440

(2) INFORMATION FOR SEQ ID NO:1247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1247:

GAATTCGCCT TTATGGCCT AGCCNAACAA AATGGCGGCG GCAGCGGTGT CGTTTTGTTT 60
 CCGGGGNTCC TCGCGCGGTG GCAGTGGTAG CGCCCTTTGA GCTGTGGGGA GGTTCAGCA 120
 GCAGCTACAG TGACGACTAA GACTCCAGTG CATTCTATC GTAACCGGGC GCGGGGGAGC 180
 GCAGATCGGC GCCCAGCAAT CACAGAAGCC GACAAGGCGT TCAAGCGAAA ACATGACCGC 240
 TGAGCCCATG AGTGAAGCA AGTTGAATAC ATTGGTGAG AAGCTTCATG ACTTCCTTGC 300
 ACACCTCATCA GAAGAATTTG AAGAAACAAG TTTTCCTCCA CGACTTGCAA TGAATCAAAA 360
 CACAGGTAAA TTGAAAAAGA ATGTGCTATA CCTTCTAGTC TTTTCTCTAT TTTTCTTAA 420
 CACTTATGGA GGTAAACATT TATTTTATTC AGAGAGCACA CTCGAG 466

(2) INFORMATION FOR SEQ ID NO:1248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1248:

TTTTGTTTTG TTTTGTGTTG TTTTGGTAG AGTTGGAGTC TTGCTGTGTT GCCCAAGCTG 60
 ATCTCCAATT CTGACCTCA AACAGGTCTC TCACCTTGGC CTCCCAAAGT GCTGGGAATT 120

CAGGGGTGAA CCACCTCACC CAGCCAAGAT CACATTTTGA ATCTAATTTT TTTTTTTTGA 180
AACAGTGTCT CGAG 194

(2) INFORMATION FOR SEQ ID NO:1249:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 523 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1249:

GAATTCGGCC TTCATGGCCT ACCTGTGCAA GAACATGAAA CATCTGTGGT TCTTCCTTCT 60
 CCTGGTGCCA GCTC[^]CAGAT GGGTCCTGTC CCAGGTGCAG CTGCAGGAGT CGGGCCCAGG 120
 ACTGGTGAAG CCTTCGGAGA CCCTGTCCCT CACTTGCACT GTCTCTGGTG GCTCCATCAG 180
 TGATCACTTC TGGACCTGGA TCCGGCAGCC CCCAGGGAGG ACGCTGGAGT CGCTTGGCTA 240
 TATTCATTAC AGTGGGATCA CCAACTACAA CCCCTCCCTC AAGAGTCGGG TCACCTTTTC 300
 AGTAGACACG TCCAAGAACC AGCTCTCCCT GAAGCTGAAG ACTGTGACCG CTGCGGACAC 360
 GGCCGTGTAT TACTGTGCGA GATTTAGTGG TTATTATACT AACCTTCCT ACTACTACTA 420
 CATGGACGTC TGGGGCAAAG GGACCACGGT CACCGTCTCC TCAGCCTCCA CCAAGGGCCC 480
 ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACTCTC GAG 523

(2) INFORMATION FOR SEQ ID NO:1250:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 194 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1250:

GCCAGAGGGA TGACCGGTGG CTGCTGGTGG CACTCCTGGT GCCAACGTGT GTCTTTTGG 60
 TGGTCCTGCT TGCCTGGGC ATCGTGTACT GCACCCGCTG TGGCCCCCAT GCACCCAACA 120
 AGCGCATCAC TGACTGCTAT CGCTGGGTCA TCCATGCTGG GAGCAAGAGC CCAACAGAAC 180
 CCATACCCCT CGAG 194

(2) INFORMATION FOR SEQ ID NO:1251:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 503 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1251:

GAATTCGGCC TTCATGGCCT AAGCCCACTG GCATCAGACA TGCTTTGCTG TAGTGACAC 60
 TTCNTTTTTC NTTTTNTT TTTTTTTT CACACAGAGC CNGGNTCCGT CCCCCAGGCC 120
 TGACTGCAGC GGNANAATCC CACCCACNG CCACNTCCGC CACCCAGGCC CAAGGGTTC 180
 CCTAACGGCT AATGATGTTG AACATCTCTT CATGGGGTTA CATGCCATCT TTATATCCTC 240
 TTCAGTGAAA TGTTCTTAA CATCTTTTGC TGTTTTCTAA TTGGATTACT TGGGGTTTTT 300

TAATACTGAG TTTGGAGTTA TTTATATATT CTAGACAGTA GTCTTTATTG GATATGTGGT	360
TCAAAAATAT TTTCTCCCAG TCTGTAGTTT GCCTTTTCAG CCTTTTAACA TGGTCTTTAG	420
CAGACCAAAA TGTTTTAGTT CTTATGAAGT CCAACTTACC AATTTTCTCT TTTCTAGATC	480
ATACTTTTGG TGCAAGTCT CAG	503

(2) INFORMATION FOR SEQ ID NO:1252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1252:

GAATTCGGGC TTCATGGCCT AATTGAATTC ATGATTGTGC TCTCTGCTTG CCTGTTGTTG	60
GTGTATAGGA ATGCTAGCAA TCTTTGCACA TTCATTTTAT ATCCTGGGTT TCAGTATTTT	120
AAAAACTTAC TTCAGGTGAT TCTATGTGTG CAACCATGAT TGAGATACAC TGTTATAGAA	180
TCTAGGATGT GATAAACTAG AAGAACATAA CTAAAGTTTT GCATTTTTCG GGTGTCTCAG	240
TTTCTCATT TATAGATGGA GTTGGTATGT GTACCAAGTT CATAGGCTTG TTCTGAGTAA	300
ATTAGTGCAT GTAAAGTGCT CCACAGAATG TTAGCTGTTG TGATGCTTTA CTTTCCATTG	360
CACCTCCTGA CTCCTAGCCT TTCTTTTCCT TGGCTCTTTT TATGCTCATG TCAGATGCCT	420
CTATTGTTTC TTTCCCCCA GAATATCCTC CACTTTATCT TGCTCTGCTC AACATCTTTA	480
AAGTATAGAA TCAACAGACT GCCATGCCAC CCAGTCTGTC TGACAATTGA GGCAAATTCC	540
CTAAGTCCTC TTGTTCTCCT TCTGAGATTT CCACCTGCTC TAACTCGAG	589

(2) INFORMATION FOR SEQ ID NO:1253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1253:

GAATTCGGCC TTCATGGCCT ACATTTATCG AGTCTTTAAT TAATGCCCTG GGTAACATA	60
AGGTTGGAAC TGTAATTGTC ACCATATTGA TGATGAGAAA CTTGAGAAAG GATAAGTGAC	120
TTGTCATAAA TCACACAGTA AAACCTCAAA TCAAACCCAG GCCCTCTGGC TCCAGACTCT	180
AAATTACT CTGAATGATA CTCACTGATT GTCCGAGGAC ACAAAGACTG TCGAGGCACT	240
ATCTGCTGGG TGTCTGCAGA ACCTTACTGT TCTAAAGCAA AACATTTTAC CCCTGGACAA	300
GAGCAGCAAA GGTGGCGTTC GGCCCTCCTT GGCTCTCATT TGAAGTGTCA AAGCCAGGTG	360
CTTTTCTTTC TTGGGTGAGA ACGTATTTTC AGCAGCATTT TGAAGCACCC CTGGCGTGCA	420
CTGCACAGGG AAACCAAGGAC CACATTGGTG TGCTGTGTCC TCCTTACCAA CTGGCTCTTG	480
GAGAAGGTGA GACAGAAGTA GCTGAGACTC CATTCTGAG ATCTTCACTT AACAACTCCT	540
GCAGCTTGTG CAGAGCCTTA CTAGAAATAC TGAAGGCAGA AGTCCCTGGA AAATAGGGCC	600
CATAACTAAT TAGTAATTTG TTTTGTAGTA ATTTCTTACC GTTATTTGAG CACATTCTGC	660
AGTCCAGGCA TTTTGCTAAA CTCTTACATG GCAGGACTCG AG	702

(2) INFORMATION FOR SEQ ID NO:1254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1254:

GAATTCGGCC	TTCATGGCCT	AAGCAAGTAA	ACACTGTATA	TCTGTAATTG	GAAAGTTGGT	60
GGGAAGATT	CTTTTCCATT	CTTGATGTGG	CAGCCTTAAG	TGCCATCACA	GCTTGTCTG	120
TGGTTTGCCT	TTTTTTTTC	AGTGACCTCA	GCTCACTGCA	ACCTCCACCT	CCCTGGTTCA	180
AGCAATTCCC	CTTCTTCAGC	CTCCCAAGTA	GCTGGGATTT	CTGGTGCAATG	CTACCAGGCC	240
TGGCTAATTT	TTTTTTGTAT	TTTAGTATA	GACAGGGTTT	CATCATGTTG	GCCAGACTGG	300
CCTCAAATC	CTGACCTCAG	GCAATCTGCC	CACCTCAGCC	TCCCAAAGTG	CTGGGATTAT	360
AGGTGTGAGC	CACTGCGCCC	AGCCGACTTT	CAAATTTTTT	AACCACAGCC	CAGTGTAAAC	420
CTGTGTGTAT	GTGTGTGAGT	GTGCTTGAT	GTGTGTTTGA	AATAAAATTT	TTCATGTGCT	480
TAAACATTCT	GATTTTTTTT	TTATCAGAAC	CACTAATGAG	ATGAGACCAT	AGTTTGTAAA	540
ACCTCATGCT	CGAG					554

(2) INFORMATION FOR SEQ ID NO:1255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1255:

GAATTCGGCC	TTCATGGCCT	AGCTCGGCA	CATGGCAGGC	ACTCAGGGAA	AGTATGTAGC	60
CTTATGAACT	GACTGATCTG	AGGGAGGCAC	TTCTGTAAGC	CATAGTATTG	GTCACATGGCA	120
TGAGGCCACC	TACTGGATCC	CTGCCATCCA	GCCCTGGGAG	TAGCATGAAG	CAGCATGGCA	180
CTGGCCTTCT	GGAAGCTTGG	AGAGGAGTCT	TACCCAAGCT	TTGCTCCTAG	ACATTAAACT	240
TCCCAGCTGG	GCACTAACAT	GTGGCTGCAG	AACCTGCCCT	TGCTCAGTCT	GTCCCTGGTG	300
CAGCTGCTGG	GAGAGCCTGC	CTCGAG				326

(2) INFORMATION FOR SEQ ID NO:1256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1256:

GAATTCGGCC	TTCATGGCCT	ACATTAAGGC	AGCTTTGTAA	GTAAGTACAA	AATATATTTT	60
AACCTACACA	ATTTTTATTA	GTTTCCCTCT	CTTTTAGAAG	TACACCGACT	CTAAAATGAA	120
TGAAAGTCTG	ATTACTTGCC	TAGGTTGGG	GGCTTTATCC	AAGCTCTACT	AAGTGAAGCT	180
AAAATAAAGG	ACATTGTTGT	ATATTGTATT	TTAATGTATA	CATTATTACC	TCCTCAGCAA	240
AGTGAACAT	AGCTAAACT	TGAGTATATA	TTTCCTTCAT	TTCTCTTCTT	AGTTCCTTTT	300
TGGCATCTCA	TGCTGAACAA	ATCCAAAATA	GATTTATTAA	TGCCTTCCCC	CAACACAAAC	360
AAAACCAGAA	GAGTCTTTCG	CTTCTAGACC	TGCCTCGAG			399

(2) INFORMATION FOR SEQ ID NO:1257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1257:

GAATTCGGCC	TTCATGGCCT	ACTGAGTACA	GGTTTGGGAT	CTACATACCC	AGATCAACAG	60
CATGTGGCAT	CACCTGGCCC	AGGTGAGCAT	GACCAGGTAT	ACCCAGATGC	AGCTCAGCAT	120
GGCCATGCTT	TCTCTCTCTT	TGACAGTCAT	GATTCAATGT	ATCCTGGTTA	TCGTGGCCCA	180
GGGTATCTAA	GTGCTGATCA	GCATGGCCAG	GAAGGTTTGG	ATCCAAATAG	AACACGAGCC	240
TCGGACCGAC	GTGGAATTCC	TGCCCAGAAG	GCCCCAGGCC	AAGATGTCAC	TCTTTTCAGG	300
AGTCCAGACT	CCGTCGACCG	AGTCTTATCA	GAAGGGAGCG	AAGTCTCGAG		350

(2) INFORMATION FOR SEQ ID NO:1258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 335 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1258:

GAATTCGGCC	TTCATGGCCT	AATTGAATCG	AGCTGGTTAA	GTTTCACTAG	GAGGCGCNAA	60
AAAGGAGCCG	TTTTTGACTT	AACATTTTAA	TTCTAGTAGA	GATAAGAAGA	GCTTGTGTGG	120
GCTTACAGTC	CTTCACCTGA	CTGTCCTTCA	CCAGTGAGTA	GCATACCACT	TCTTCAAATG	180
TCCTATACTT	TGGAAAGCAG	ACCCGACTCT	GGAGCACTCG	CCTTAATTAG	ATTCTGAATT	240
TCCTTGAATT	TTGGATGGTC	CTTATCAGCT	ACCAGCTGAA	GCAGAACAGC	CTCACTCGTG	300
GTCACATATGA	TCCCGGTTTC	AGCGAGACGC	TCGAG			335

(2) INFORMATION FOR SEQ ID NO:1259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 621 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1259:

TCCAGTTGAA	TTTAATAGAA	TTCGGCCTTC	ATGGCCTAGC	CGACCGTTGA	CTATTCTCTA	60
CAAACCACAA	AGACATTGGA	ACACTATACC	TATTATTCGG	CGCATGAGCT	GGAGTCCTAG	120
GCACAGCTCT	AAGCCTCCTT	ATTCGAGCCG	AGCTGGGCCA	GCCAGGCAAC	CTTCTAGGTA	180
ACGACCACAT	CTACAACGTT	ATCGTCACAG	CCCATGCATT	TGTAATAATC	TTCTTCATAG	240
TAATACCCAT	CATAATCGGA	GGCTTTGGCA	ACTGACTAGT	TCCCCTAATA	ATCGGTGCCC	300
COGATATGGC	GTTTCCCCGC	TGCATGCTAG	TTATATTTCT	CCAACATAGA	TTAAATACAT	360
ACATGACTAT	TAAAATCTCA	GGGTTCTTCT	ATGTGTCCCC	TAAAAGCATG	ATGTATGCCA	420
GTGGTCATCT	GTCCACCACC	ATTTGGGGAC	CACGGCATT	AGGTAAAGTG	GGTCTCGGAT	480
GACCTCCTTC	AGCTTAACAG	CAGGAGTTGA	GATGGAGCCC	TTGCAATTTT	CCCACTGAAT	540
TCCAGAAGCA	AGGAGAAAGA	CTGAAGTGAC	AAGTACCGCA	AGACAGACTT	CAGGAACAAT	600
TCGTTTAAGC	TGCAGCTCGA	G				621

(2) INFORMATION FOR SEQ ID NO:1260:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1260:

```

GTTTTGTGAT TCTCCAGGAC AGATGATGAA AAACAGTGTA GATAGTGTC AAAATTCCAC      60
TGTAGCCATA AAATCTCGAC CTGTTTCAAG AGTTACCAAT GGAACCTCCA ATAAAAAAG      120
TATTTCATGAA CAAGACACTA ATGTAAATAA CAGTGTAATA AAGAAAGTCA GTGGCAAAGG      180
ATGTAGTGAG CCAGTACCAC AGGCAATTTT GAAGAAAAGA GGAAGTAGCA ATGGATGTAC      240
TGCAGCTCAG CAGAGGACAA AGAGTACCCC ATCTAATCTT ACTAAAACTC AAGGATCCCA      300
AGGAGAGTCA CCAATACTCG AG                                     322

```

(2) INFORMATION FOR SEQ ID NO:1261:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1261:

```

GCCCTCATGA CTCGGATCCA ACCTGCCTCG CAGGGAGTCG AGCTCTCCGG CCTCTCAGCC      60
GCCATCAGCC ACTTCCTGAA CTGCTTCTCG AGCTCCTACC CAAACCCCGT GGGCCACCTG      120
CCCGCCGACG AGCTGGTCTC CAAGAAGCGG AATAAGAGGA GGAAAAACCG GCCCCCGGGG      180
GCTGCAGATA ACACAGCCTG GGCTGTCATG ACCCCCCAGG AGCTCTGGAA GAACATCTGC      240
CAGGAGGCCA AGAACTACTT TGAATTCGAC CTCGAG                                     276

```

(2) INFORMATION FOR SEQ ID NO:1262:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1262:

```

GAATTCGGCC TTCATGGCCT ACAAGAAAAG CAAGCCACAA ACAATAATGA AGCAAAAAAT      60
GGAATCTAAG AATCTTTTGG TATGGAATAT TACTTCTATC AGAAGATGAT CAAGATGTTT      120
CAGTCCAGTG CACATCAGCA TTGCTGACAT TTTATGGATT CTAAACTTGT GTTGTTTCTT      180
TTTTAAATCA ACTTTTAAAA AAAATAAAGT GTAAATTAAC CGACTAGAGT ACTTGGAAAA      240
TGTGATCAGT ACAAGTGAAC TTAGGTGTGT GCCAACAGGG TCCGTACTCG AG                                     292

```

(2) INFORMATION FOR SEQ ID NO:1263:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1263:

```

GCGATTGAAT TCTAGACCTG CCTTGATGCC AACTAAGGAA ATTTGTTTAG CATTGAATCT    60
CTGAAGGCTC TATGAAAGGA ATAGCATGAT GTGCTGTTAG AATCAGATGT TACTGCTAAA    120
ATTTACATGT TGTGATGTAA ATTGTGTAGA AAACCATTAA ATCATTCAAA ATAATAAACT    180
ATTTTATTA GAGAATGTAT ACTTTTAGAA AGCTGTCTCC TTATTTAAAT AAAATAGTGT    240
TTGTCTGTAG TTCAGTGTG GGGCAATCTT GGGGGGGATT CTCTCTAAT CTTTCAGAAA    300
CTTGTCCTGC GAACACTCTT TAATGGACCA GATCAGGATT TGAGCGGAAG AACGAATGTA    360
ACTTTAAGGC AGGAAAGACA AATTTTATTC TTCATAAAGT GATGAGCATA TAATAATTCC    420
AGGCAAATGG CAACTCGAG                                     439

```

(2) INFORMATION FOR SEQ ID NO:1264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1264:

```

GAATTCGGCC TTCATGGCCT AGGGGAGGCC GCGGNGGGGA AAATGGCGGA CGGGAAGGCG    60
GGAGACGAGA AGCCTGAAAA GTCGCAGCGA GCTGGAGCCG CCGGAGGTGA ACACAACCCC    120
AGCGTCGTGG GCAGCGTGGG ATGCTCCGGG CTTTCTTTG AGCTCCCAAG GTGGGGGGAG    180
TGGGGTGGGG CGAAAAATGGG CGGATCTGGA CCTCACCCGG ACAGGTGTTG GGCCAGACC    240
TGCCTCCGGG CNOGCCCGA TGCGGCCCTC CTGGGCTCCG GGCCTACATC GCCTCCTTGC    300
CTGGGGAGAG CCGGCCACTG TTCGTACCTT CCTGGCCCCA GCGGAGGCCC TGATTCCGAG    360
GAGAAGGGAG ATGGGCGCCA GAAAGGGAGA CCGAACTCGG GGTGGGACCA GGAGCGGCGG    420
TGCAGGAGCC GCTACCGCCA CACCGGAGAC GCACATCACA CAAAACACAC ACACCGGATT    480
CTCGAG                                     486

```

(2) INFORMATION FOR SEQ ID NO:1265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1265:

```

GAATTCGGCC AAAGAGGCCT AATTTATTGT TGGATCAATC AAAATTTTCA TCACTTAAAA    60
GAACCATGTC TATTAAAGAA TCTAGCTCAC TGGAGTGCAT TGCCATTCCA AAAAAGAAGA    120
TGAATTTAAA AGATAAAGC CATGAAGGTG TTGCTTGTGT CCAGAAAGAA AAATCAGTAG    180
TTAAACCTG GTTCTGTGAA TGCAATCAGC GATTCCCAAG TGAAGATGCA GTAGAAAAGC    240
ATGTTTCTC AGCAAACACA ATGGGTTATA AATGTGTGGT CTGTGGAAAG GTATGTGATG    300
ATTCAGGGGT TCTCGAG                                     317

```

(2) INFORMATION FOR SEQ ID NO:1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1266:

```
GAATTCGGCC AAAGAGGCCT AATCTTTTCC TTTCTGTAA GTTAGAAGAA ATAACCTCTT    60
CAGTTAAACC TTCAGTGAAG GTTCTTTTAG TTTTCTGTTT TGCTTTCTAA AAACATAGAC    120
TCTGTTCTTT AGAGCAACTT ATGACTCTCA TCTCTGCTGC ACGAGAATAT GAGATAGAGT    180
TCATCTATGC GATCTCACCT GGATTGGATA TCACTTTTTC TAACCCCAAG GAAGTATCCA    240
CATTGAAACG TAAATTGGAC CAGGTAATC CTTACTTTTT ATTCATTTTT CCTGACTATG    300
TACTTGAAAC TAGAAGTTTA CTCAGTTGCT TTTACGATGT TAAAAGGAAA TCAAATTCCT    360
ATTTCTTGT TTTCTTTTTT TGTTGTTTG TTTTGTTTT TGAGACAGAG TCTTGCTCTG    420
CACTCCAGCC TTGGGCAACA GAGCAAGGCT CTCAAAATAA AAAAGCAGCG ACACTCGAG    479
```

(2) INFORMATION FOR SEQ ID NO:1267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1267:

```
GAATTCGGCC AAAGAGGCCT AGGGTTTATG CCAACAAAAG GAGAGGGAGC CATAGGTTCT    60
CTAGATAACA CTCCTGAGGA AAGAAGAGCA CTTGCCAAAA AATCACAAGA TTTCTGTTGT    120
GAAGGATGTG GCTCTGCCAT GAAGGATGTC CTGTTGCCTT TAAATCTGG AAGCGATTCA    180
AGCCAAGCTG ACCAAGAAGC CANAGAACTG GCTAGGCAAA TAAGCTTTAA GGCAGAAGTC    240
AATTCATCTG GAAACACTAT CTCTGAGTCA GACTTAAACC ACTCTTTTTC ACTAAGTGAT    300
TTACAAGATG ATATACCTAC AACATTCCAG GGTGCTACGG CCAGTACATC GTACGGACTC    360
CAGAAATTCCT CAGCAGCATC CTTTCATCAA CCTACCCAAC CTGTAGCTAA GAATACCTCC    420
ATGAGCCCTC GACAGCGCCG GGCCAGCAG CAGAGTCAGA GAAGGTTGTC TACTTCACCA    480
GATGTAATCC AGGGCCACCA GCCAAGAGAC AACCACACTG ATCATGGTGG GTCAGCTGTA    540
CTGATTGTCA TCCTGACTTT GGCAATGGCA GCTCTTATAT TCCGACGAAT ATATCTGGCA    600
AACGAATACC TCGAG                                     615
```

(2) INFORMATION FOR SEQ ID NO:1268:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1268:

```
GAATTCGGCC AAAGAGGCCT ACAGAACTTT TGTCAAATGG AGTGTACCC ACAGTCAGAA    60
TCTAGCCACC AAAATGGGAA GGGAGTGNAG CTGCCCTGTC CACAGGCTTC TCTATGGGAA    120
ANGCTGCTGT TCTGTAAAC ATGNTGGGGC NGGCTGTGGG GANGAAGGCA TTTTCTGGAC    180
CACATGNACG AATTGGAATT GGGGACGGT CCTACCCAG TGAGGAAGCT GAAAGAAATG    240
GGCCTGATTT GGTGCAGGAC ANCCCCTGAA GACCGTGAGG CCCCTGGCCT CTGCCGAGA    300
```

TGGGAGCCTC AGCAGCANGG TTTAGGGCAG CACCCAGGGC ATCCTTGCCA CGTGAGGCTG	360
CCGTGCGTGC CTGGGCATCA GTAGCTCAGG CTGGAATAAT TGGAAAGGAA AAGGCAGGAG	420
GANCCCTGA GGCCAGGCCA TTGGGCTGGG GAGCTGTTAA GCTGAGGTGG CCCTAGGGCC	480
TGCCGGGGCT GGGGTGGCA AGCCAACTC TCGAG	515

(2) INFORMATION FOR SEQ ID NO:1269:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1269:

GAATTCGGCC AAAGAGGCCT AGTGCAACTG ATCTGTCCAG TTTGTGTATG AAATGGATT	60
GATAAAGTTT TTGCTAGTTA TTTACTACAT TTTGGGATTA ATAAGTGATT TATATGCATA	120
TTTTTCTGTA AATCTACAGT TTTTGTACA AGATATTCTA CAAGTTATGA AGCTAAGGGA	180
AGAAATGCC AAAGATACCT CTAGTTATGT TGAACACAGC CAGCTCGAG	229

(2) INFORMATION FOR SEQ ID NO:1270:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1270:

GAATTCGGCC AAAGAGGCCT AGTATGCCCT TAAATCTGGT TATTAGGTAA TTCTTTTCCG	60
AGTAGGAGCC CAGATCAACT CACAGTGTTC CTGAGTCCTG GGAGATTGAA TTCTAGACCC	120
GCCTCGAG	128

(2) INFORMATION FOR SEQ ID NO:1271:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1271:

GAATTCGGCC AAAGAGGCCT ATTAGCACA AATTTCTTTT TGCTTGCCTT TTCAGATTTT	60
AAAACTATTA GAGAAAAACA TACTTGATTG CTAAAATTG TCAAACATAA ATAGTAGACA	120
CAATTTAGTA ATAATCATAT TAATAATCAT AATCATTAACT ACTCATAATA ATCANACAGA	180
GGACGCCCTA AAATGTACAC TGATTAAATT TTATTTTTTT CCCATGCATA GCTAGCCTGT	240
TTGTACAACT TTACTTTTGC TGCTGCATGT AACCAGATGA TTTTTTAATC AGATTACTGC	300
CTTCTGATT TATTTAGAAT TTTTTTCTT TTTTTTTTTT AAGAGACGGG ATCTTATTCT	360
GTGCTCAGG CTGGGTGCA GTGATGTGAT CCTAGCTTAC TGTATTCTCG AG	412

(2) INFORMATION FOR SEQ ID NO:1272:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1272:

```
GAATTCGGCC AAAGAGGCCT AGTTTAAAG GACAGGTTTA AATAGGCTTA CTTTTTCTT    60
TTAAGTTCAG ATACCTAAGC CTTATGTCCC TAGCCGCAGT TTTCAGATAT TTGCAGCTAA    120
TTAATTCTTA GGAAATCTAA TCTGAATTGA ATTAATTTTC CCTTTTAGGG CACACGAAGC    180
AACTTTTAGG TAAGAAAAAA AATGAAAACA GCTTTTGTG CACATAATTC TTGCAACTAA    240
TGAAAAGTAA TATTGCTGTT CCCTTCAAAT AATGCAATAA CAAAACACCA AATGAGAGCA    300
TTGCATTGTA TTGTTATATT TGCTGTTTAA ATAATTTAGC TGCAAAAATC TGAGGGCTGC    360
TTTAGCTGTA ATTAATTATT CATTAAATGAC ATGCTAATTG CACAATACCT TTGAATATTT    420
AACAAAATGC AAAAACCAGG CTCTGAAGTT ATGTTTTTAG TGCAAGGGGG ACACCTCGAG    480
```

(2) INFORMATION FOR SEQ ID NO:1273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1273:

```
GAATTCGGCC AAAGAGGCCT AAGACCAGCC TGGGTGACAG AGCGAGACTC CGTCTCAAAA    60
AAAAAATTGA ATGAAGCAGA AATTATTTCT TTAAAGCCCA TTAGCTGTT ACACACATAG    120
TTATAGCATA TTCTCTCTTG AGATAACTTG CTTTAAATTG GAAAACTAAT TCATTAAATA    180
TCCAACTCT ATATCATTTC TGAATAAGT GATTTTAGCA ATTTTGATA CTTATTCTAA    240
CATGATGCAT ATATTGAGTA TGTACTTTTC TTAAATGCA GGCAATACTC GAG          293
```

(2) INFORMATION FOR SEQ ID NO:1274:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 194 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1274:

```
GAATTCGGCC AAAGAGGCCT ACCGCTTTTT TTTTTTTTTT TGATAAAGAG AAGCCACCAC    60
CAGGAGGAGG CTTGAAAGCT TGAATTTAAT TACTCCTCCA TCTCCTCATT ATTCCACCCA    120
ACTCCCTACT TCCCATCTC ATTTCACAGC CTCACCAGC TCTCCCTCA GGCCTCCTAG    180
ACATCGCGCT CGAG          194
```

(2) INFORMATION FOR SEQ ID NO:1275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1275:

GAATTCGGCC AAAGAGGCCT AAGAAGAAGA AAGAAAAATT GGAGAGAAAA AAGGAGTCTT	60
TAAAAGTTAA AAAGGGTAAA AATTCAATTG ATGCAAGTGA AGAGAAGCCA GTTATGAGGA	120
AAAAAAGAGG AAGAGAAGAT GAATCATACA ATATTTCAGA GGTC	164

(2) INFORMATION FOR SEQ ID NO:1276:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1276:

GAATTCGGCC AAAGAGGCCT ATTGGATGG CAACGAGCTC ACCCTGGCTG ACTGCAACCT	60
GTGCCAAAG TTACACATAG TACAGGTGGT GTGTAAGAAG TACCGGGGAT TCACCATCCC	120
CGAGGCCTTC CGGGGAGTGC ATCGGTACTT GAGCAATGCC TACGCCCGGG AAGAATTTCGC	180
TTCCACCTGT CCAGATGATG AGGAGATCGA GCTCGCCTAT GAGCAAGTGG CAAAGGCCCT	240
CAAATAAGCC CCTCCTGGGA CTCCTCAAC CCCCTCCATT TTCTCCACAA AGGCCCTGGT	300
GGTTCCACA TTGCTACCCA ATGGACACAC TCCAAAATGG CCAGTGGGCA GGAATCCTG	360
GAGCACTTGT TCCGGGATGG TGTGGTGGAA GAGGGGATGA GGGAAAGAAA TGGGGGCGCT	420
GGGTCAGATT TTTATTGTGG GGTGGGATGA GTAGGACAAC TCGAG	465

(2) INFORMATION FOR SEQ ID NO:1277:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1277:

GAATTCGGCC AAAGAGGCCT AACTGTGGTT CTTACATCCT AACAAAAGCT GCCCTCCCCG	60
CACATTCTTT TGTATGTTCC TTAAGCTTAA AGATGAATAG ATGCTTAAAG TATGCAACTA	120
TGGCATTGAG AGTGCAAGAC AACTTGAAAA AGAGTGTGAA AACATTGTCA GATATAAAGT	180
TACTTCAATT CTTTGGAGTC TGTTCTCTGT CATGCTTAGA TGTTTGGAAAT CTTAAAGTTA	240
CAGAGGAACT GTTCTCTGGT AACAAAGACAT GTCTGAGTTT GTGGACTGCA CGCGATCTCG	300
AG	302

(2) INFORMATION FOR SEQ ID NO:1278:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 401 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1278:

```

GAATTCGGCC AAAGAGGCCT ATAGGCCTCT TTGGCCGGGT TAGCCTAAAG GAGAAAAAAG      60
CAAGGCTCAA GAGAAATTAG ACAGCAGCTT TCAAAATATT TTAGAGAACT AGGTTAATTA      120
TGGTAGTCAT TCAACAAGGT AGAAATCATA CCAAGCATGA AGTCACAGGA ATGTCCCAGG      180
AGTGTGCAAC CATTGGAAC GTCCATAGTA AAATGGGCCA GCTTGAGCAA TAAAAGTCTC      240
CTAGTACCAG GAAATGCTTA GAGGTTGGGG AAAGTGAAAA AAAGGGGGAA AGTTTGGTCA      300
GGTTGGGGAG CAGTCACACT TCTTCTGAG AGGTAGTAAA TACCAGGCTC TCCATCTGGA      360
GGAGGGGTCA GTAAATCAGG TTGCAAAGG AATATCTCGA G                          401

```

(2) INFORMATION FOR SEQ ID NO:1279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1279:

```

GAATTCGGCC AAAGAGGCCT ACCCACCCT ACTCCTCAAC ACTTCTGGTT TGCCCTGACT      60
TCTCTACGGC TCTGGCTTCT TCCCGAAGAG ATATAGGAGC CATGTAAGCA CGCAGTGGGT      120
GAACTGCTTA ATTCACTAC ATGTTGATGT ACTTGTCTTC CGTCCTGTAG GTCTTTTCTA      180
TATAACTTTA TGCCACCCTT AAATGAATCA TTGGGTATAC CTGTCATGTT GGATCCTGTA      240
ATCACAGTTT TCCCTGCTCA CCTTTTGTG TAAGATCTAT TGAGAAAGGG AAATATGGGA      300
AGGAGAACCA TTTGATCAGA ATACAACCA TAGTCTTTAA GCATTGTAA AGTATGAAAC      360
TGAAATACAT TCAAAACACT TTACACTCGA G                          391

```

(2) INFORMATION FOR SEQ ID NO:1280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1280:

```

GAATTCGGCC AAAGAGGCCT AGGACTCCAC ACTCCCCAGA TCCCAGTATG ACTACATCTT      60
GCCTCAAGTT TCTTTCACCG CAGTGGGCTA CCATAACAC ATCACCTTGA TTTTAAATCC      120
CACGAGGAAG CTGCCTGAAC AGGACATCGC ACAAGGATCC TACATTGCCC TGCCATTGAC      180
GCTGCTGGTT CTGCTGGCCG GTTACAACCA TGACAAGCTC ATTCCTTTGC TGCTGCAGTT      240
GACAAGCCGG CTACAGGGAG TCCGCGCGCT CGGCCAGGCA GCCTCTGACA ATAGCGGCCC      300
AGAAGATGCA AAGAGACAA CTGAG                          326

```

(2) INFORMATION FOR SEQ ID NO:1281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1281:

GAATTCGGCC AAAGAGGCCT ACAGATGCAG ACACGGTGTC CGACGAGTAT TCTGACGAGG	60
AGGTGGTGGA GGACGTGGAT GATGCCGCCT ACTCCATGGT CAGTGCCTCC CATGTGACCG	120
CCCGCACCTG GGCCGCTGTC CGTCTAGCGC TCTAACAGTC TTACACCTTG GCTTTCTCTG	180
TCCCTTGAAA GAATTAATA TATCTACTGT GGACTGTTTC ATAAAACCAA CCTATGGTGT	240
TGCCGGGCAC AGAACAAAGC TGTGTTTCAC TACTGAAGGG ATGATTGGGT TTCTATATCA	300
TAATTACTTT TAGCTTCAGA ACAGACCCTT GTTCAAACAT CTCATGATCT TCGCTAACCA	360
TCTCGAG	367

(2) INFORMATION FOR SEQ ID NO:1282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1282:

GAATTCGGCC AAAGAGGCCT AAGAGAAGTG TCAGCCTCAC CTGATTTTTA TTAGTAATGA	60
GGACTTGCCT CAACTCCCTC TTTCTGGAGT GAAGCATCCG AAGGAATGCT TGAAGTACCC	120
CTGGGCTTCT CTTAACATT AAGCAAGCTG TTTTATAGC AGCTCTTAAT AATAAAGCCC	180
AAATCTCAAG CGGTGCTTGA AGGGGAGGGA AAGGGGGAAA GCGGGCAACC ACTTTTCCCT	240
AGCTTTTCCA GAAGCCTGTT AAAAGCAAGG TCTCCCCACA AGCAACTTCT CTGCCACATC	300
GCCACCCCGT GCCTTTTGAT CTAGCACAGA CCCTTCACCC CTCACCTCGA TGCAGCCAGT	360
AGCTTGGATC CTTGTGGGCA TGATCCATAA TCGGTTTCAA GGTAACGATG GTGTCGAGGT	420
CTTTGGTGCG TTGAAGTATG TTAGAAAAGG CCATTAATTT GCCTGCAAAT TGTTAACAGA	480
AGGGTATTAA AACCACAGCT AAGTAGCTCT ATTATAATAC TTATCCAGTG ACTAAACCA	540
ACTTAAACCA GTAACGAG	560

(2) INFORMATION FOR SEQ ID NO:1283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1283:

GAATTCGGCC AAAGAGGCCT ATTTTCATCA ATAGTAAGTT TTTATTGTCT GCTAATTTGG	60
TAGATAAGTT GAGACATCTC ATTGTTACTT TAATTTGCAT TTTCTCCACA TTAGAAAATA	120
TTTTCATGG TTTATTGACC ATTTGCATT CTCTTCTATA AATTGACTTT TTATATTIAT	180
TTGTCTCTAT TTCTGTATTC TGTGATAGT CAATTTATAG GAACCTTCTG ACAGATATGC	240
ATATTCATT TATGTGTGAG TTATTTTGT GGCACCTACT CGAG	284

(2) INFORMATION FOR SEQ ID NO:1284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1284:

GAATTCGGCC	AAAGAGGCCT	ACTTCGGTTG	CGGGATTCTT	CCTCTGCCTG	GGTCATTCTT	60
TCTCGTGTCA	TCTGATACGA	GTCGTTTGTT	GCACACACTG	TAATTTTATC	TTGTATAAAT	120
CCCAGGCAAT	TGAGCTGGGA	GGCTCCAGAG	CTGGAGAATG	TTTGCTGGAT	GCAGTCAAAG	180
CTGCCCTGAG	GGTTGTCTTT	GCCCACATTT	GACAAATAAA	AGTTAAAGTT	ATGAACCTCA	240
TTGAGGGGAT	CATTTTGGG	AATTTTGACA	AGCCCGTGA	GTCCTTGGAA	CTGGATTGAA	300
GGTCGAAAAG	GAATTAAATT	CTGTGGCTC	TGGTAAGTCT	CGAG		344

(2) INFORMATION FOR SEQ ID NO:1285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1285:

GAATTCGGCC	AAAGAGGCCT	AGGGAATTG	TTTTTGCATA	GGGGAATAGG	TAAACCAAAA	60
GTGGTATTAA	AAGCAGTGCT	ATAGTAAAAG	GAGATTTTTT	TTAACTCCAC	AATAAAAAGT	120
TTAGGCCCAA	TTTCATAGTA	AACTATTCT	AATTAAGGAT	TGAACATATT	ATCACTTGCC	180
TTGATTTTGA	CCAGTGACAT	TTTTTGGCTT	CTTCATTTCA	CTGTGACCA	TCTGAATGCT	240
TTCTATTG	CTCTTTAATG	CCCAGATTTT	ATTGACATTG	GTGGCGAATC	CCTATTTCATA	300
CACAGACAAA	GCATCTGACT	TTGTCCAAGA	AGCAAGCATG	CTGCAGGCCA	CTATGACGAA	360
GCAAGAAGCC	GATGACATGA	GCATTTCCAT	CTCCACATT	GACGATGTTT	TCGACATGGT	420
GGATGTCCTG	GTGGAGGGCA	GTGAAGGCTT	GGATGAGGAA	ATAGGGTTCA	CGTTGAGTGA	480
AGACATGATC	CTGCTCACGT	TCCCATTCAG	TGCGGTAGTC	CCTGCGGCCC	TGGAAGCCAG	540
GAATAAGTTG	CTCCTTGGGA	CAGGCAATGA	AGCAGATACC	CTCGAG		586

(2) INFORMATION FOR SEQ ID NO:1286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1286:

GAATTCGGCC	AAAGAGGCCT	AGTTGAACAT	AACCTGTAGT	GTGAATATGG	TTAAACAAA	60
GGACACCTGA	TGTCTGTGAA	GTCTGCTAAG	GACAGGTACA	AAATTTATGC	ATTGCTTTTT	120
AAAAAGTTTA	AAATGAGGAA	TGCTTTTGAT	AATCAGAAAG	ACTAATGTAA	AGTGCTGACT	180
GATGTCCTGT	CTGCAGTTAA	GGAAGACACC	CAACTCTCTT	CTTCCTCATC	ATGGTATTCT	240
CTATGTATAG	ATCTCTAAAA	ATGCAAACTT	CCTATGGACA	AGACAATATG	ATTTGCTATA	300
ATATGAATTA	AGATATGGTA	ATATCTAATA	GTCTCCACTG	CTAGGATTCT	GAGTAACACA	360
AAAAATAGGT	TTTATAAAAA	GCCCATGCAC	TTCAATTGGT	GGGGGAAAAG	AATAAAGTCA	420
TTTTCAGTCG	ACTGACTCTG	TAAACAGAT	TACCAATATA	ACAAGCTATG	TTATCTAAAT	480
TGCCCTGGCT	ACTCGAG					497

(2) INFORMATION FOR SEQ ID NO:1287:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1287:

```
GAATTCGGCC AAAGAGGCCT ACAGGAGTTC ATTTTCATCC AAAACAAACA CTGGACTTCC    60
TGCGGAGTGA CATGGCTAAT TCCAAAATCA CAGAAGAGGT GAAAAGGAGT ATAGTAA AAC    120
AGTATCTAGA TTTCAAACCT CTCATGGAAC ATCTGGACCC TGATGAAGAA GAAGAAGAAG    180
GGGAGGTTTC AGCTAGCACA AATGCTCGGA ACAAAGCAAT TACCTCACTG CTTGGAGGAG    240
GCAGCCCTAA AAATAATACA GCAGCAGAGA CAGAAGATGA TGAAAGTGAT GGGGAGGATA    300
GAGGAGGAGG CACTCCCGGG GAACTCGAG                                     329
```

(2) INFORMATION FOR SEQ ID NO:1288:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 459 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1288:

```
GAATTCGGCC AAAGAGGCCT ATGCATCGCG GGAGGCGCAT GCGGGGATG GCGCTGGCGC    60
GGGCCTGGAA GCAGATGTCC TGGTCTACT ACCAGTACCT GCTGGTCACG GCGCTCTACA    120
TGCTGGAGCC CTGGGAGCGG ACGGTGTTCA ATTCCATCCT GGTTTCCATT GTGGGGATGG    180
CACTATACAC AGGATACGTC TTCATGCCCC AGCACATCAT GCGGATATTG CACTACTTTG    240
AAATCGTACA ATGACCAAGA TCGGACCAGG ATCAGAGGTT CCTTGGGGAA GACCCACCCT    300
ACGAAGTTGG AATGAGACCA TCAGATGTGA TAAGAAATC TTCTAGATGT CAACATAACC    360
AACCTTATAA AGACTAAAAT TCATGAGTAG AACAGGAAAA TCATCCTGAC TCATGTGTTG    420
TGTTCTTTAT TTTTAATTTT CAAAGAGGCT CAGCTCGAG                                     459
```

(2) INFORMATION FOR SEQ ID NO:1289:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1289:

```
GAATTCGGCC AAAGAGGCCT ACTACCTGCC TGAAATTCAA TGCGTGTTC CTTCTGGACC    60
AGTTTTAAGC CATCTCTTCT GTTGTTCCTT TCCTCCCAA GATGTAGACT TTTCCACTTA    120
AAAGCATTTT CAAGATTCTA TTTTTCATC CTTTTCCTG TCCCTATTCT CTTTCACTCC    180
CCACACTTGT TCCTAGCCTG TCTCTGTTGC TCTGATGTCC ATGTTGATGG TGGCGGTCTT    240
CAACCATGCC ATCCGTGTGC CAACCCAGCA CTTTCCTGCC ATCCCTGTAG CCCTTGCCCC    300
AACATCTGTG CATTTGACTC CCCACCACTC GAG                                     333
```

(2) INFORMATION FOR SEQ ID NO:1290:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1290:

GAATTCGGCC AAAGAGGCCT ATCCACCCGC CTCAGCCTCC CAAAGTGTG GGATTGCAGG	60
TGTGAGCCAC TGCGCCTGGC CTAAACAAAC TTTTGAAAA GCTGTTTCTA AAAGATTCTT	120
TAAATTCAGA TATGACAGCT AATTACCTCA TCATAAATTA CTTTATACT AATTGTTTCC	180
AGGGTTTTAG AGTAGTTGAA TGTTTATTTC ACAAGGCACC CTAAATTCTA TAGAAATAAA	240
ACCTCAGATG AGTCTCCTTC TTAGAGTGTT ACAATGAATG GGAGTTTACA ACTTTTATGT	300
GTCATGTTTC CAACAGCTAT CTCGAG	326

(2) INFORMATION FOR SEQ ID NO:1291:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1291:

GAATTCGGCC AAAGAGGCCT ATTGAATTCT AGACCTGCTG CTTGCTGCTC GTCCAGTACA	60
TTGGCTTTGA AATATACTTG AATTTGTGGA GGCAGGGTGT AGAATGACAA AAACAAACAA	120
AAACCCACCA ATACAGACCA AATTGGGGTA CACACGGACA GATTGGTTTT AATTTTATTT	180
TAATTTTGA GTTCTATGA GAAGAAGAAT GAGGAGAGAC AAAAAAGGGG AAGAGTGAGA	240
GATAGTATAT TTAGGGTATG ACAAATCAGG GATGGCTCGA G	281

(2) INFORMATION FOR SEQ ID NO:1292:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1292:

GAATTCGGCC AAAGAGGCCT AATTAACTA AATCTTAGGG ACTTAGGGAT TTAAACTAAA	60
TCCCCACCAC ATCTGATTC CCCTCCTCG AAATACCAAT AGTACGTGCA ACACAGACTT	120
GTAGCTCAGA GGTGCATGC TGTTCAAAT TCTTGGGATA TGCATGTTAC TTTTTTTAA	180
AGAAGTGGTA TATCAGACAC CTGAAGTCA AGTCTCTCTG TGCCACCAAC AAACCTCTCGT	240
GACCTTGAGC CCCTCCTCTC AATTCCTCTT CGGTAAAAGA AATACCTCAC AGTGGCTGTG	300
CAATCACCAA ATAGGAACTA CAGGTGGCAT TATTTATCTT TTGCCCTTGT GTAAGAAAAG	360
ACTCGAG	367

(2) INFORMATION FOR SEQ ID NO:1293:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1293:

GAATTCGGCC AAAGAGGCCT AGGATATTTT AAATTTTGGT AATTTTGGTT CGTGGTCTCT	60
GCCTGAATAG ACAGGCACTT GCCTGGAACG TAATACTGTT TCACTGCCTC GTTTTACCT	120
GTTTAATCTA GAACCAAATT GTGTCAATGT GTCAGCCCGT TTGTGCTTTT ATAACAAAAT	180
ACTACAGACA GTAATTTATA AAGAATAGAT ATTTATTTCT TCACAGTTCT CGAG	234

(2) INFORMATION FOR SEQ ID NO:1294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 562 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1294:

GAATTCGGCC AAAGAGGCCT ATACTGATCC TCTCCCTTG TGCATCACTT TTTCAGTGCA	60
GATATCTTGT AGCTCOGTGT CTAGAGGTAG CCAAGGTATC CTCCTAGCTT GCCTTCTTGG	120
TTTTATACAT GCTTCAGTAT GTAAGACAGC TTGTAGTCCA AACTCATGAG ATGACTATTG	180
TGCCTGCCCC ATCTTACCTC AACAAAGTGAG CCTGCATGCA TGTGCTCCTC AGTCTAGTCC	240
CAGGATAGGA GGTAGGGGTC TCACATCGAC CTCAGTTCA TATGACTTTT TCTAACTCAC	300
CTTTACCACA CAGCCCTAC TGTGGGGCTT ATAAAGTGTG ATGGAGATTG GTGAAGTCAA	360
TGTTTCCTTT CCTTGTTTAT GTGCTTTATA AATTAGGTCC CTCTCCAAAA CTTTTCATC	420
ATCCTAAACT GAAACACTAT GCCCATGAAG AAGTCATTAA ATAAAAGACT GATAAATTG	480
ACTCCATAAA AATTAAAATT TTCTATATAG GAAAAAATGC CTCAAAGTCA AAAGTCAATC	540
ACCAAACCTGG GAGTTACTCG AG	562

(2) INFORMATION FOR SEQ ID NO:1295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 322 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1295:

GAATTCGGCC AAAGAGGCCT AGACACCCGT CATTGCAATT TATATTTTAA CAAAGGCTTC	60
TGATCCTAAT TTCAGGAAAT AGCCTCTAAA CTCATCTATT AGTCCCAAAT TCTTTACCCA	120
TTAAATCTGC TATTTTATGC CTCCTATATT CTTACCTTCA GATGTTGAGA GGTGGGGCA	180
TAAAACTTTG CAGCAGTCT GCAGTCTTCC CTCTAGAGTG AACTTGATCC TGCTGTTTGT	240
TCTTTTATT CTCTTCAAAG TTAAATCATA TTCCAGCATT CATGGTATTT CTCCAGCTTG	300
TCCTCCACAC TCACCCCTCG AG	322

(2) INFORMATION FOR SEQ ID NO:1296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1296:

GAATTCGGCC AAAGAGGCCT AAGCTGTTTCG GGTACTTGTC AAAAATGGCT TCCAAATATA	60
TTCTTTTAA TACAGGATGT GAAACACTT CCTAATAAT TCCTGCAAAA TTAGATGATA	120
CTGTATGTAC TTCTGAAGGA CAGACAAGAA AGTAACCTAA GACCAAAACA ATAGAGGTCT	180
CCTACTACTG GGGAGAAGGA GGATTATCAA GAATAGAGGA AAACAGAGCC TGCCTAAGAC	240
TAATACTGGT CTAGAACAAA AGAGAAAGCT CAATTCCTAC CACCACAAAG CTAACAGCA	300
TCCAAGGCCT CGG	313

(2) INFORMATION FOR SEQ ID NO:1297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1297:

GAATTCGGCC AAAGAGGCCT AGATTTTGT CTTAATTCT CTGTGTTTC AGNACCTGC	60
GATTTTAAA GTATATTAAC CTTTCTCCT AGATGTTTAC CTTTGAAATA CCTCTCTC	120
CTAATGATT AGACCTATGT GTCCAACCTAC TTTTCGGACA TGTTCCCTA GATGTCTCAT	180
GGTTAACTCC AATTAAACAT TTCCAAAGTT AAATTTATT TATTTTACCA GACTTGGGT	240
TTTGTTTC TTTGTTTTC CTTTTCCT TTTAAGATA TCCTGGAGTC ACCAGAATCC	300
TATCTAGATA CCCTTGTTA GAGTTGCTCA TGATCTCGAG	340

(2) INFORMATION FOR SEQ ID NO:1298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1298:

GAATTCGGCC AAAGAGGCCT AGCTTCTTCT GAGAGAGTCT CTAGAAGACA TGATGCTACA	60
CTCAGCTTTG GGTCTCTGCC TCTTACTCGT CACAGTTTCT TCCAACCTG CCATTGCAAT	120
AAAAAAGGAA AAGAGGCCTC CTCAGACACT CTCAAGAGGA TGGGGAGATG ACATCACTTG	180
GGTACAACT TATGAAGAAG GTCTCTTTA TGCTCAAAAA AGTAAGAAGC CATTAATGGT	240
TATTCATCAC CTGGAGGATT GTCAATACTC TCAAGCACTA AAGAAAGTAT TTGCCCAAAA	300
TGAAGAAATA CAAGAAATGG CTCAGAATAA GTTCATCATG CTAACCTTA TGCATGAAAC	360
CACGCTCGAG	370

(2) INFORMATION FOR SEQ ID NO:1299:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1299:

```
GAATTCGGCC AAAGAGGCCT AGTTGGAGTT TGCTGATAGA AGGACTAGCT AAAGGCGTCA      60
CTGCAGGAAT TACAACTGA AGAGGACTCT GTTGGACTGT TTTTITTTTC TTTTNCITTT      120
TTTAAAGAAA AACCCATTTT TTTCCTTAAG GACTTACTAG CCAAAATTTT TTAAGCTTCG      180
AGGACTCTAC TAGCCATGGC CGAGCCATTC TTGTCAGAAT ATCAACACCA GCCTCAAACT      240
AGCAACTGTA CAGGTGCTGC TGCTGTCCAG GAAGAGCTGA ACCCTGAGCG CCCCCCAGGC      300
GCGGAGGAGC GGGTGCCCGA GGAGGACAGT AGGCATCTCG AG                          342
```

(2) INFORMATION FOR SEQ ID NO:1300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1300:

```
GAATTCGGCC AAAGAGGCCT ATCTAGACCT GCCTCGAGTT GGTCTATCCT ATGCTTTATA      60
CGCTAAGAGA GACCACATTT TATTTGCTGT GTCCAACACA GGAATTTAAT AAATGTTGAT      120
TTTAGGAATG CCTCAAGTT CCTCTTATC TTTATATCTC TTTCTACTTT GGCTTCTCCT      180
CTCTAGAGAA GTTCTAGATC TTTCCCAAC TCTCGAG                          217
```

(2) INFORMATION FOR SEQ ID NO:1301:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1301:

```
CCTTCGGAGA GAGGCACGCC CGGCCCGGAC AGTTCAGGCT CTCTCGGCTC CGGGGAGTTT      60
ACTGGCGTGA AGGAGCTTGA TGACATCAGT CAAGAGATTG CCCAGTTACA AAGAGAGAAA      120
TATTCAGTGG AACAAGACAT TCGAGAAAAG GAAGAGGCAA TCAGACAGAA AACCANCGAG      180
GTGCAGGAAT TACAAATGA CCTAGACCGG GAAACAAGCA GTTTGCAGGA GCTCGAG       237
```

(2) INFORMATION FOR SEQ ID NO:1302:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1302:

GAATTCGGCC	AAAGAGGCCT	ACAAAGGAGA	CCCTTCATAT	CAAAATACAG	TTATCAAAAT	60
ATTTTAAAGT	TATATATAAT	TATGTGCTTC	TNCTACTAATG	TCTTAAATAA	TGAGATCAAA	120
CAGCAGATCT	TAAAAACTGT	CATAATATTT	GGAGTAGTGA	TGGGCATAAA	AGTTATTCTG	180
AGATCTCCGC	AGGAACTGTA	ATGTGATATG	AAAAAGTCTG	TGACTCCTGT	TACCAACAAA	240
GTCTCAAGTC	TCAAGTCTAC	TACTAGGGTA	TGTTACCTAC	ATTCCCTAAG	TGAGGGAAAT	300
GTTATGTTTC	AGTTGAGGGC	AAATGATGGC	AATGATGTAA	TTTTTTTCTC	TTTCAAGTTC	360
ACAGCCCCCC	CCGCTCGAG					379

(2) INFORMATION FOR SEQ ID NO:1303:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1303:

GAATTCGGCC	AAAGAGGCCT	ATTTTGCTGA	TTTCTTCTTA	CATATGAATT	ATGTGGGTAT	60
GTTTAAATTT	AAGTTAGGAT	AAACAGGCGT	TAAGTAAGGG	TTAGTGTAGA	ATTTAAGCAT	120
GTCATTTTGG	TAATCTCATC	GGGCCTTGAT	TTCATTAGTT	TAGGCCCTCC	ATTTTATAGA	180
TAGTGGTTCC	CAGACTTCCC	GGCTGCCTCA	ATCTCCTGGG	TCTTTGTAA	ATAACCTTAA	240
GCAAGCTCAT	TTCCCCAGT	GTGTTGAGTT	CACAGAAAGC	TCGAG		285

(2) INFORMATION FOR SEQ ID NO:1304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1304:

GAATTCGGCC	AAAGAGGCTT	AGTTGGTATC	TGCCCAGGGA	TAATTGCTCT	TAGGGTAAGA	60
CTTTTAACAT	GTAAGCCAGC	CTGTCAAAAG	TGCACCTAAA	AGTTCTCTTT	CAGTCATTTT	120
CTGAGTTACT	GATAGGAACA	TAGGTACTGT	GTGAATCAGA	TCTGAGAGGA	TTATGAATGT	180
TATAGAATGC	CTTTTGTTAG	GGAATTTAAG	CCCAGAAGAA	GTTGGGAAAG	TGACAGATTT	240
ATATAAATGC	GAGTGACAAA	ACCAAGTAAA	ATGTTCTGAC	TCAACCTGAA	ATATGTTGGA	300
CTATATAATA	AATATAATAT	TGTGAGATAT	TCTGAAGTAG	ACTCAACTCG	CTCGAG	356

(2) INFORMATION FOR SEQ ID NO:1305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 489 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1305:

CTCGAGTACG	TAGCGTAGAA	ATAGAGAATA	GGTCATCAGG	TTGGAGGTGG	AGTGTTTAAG	60
------------	------------	------------	------------	------------	------------	----

GACAAAGTTA TAAAGAAGTT TTTTGGTTTG AAAAATTAGA GGATAGGTTT GTACCATAGA	120
CAATGGATA AGTTCGGAAA AAATCTTTT TTTTTTTTT TTTTTTTTAA AAAAAAGCC	180
ACGTCTCAC TATGTTGACC AGGCTACCAG GTCGTCTCA AACTGCTGGC CTCAAGCAAT	240
CCTCCCACCT AGGTCTCCCA AACTGCTGGG ACTACAGGCA TGAGGCAGAA TCGCCCGAAC	300
CCAGGAGGCA GAGGCTGCAG CGAGCCAAGA TCACGCCACT GCACTCCAGC CTGGGTGACA	360
GAGCAAGAAT CCGTTCTCCA AAAAAAAGA AATAAATAA ATAAAAAAGG GTGTTCCATA	420
GGGGTGATGG GGAGGATGAA ACGTCATCAA ACAAGTTTAA GAAACATCTA GGCCTCTTTG	480
GCCGAATTC	489

(2) INFORMATION FOR SEQ ID NO:1306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1306:

GAATTCGGCC AAAGAGGCCT AAACCTCAAAT AAAGAAGAAA TACAGGAAAA GGAGACAATC	60
ATTGAAGAAT TAAACACAAA AATAATAGAA GAAGAAAAGA AAACCTTTGA GCTAAAGGAT	120
AAATTAACAA CTGCTGATAA ATTACTAGGA GAATTACAAG AACAGATTGT GCNAAAGAAC	180
CAAGAAATAA AAAACATGAA ATTAGAGCTG ACTAATTCTA AGCAAAAAGA AAGACAGTCT	240
TCTGAAGAAA TAAACAGTT AATGGGGACA GTCGAAGAAC TTCAGAAGAG AAATCATAAA	300
GACAGCCAAC TCGAG	315

(2) INFORMATION FOR SEQ ID NO:1307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1307:

GAATTCTAGA CCTGCCTCGA GTAAAGCCTG TAGGTAAAT GGAGACAGAT TTGAAAGAAA	60
TTAGAGAAGA AATTTCCTCA AGGGAAAAGG TGCTAGCAGA GATCAGTGCT ATAAGGGAAA	120
AGGAGATTGA TTGAAAGAA ACTGGAAAAA GAGACATTCC CATGATGGAG AAAGTATCAG	180
GAAAGATGGC TGTGTTGAA GGACATCTCG AG	212

(2) INFORMATION FOR SEQ ID NO:1308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1308:

GAATTCGGCC AAAGAGGCCT AGAAATATTA ATGAAATCGC TGAAGAGCTT TGCCTTCGAG	60
AGGCCAGAAG CCTCGCGGAA TGTCTGCAAG TCCTAAGACG CGTGTGGGTT GTGCCCTGAA	120

GTGCCGTCCA GCAGGCGCGT GCGGCCGGGC CGGCCTGTGC GTGTGGCCTT TGCCTTCTTC	180
CCTTTCTTCC TGTTTTCTGT TTTTAAATT TGGGGACTGG TGAGGGCTCG TCCATGTCCT	240
TTGTCAGGTC TTCTTGCTCC TCCCCTCGAG	270

(2) INFORMATION FOR SEQ ID NO:1309:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1309:

GAATTCGGCC AAAGAGGCCT AGTCTTATAC CTGGGATGTA GCTGACAAAT TATTGCATTG	60
TAAATGAGT CACGTGAATC ACGGAAGCTT TAACTTTTT CTTTTATAG CCCTACCTGA	120
ACCCATCCTT CCATCCCTCC AAAAAATTTA CCCAGTAAGT GTTCTTATA AATTATTATA	180
ATACATTTTA TGTCAAGTGT ATGTAGAACT ATTATAAGTA GTATTAATGT GATTATAAAA	240
GTAGTAAGGC TAAGTACATG ATAACATTTT CTATATATAC CAAGAGAACA TTTAAATGT	300
TTCATATACT GTTTCAGAAA ACTCTCTTAC TTGTTATTTT GTTATTGGCA GACAGTCTGG	360
TCAGTTGTGT TAATGGTGGA CTCGAG	386

(2) INFORMATION FOR SEQ ID NO:1310:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1310:

GAATTCGGCC AAAGAGGCCT ACCATTTTAG CCTGCAGGCT TCCTTGGGCT TTCTCTGTGT	60
GTGTAGTTTT GTAAACACTA TAGCATCTGT TAAGATCCAG TGTCCATGGA AACATTCCCA	120
CATGCCGTGA CTCTGGACTA TATCAGTTTT TGGAAAGCAG GGTTCCTCTG CCTGCTAACA	180
AGCCCACGTG GACCACTCTG AATGTCCTTC CTTTACACCT ATGTTTTTAA GTAGTCAAAC	240
TTCAAGAAAC AATCTAAACA AGTTTCTGTT GCATATGTGT TTGTGAACCT GTATTGTAT	300
TTAGTAGGCT TCTATATTGC ATTTAACTTG TTTTGTAAC TCCTGATTCT TCCTTTTCGG	360
ATACTATCTC GAG	373

(2) INFORMATION FOR SEQ ID NO:1311:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 402 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1311:

GAATTCGGCC AAAGAGGCC TAAACAGATA TTTACTGAGC ATTTACCATG TTCAGTAACC	60
AGGGCCCTGG GAATATAATA GGAGAAGGCA GATGAGATCC TTGCCTTCAC CAAGCTTATG	120
TTTTTCTATT TTAAGTAAAA TTGCCATGA CAAATTTCT ATCAGCGGAA GAGCCAGTAA	180

CTCTTATTGT AATAGGTTTT ACCCAGTTTT AGAAAAGGAA AGTAGCTAAA CTCTTGTTTC 240
 CTTGGTGTGT GTTTTGTGTT GTTCATTTCT AGTACTTGTC TATGCTTTTG GGGTAATTTT 300
 TGATTTAGAA TTTTGTAGAA ATTACTCGGC ACAGTGTAGT TGAGGTGAAT ATAGGCAAGA 360
 AGGCTTAGGA AGCCTACAAC AAAGGAATCT GACACACTCG AG 402

(2) INFORMATION FOR SEQ ID NO:1312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1312:

GAATTCGGCC AAAGACGCCT AATTGAATTC TAGACCTGCC TCGAGTTGGA CCCTGAGTGT 60
 ATCACTCCCA AGTGTGTACT ATTTATACAC AGCAGTTTCC AATGTACTCA AATCAACCTC 120
 ATGTTCTTTG CTGTAGTAAG CTGAATGAAC ATGACTCTTG AATCACCTTA AATATGCTTG 180
 ATAACATGTC AGGATTCAGA ACAGCAAAAA AGAAAGCTTT AAAGGGGAGAT ATGCTGGGCT 240
 CATTACATC AAACCTGCAGG GGAAACCTGG TTTATGTCCC ATAGCTACTA GAATTCCTAC 300
 ACTTGGCCAG CTTATTTTAA TAGACCATT CTCAACTACT CTAGCTGTTT TGTCTAGTTC 360
 TAAATAAAAA GCTAGGTAGT TGGGTACTAA AAGGCAAATA TGAATATATC AGTGGCTCTG 420
 TATCATCTGC AGCAGTGGTT CTCAGTGTGA TTCCTGGACA GGCAGCACAA GCATCATCAG 480
 GGAACCACTC GGTAAATGCA ACTCTGGGGC GCACTCGAG 519

(2) INFORMATION FOR SEQ ID NO:1313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1313:

GAATTCGGCC TTCATGGCCT ACGAGGACGT GAGCAGATAT ACCAGCCCAG TGAACCCAGC 60
 TGTCTTCCCC CATCTGACCG TGGTGCTTTT GGCCATTGGC ATGTTCTTCA CCGCTGGTT 120
 CTTCTGTTTAC GAGGTCACCT CTACCAAGAC ACTCGAG 157

(2) INFORMATION FOR SEQ ID NO:1314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1314:

CTCGAGTTCA CTACCATGAC AATCATTAAAT TAATTTGGTT TCTCTAGTGA GGTAGTTGTC 60
 TTTCTTCCCT TCCTCCAGCA TCTGACCAAG GTCTGATTCT ACAGCTATTT GGGAAACAGT 120
 AGTTTCTGGT GACATAGCTG AAGACCCTGA TGCTGTCATA GTCTGAATTC CAGAATCTTT 180
 AGAATCTTGA GTTTCAGTAT CAGTTTGCTT TTCAGTAACA GGTTCCTCTT CTTGAAATAT 240

TAATTTGTCA TCATTACCAA ACATGTCCAG TTTTTCACCG GCTTCAGATG CAGCTGGAGA	300
CAAACGTGTTA TCTTGGAGCT CTGTGGGTAG ATTAGCTTCC TCAGTAGGAC TGCCTTCTAC	360
TTTCAGTTCC ACATAATCAT CATCTTCCTC TTCCTCTACT ATAGATTTAT CCAAGAATTC	420
TGGCATCTCT GAGGCAGGTC TAGAAATTC	449

(2) INFORMATION FOR SEQ ID NO:1315:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1315:

GAATTCGGCC TTCATGGCCT AGTGAATAC TAGGATATTT GTTGGCAGC AATAGAGCGG	60
CAACACCCCTT CTCAGACTCG TGGTACTACC CGTCTATCC TCCCTCCTAC CCTGGCACGT	120
GGAAATAGGGC TTACTCACCC CTTTCATGGAG GCTCGGGCAG CTATTCGGTA TGTCAAACCT	180
CAGACACGAA AACCAGAACT GCATCAGGAT ATGGTGGTAC CAGGAGACCA TAAAGTAGAA	240
AGTTGGAGTC AAACACTGGA TGCAGAAATT TTGGATTTT CATCACITTC TCTTTAGAAA	300
AAAAGTACTA CCTGGTTAAC AATTGGGAAA AGGGGATATT CAAAAGTTCT GTGGTGTAT	360
GTCCAGTGTA GCTTTTGTG TTCTATTATT TGAGGCTAAA AGTTGATGTG T	411

(2) INFORMATION FOR SEQ ID NO:1316:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 274 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1316:

GAATTCGGCC AAAGAGGCCT ACATCCAACA AGAAGCCATA ACTTTATTTA TGATAGAAAC	60
AGTACAAATT TCAAACCAAG CTGCAGTTAC TCCTTTGAGA CACCAAAAAA AGTTGCCTCC	120
ATATGGTTAC ATTGTTAATT CCATAATCGC ATTACAATA TCATTACTGT TGTCTTCAG	180
GGCTCGGACT GCCTTTGCTC TCGACACATT TGCTTGTGAC ATGACCAATT CTATGTCCTT	240
AACITCTACA CCTGTTTCAC TTCCTCTTCT CGAG	274

(2) INFORMATION FOR SEQ ID NO:1317:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1317:

GAATTCGGCC AAAGAGGCCT AGGCGGAGGT GCAGGTCCTG GTGCTTGATG GTCGAGGCCA	60
CTTCCTGGGC CGCTGGCGG CCATCGTGGC TAAACAGGTA CTGCTGGGCC GGAAGGTGGT	120
GGTCGTACGC TGTGAAGGCA TCAACATTTC TGGCAATTTC TACAGAAACA AGTTGAAGTA	180
CCTGGCTTTC CTCCGCAAGC GGATGAACAC CAACCCTTCC CGAGGCCCTT ACCACTTCOG	240

GGCCCCAGC CGCATCTTCT GGCGGACCGT GCGAGGTATG CTGCCCCACA AAACCAAGCG 300
 AGGCCAGCC GCTCCTCGAG 320

(2) INFORMATION FOR SEQ ID NO:1318:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1318:

GAATTCGGCC AAAGAGGCCT ATAATTTTTC CCATCATTTA CCCTGATAAT CTGCCTCTTC 60
 TCCATTCTC CTTCCCTTAC TACCTTCTT TGAATTACTG TAACTGATTG GTCCCACCAA 120
 AATTTTAAAG TACATGAAGT ATCTTCATTG GTTCATCCTC TTGCCCCCTC CAGATCTCAA 180
 AAAACTTTAT CTGCCCCCT TGCCTCCACC CGATGGCCCA CTCGAG 226

(2) INFORMATION FOR SEQ ID NO:1319:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1319:

GAATTCGGCC AAAGAGGCCT ATGAAGCTTC TGAGTTCTGC GGCCTCACNT CTGAGAAAAC 60
 CTCTTTGCCA CCAATACCAT GAANCTCTGC GTGACTGTCC TGTCTCTCCT CGTGCTAGTA 120
 GCTGCCTTCT GCTCTCCAGC GCTCTCAGCA CCAATGGGCT CAGACCCTCC CCCCCTGGC 180
 AAATCTCTCG AG 192

(2) INFORMATION FOR SEQ ID NO:1320:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1320:

GAATTCGGCC AAAGAGGCCT ATTTATTACA ACAGATCTTT TAATGACTAT TTTTAACATA 60
 AAGATTGTTG TTTTGGGAAA CATCTATTCT CTTTGAACAT TTCCTAAAT TTTCAATGTA 120
 TTAAATAACT GACAGAAATA AGTTCTGTGT TCTGTACAAA TTAAAGGTCC CATGAATACA 180
 TAACCCAC CCCCCCCC TCCACTCGAG 210

(2) INFORMATION FOR SEQ ID NO:1321:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1321:

GAATTCGGCC AAAGAGGCCT ATTTTITTTT TGATCTATGA ATGATTTATT AGATAAATTC	60
TATACATACA AAGTACAGAT TCTTCATTGA GCATTGATTT ACTTCTTAGT TTTCATCTTT	120
CTGACTATCC AAACCGCTGA CTCGAGGCAG GTCGAG	156

(2) INFORMATION FOR SEQ ID NO:1322:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 199 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1322:

GAATTCGGCC AAAGAGGCCT ATTTTGTCTA CACTATGTGA CAGAACAGCT TATAAACTA	60
GGTATGAACA TTAAGTGTGA GTGTAAACAG TAGGACTACC ACTTGTCAAA AGTTTAAAC	120
ACTTGAACGT GAACTGGTAC TGGTTATTCA TCATTTTCAT TGTTTCTAT TTCATCCCCC	180
CCACACCCCT CTGCTCGAG	199

(2) INFORMATION FOR SEQ ID NO:1323:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1323:

GAATTCGGCC AAAGAGGCCT ACACGGTACC AACACAACCT CAAGCATCGA CTCCTCCGCA	60
GACCCAGACC CCTCAGCCGA ATCCTCCTCC TGTGCAGGCC AGGCCTCACC CCTTCCCTGC	120
CGTCACCCCG GACCTCATCG TCCAGACCCC TGTCATGACA GTGGTGCCCTC CCCAGCCACT	180
GCAGACGCCC CGCCACTCAG CGCCTCGAG	209

(2) INFORMATION FOR SEQ ID NO:1324:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1324:

GAATTCGGCC AAAGAGGCCT AATCACTACT CACAGTAACC TCAACTCCTG CCACAATGTA	60
-------------------------------------------------------------------	----

CAGGATGCAA CTCCTGTCTT GCATTGCACT AAGTCTTGCA CTTGTACAA ACAGTGCACC	120
TACTTCAAGT TCTACAAAGA AACACAGCT ACAACTGGAG CATTACTTC TGGATTTACA	180
GATGATTTTG AATGGAATTA ATAATTACAA GGCTCCAAAC TCACTCGAG	229

(2) INFORMATION FOR SEQ ID NO:1325:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1325:

GAATTCGGCC TTCATGGCCT AGCTTTCCCA ATCTCTCGGA GCATGCACAT CAGGGCCACG	60
TTGGTCTTCC CAGCACCAGT AGGAGCACAC AGCAGCAGAT TCTCATCCGT CTCAAGGGCA	120
GCACGGTAGA GCTTACTCTG GATCCGATTC AGTGTTTGA AGCCCTCAA CCCAGCCTGG	180
ATTGAATTCT AGACCTGCCT CGAG	204

(2) INFORMATION FOR SEQ ID NO:1326:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1326:

GAATTCGGCC AAAGAGGCCT AGCCGATCTC CAGCCCAAGA TGATTCCAGC AGTGGTCTTG	60
CTCTTACTCC TTTTGGTTGA ACAAGCAGCG GCCCTGGGAG AGCCTCAGCT CTGCTATATC	120
CTGGATGCCA TCCTGTTTCT GTATGGAATT GTCATCCCC CAGAGCGTCT CGAGGCAGGT	180
CTAGAATTCG AG	192

(2) INFORMATION FOR SEQ ID NO:1327:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1327:

GAATTCTAGA CCTGCCTCGA GAATAGGATA GCATTAGTA ATTCACTTAA CAATTTTAT	60
TGAATATCTA TTGTTTTATT GAATATGCTT GTTCTCACCT TAGCACATT GCCCTTGTTT	120
TCCCTGGGAT ACTATCCCC TAGATCTGAT TTTTGGTTTT TGTGTTTGT TGTTTTAATT	180
CTCTGCCATC TTTCTCCAGT CAAATGTCAC CACTCTCTG AG	222

(2) INFORMATION FOR SEQ ID NO:1328:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1328:

```
GAATTCGGCC TTCATGGCCT AAGAAATGTT CACTTTTCCA ACTTAAAAGG ATTTTAAAAA    60
ATACAAACAT AATTGACCTA CTGGTTCAA AGAACAGAAG TGAGGAGAAC TTGCTTAAAG    120
GTATTGATGT TATATTTTCT CTGACTGAG TGCTTGAAAA AAAATTTTAT TGAACATATG    180
TTCTCCTTCC GTGGCTTTT TGTCTTGCT TTTTGTGTTT GTTTGTGTT TTTTCTTT    240
GAGATGGAGT CTCACTCTCT GCTCGAG    267
```

(2) INFORMATION FOR SEQ ID NO:1329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1329:

```
GAATTCGGCC TATGGCCTAA AAAAAAAG AAAGAAATAG GATTGATACA GGTATAGATA    60
CATAGATACA TGAGAAGGGA TTTATTATGG GAATGGGCTC ATATGATTAC AATGATTACA    120
GAGGCTGAAA ATTCCACAA TAGGCCATCT GCAAGCTGGG GACCAGGGAA GCCATTTATG    180
TGGTACAGTC TAAGCGTCAA TCAGGAAAGC CAGTTGGGTA ACTCTCAGTC TGCAGCTGAA    240
GGCCTGAGAC CCGGAGGTCC ACTCGAG    267
```

(2) INFORMATION FOR SEQ ID NO:1330:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1330:

```
GAATTCGGCC TATGGCCTAA AAAAAAAG AAAGAAATAG GATTGATACA GGTATAGATA    60
CATAGATACA TGAGAAGGGA TTTATTATGG GAATGGGCTC ATATGATTAC AATGATTACA    120
GAGGCTGAAA ATTCCACAA TAGGCCATCT GCAAGCTGGG GACCAGGGAA GCCATTTATG    180
TGGTACAGTC TAAGCGTCAA TCAGGAAAGC CAGTTGGGTA ACTCTCAGTC TGCAGCTGAA    240
GGCCTGAGAC CCGGAGGTCC ACTCGAG    267
```

(2) INFORMATION FOR SEQ ID NO:1331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 494 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1331:

ATGGATTGGT	TGCGTGGTC	TTTACTGCTT	TTCTCCCTGA	TGTGTGAAAC	AAGCGCCTTC	60
TATGTGCCTG	GGGTCGCGCC	TATCAACTTC	CACCAGAACG	ATCCCGTAGA	AATCAAGGCT	120
GTGAAGCTCA	CCAGCTCTCG	AACCCAGCTA	CCTTATGAAT	ACTATTCACT	GCCCTTCTGC	180
CAGCCCAGCA	AGATAACCTA	CAAGGCAGAG	AATCTGGGAG	AGGTGCTGAG	AGGGACCGGA	240
TTGTCAACAC	CCCTTTCCAG	GTTCTCATGA	ACAGCGAGAA	GAAGTGTGAA	GTTCTGTGCA	300
GCCAGTCCAA	CAAGCCAGTG	ACCCTGACAG	TGGAGCAGAG	CCGACTCGTG	GCCGAGCGGA	360
TCACAGAAGA	CTACTACGTC	CACCTCATTG	CTGACAACCT	GCCTGTGGCC	ACCCGCTGTG	420
AGCTCTACTC	CAACCGAGAC	AGCGATGACA	AGAAGAAGGA	AAAAGATGTG	CAGTTTGAAC	480
ACGGCTTACT	CGAG					494

(2) INFORMATION FOR SEQ ID NO:1332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1332:

GAATTCGGCC	TTCATGGCCT	AGCTGATATT	ATTTCTGAGT	TTTGTCTTAT	TTGCTTTCTA	60
CATAGAATCA	ATAAAATTGA	CAACTAGCAT	TGCCTATATA	TGCAGGTGTG	ATACTATTCA	120
GGGTACTAGT	ATATTGGCCA	CTCATTATGA	AACTTTCAGG	TCCTCATATA	TTTTCTTTTA	180
TTACAATGAT	CTACTTATTT	CTGATAAATA	TTGGATTTCAT	AGAGGCTAAA	GGGCTGGGAA	240
AGGAAAACAT	TCGTGACTAC	TTACAACCAT	TTGATACGAG	TTGTGTCAAT	ACAGACCTCA	300
CACAGCAGCA	CCTCGAG					317

(2) INFORMATION FOR SEQ ID NO:1333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1333:

GAATTCGGCC	TTCATGGCCT	AGCTTTTCTA	GCCTTTCTCA	AAGAAATGCA	AACAGCTTGT	60
GTTTTTTCCC	CTTGGGTCTT	ATTGTACCTA	CTTTGTGTTG	ATGGTCTCTC	TGTCTCCCAT	120
GATGCCAGTG	AATGTAGCAG	TTTCTCTCCA	CTTCCACCAG	TGCCTGGGGA	AAATTTGGTA	180
TTGGCAAATT	TGAGTTCTGC	CTTTTTCGAG	CTTGCAATTGC	TGGATTCAAC	CTTAGGAGCC	240
TCAGTTACCC	TCGAG					255

(2) INFORMATION FOR SEQ ID NO:1334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1334:

GAATTCGGCC TTCATGGCCT ACTCTTCCCC AAAAGGAAGC ATTTACTCTG CCTCTTACAG	60
TGCAGAGTGA CAGAATGGAC ACAGAAAAAC ATAGGTGGGT CAGAACAGAT CTCAGTTTGA	120
ACCCAGTAGC TACTGGCTAT AGGGTCTCTG GGCAAGTGAT TTGACCTCTC TCGGCTCTGT	180
CTTCTCAAAT GTAAAAACGG GTCAGGCGCA GTGGCTCATG CCTATAATCC CAACACTCCG	240
GGAAGCCAAA GTGGGAGGAC TCTCGAG	267

(2) INFORMATION FOR SEQ ID NO:1335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1335:

GAATTCGGCC TTCATGGCCT ACAAATGTAA AAATAACTGG GCACTGAAGT TTTCTATCAT	60
ATTATTATAC ATTTTGTGTG CCTTGCTAAC AATCACAGTA GCCATTTTGG GATATAAAGT	120
TGTAGAGAAA ATGGACAATG TCACAGGTGG CATGGAAACA TCTCGCCAAA CCTATGATGA	180
CAAGCTCACA GCAGTGGAAA GTGACCTGAA AAAATTAGGT GACCAAACCTG GGAAGAAAGC	240
TATCAGCACC AACTCAGAAC TCTCCACCTT CAGATCAGAC ATTCTAGATC TCCGTCAGCA	300
ACTTCGTGAG ATTACAGAAA AAACCAGCAA GAACAAGGAT ACGCTGGAGA AGTTACAGGC	360
GAGCGGGGAT GCTCTGGTGG ACAGGCAGAG TCAATTGAAA GAAACTTTGG AGAATAACTC	420
TTTCTCATC ACCACTGTAA ACAAACCCT CCAGGCACTC GAG	463

(2) INFORMATION FOR SEQ ID NO:1336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1336:

GAATTCGGCC TTCATGGCCT AAATTCTAGA CTGTCATCGA GGGCGGCGAC CTGATGATGA	60
CCAGCTTCGA GAGGATGCTG TCCCAGAAGG ACNTGGAGAT CGAGGAGCGC CACAAGCGCC	120
ACAAGGAGAG GATGAAGCAA ATGGAGAAGC TGAGGCACCG GTCCGGAGAC CCCAAGCTCA	180
AGGAGAAGGC GAAGCCGGCA GACGACGGGC GGAAGAAGGG TCTGGACATT CCTGCTAAGA	240
AACCGCCGGG GCTGGACCCT CCATTAAAG ACAAAAAGCT CTCGAG	286

(2) INFORMATION FOR SEQ ID NO:1337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1337:

```

CTCGAGGGTT TTTGTTTGGC TGGTTGTGTG TACACAGTGT ATACAAGTTG AGTTGTACAG      60
AAGCCCAAGA AAGAGCAAGA GACAAAGGCT AGTGGGAGCA GGGGGTGGG CGGGGGCGAG      120
AACGGGGAGG AGGGGAAAGG AGACCGATAA AAAATAGAAC CACATCCAGA CAACAATGGG      180
GGATGGGCAG TGGGTGGGGG CCAGACACAG ACAAATCGCC GTAGAAAAGG AGTGGGAGGG      240
GCAGAGAGTA GAGGG                                                    255

```

(2) INFORMATION FOR SEQ ID NO:1338:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1338:

```

GAATTCGGCC TTCATGGCCT AAGAGAAAGC ATTTTAACTT TTATAGTAAA CAATAAAAAA      60
GCCTCATAAA GCTTCTCACA ACAACTTCAT TCGTTTCAGA AGTTAAGATA TATTCCTTAT      120
GAATACCAAC ATTGTGACAT TTGTGTTGCC AATTATTTTC TCTGGAATCA TTCTTTTAAC      180
TTCACCTTCT GTTGTGTTGGG AAGACTTTGC AGAGAACATA TTTTAAATAG GCTATAATCA      240
CACGGGCAAC AGACTCGAG                                                    259

```

(2) INFORMATION FOR SEQ ID NO:1339:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1339:

```

GAATTAGAAG TATTGTTTAA TAAGTCCTTT TTTTCTACTC AACATTAAGT AGTAATCAAC      60
TTTACCTCC GCCAGTTTTT CTGCTTTTTT GCTGGTACGA TCTCTCTTC TAAATTGAAT      120
CAAAGACCTA GGTGGAAC TGAACTTAGG AGGGAAAGAC AAAATGAGGC TTGTTTCATGA      180
TCAAATTCTG TGTACTCTAG TTGCTTCTTT CCCTTGGAGT GACAGGTACT TTTATATCCA      240
GGATGATTAC AGTGATGACA TCCATTCTTT TTTGGGGGCC CTCGAG                                                    286

```

(2) INFORMATION FOR SEQ ID NO:1340:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 240 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1340:

```

GAATTCGGCC TTCATGGCCT AGGAATCAGT AGTGTACTTT GATTGTATTG TATAAGGTAT      60
TTTCAATAG AAAAGCAGGT AGCAGAAATA CTAAAAGAAT TTTTGCTTT AGTGTAAGT      120
AGATAATGAG AGGTAGATGC CTAATTTCTT AGTTTTCTTT TTAAATTAT GCTAAAATAT      180
ATCATATCAT TTACCATTTT GACTATTTTA AAAGTATACA GTCCGTGGC AAGTCTCGAG      240

```


(2) INFORMATION FOR SEQ ID NO:1341:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1341:

GAATTCGGCC TTCATGGCCT ACAAATTTGT GTCTTTTTTT TGGCAATGTT GTCTTGCCAA	60
TCCCATCCCT CCCCAGCTC TCCGAACAGC AGGATTTCCT AACGGCAGCT TGGGANAAAG	120
ACCCAGTGGC AGCTTGGGGA AAAGACCCAG CGCTCCGTTT AGAAGCAACG TGTATCAGCC	180
AACTGAGATG GCCGTCGTGC TCAACGGTGG GACCATCCCT ATTGCTCGGC CAAGTCACAC	240
TCGAG	245

(2) INFORMATION FOR SEQ ID NO:1342:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1342:

GCGATTGAAT TCTAGACCTG CCTCGAGACT GACGCCGCAC CATGACCCTC CTGCTGCTGC	60
CCCTTCTGCT GGCCTCTCTG CTCGCGTCCT GCTCCTGTAA CAAAGCCAAC AAGCACAAGC	120
CACCGCATCT CGAG	134

(2) INFORMATION FOR SEQ ID NO:1343:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1343:

GAATTCGGCC AAAGAGGCCT AAAAAGCTTC CAGCAGCAGA TGCAGAATTA CCTTAAAGAC	60
AACAAAACAG CCACTATTTT GGACAAATTG CAGAAAGAAA ATAAGTCTG TGGAGCTTCT	120
AACTACACAG ACTGGGAAAA CATCCCCGGC ATGGCCAAGG ACAGAGTCCC CGATTCTTGC	180
TGCATCAACA TAACTGTGGG CTGTGGGAAT GATTCAAGG AATCCACTAT CCATACCCAG	240
GGCTGCGTGG AGACTATAGC AATATGGCTA AGGAAGAACA TACTGCTGGT GGCTGCAGCG	300
GCCCTGGGCA TTGCTTTTGT GGAGGTCTTG GGAATTATCT TCTCCTGCTG TCTGGTGAAG	360
AGTATTCGAA GTGATGTGCA G	381

(2) INFORMATION FOR SEQ ID NO:1344:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1344:

GACCAGATGG AANGGTCACC GAACAGTTCT GAGTCATTG AGCATATAGC TCGATCTGCA	60
AGAGATCACG CAATTTCCCT TTCTGAGCCT CGTATGCTGT GGGGGTCAGA TCCCTATCCT	120
CATGCTGAGC CTCAACAAGC AACTACTCCC AAAGCAACAG AAGAGCCTGA GGATGTAAGG	180
TCTGAAGCTG CGTTGGACCA GGAACAGATT ACTGCTGCTT ATTCTGTAGA ACATAATCAA	240
TTAGAGGCTC ACCCAAAGGC AGACTTTATC AGAGAATCAA GTGAGGCACA AGTACAAAAG	300
TTTTTAAGCA GATCTGTGGA AGATGTTAGA CCTCACCATA CTGATGCAAA TAATCAGTCT	360
GCTTGTTTIG AAGCACCTGA TCAAAAGACC TTATCCGCTC CTCAAGAGGA GCGGATTTC	420
GCTGTAGAAA GTCAGCCTTC CCGGAAAAGA AGTGTTCCTC ATGGATCTAA CCATACGCGC	480
CTCGAG	486

(2) INFORMATION FOR SEQ ID NO:1345:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1345:

GAATTCTAGA CCTGACTCGA GGTGCTGGAA TTACAGATAA AAGCCACCAC ACGCAGCCCA	60
CATAAAGTGT TTATGGGAGC AACTAACAGT TGGTTTGAGC GCAGCCTAAA TAGGGGATGG	120
CAAGGTTGGG TTTTCCAAGG TTTTCTAATC TTTCTATTTC TTCTAGTGAG TCTTCAGGTT	180
ATTATGACTT GTGTTACCAG ACTATCAACA AAAGTGGGTA CCTCTTTAAA TCAGAGCCTC	240
GAG	243

(2) INFORMATION FOR SEQ ID NO:1346:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 294 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1346:

GAATTCTAGA CCTACCCCAT CCACATGCAC AGCCAGCTGG ACCACCTTAG CCTCTATTAC	60
TGCAGGTGTA CTCTGCCAGA GAATCCAAAC AATCACACCC TCCAGTACTG GAAGGACCAC	120
AACATCGTGA CAGCAGAAGT CCACTGGGCT AACCTGACTG TCAGTGAATG CCAGGAGATG	180
CATGGAGAGT TCATGGGATC TGCCTGCGGC CATCATGGAC CCTACACTCC TGATGTCCTC	240
TTTTGGTCCT GTATTCTCTT TTTCAACCACC TTCATCCTCC CAAGCACCTC CGAG	294

(2) INFORMATION FOR SEQ ID NO:1347:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1347:

AGTTTCTCCA TTTTAGAATT TTGTTGTCCT CCTTAATCAT CTGCTTACCT AGTCATTACT	60
CAATCTGCAG AAACCTCATA AAGGAAAAGT GCTGCATTGT TTTTACAAAT AACAGTTTGT	120
AGGGAAAATA TGACAAACCT CAACTATGGG AGTTGTCCAC AATACAAAAT TTTGAAAAAA	180
CATTACATAG TGATAATATC ATACTTGGTT GTTAGGCTTG TTGCTTCCCC ACCACTCGAG	240

(2) INFORMATION FOR SEQ ID NO:1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1348:

AAGTATTCTT TCAATTGCAA AGTGGCAACA GCTTTTATAT GCTAAGTCTG ACAAGTTTGC	60
AGTCAGTGAA TGATGGCACA TGGCACGAAG TGACCCCTTC CATGACAGAC CCACTGTCCC	120
AGACCTCCAG GTGGCAAATG GAAGTGGACA ACGAAACACC TTTGTGACC AGCACAAATTG	180
CTACTGGAAG CCTCAACTTT TTGAAGGATA ATACAGATAT TTATGTGGGA GACAGAGCTA	240
TTGACAATAT AAAGGGCCTG CAAGGGTGTC TAAGTACAAT AGAAATCGGA GGCATTTATC	300
TCTCTTACTT TGAATATGTT CATGGTTTCA TTAATAAACC TCAGGACGAG CTCGAG	356

(2) INFORMATION FOR SEQ ID NO:1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1349:

GAATTCTAGA CCTGCCTCGA GACCTTTCTC CTGGTCTAAT GCTCCTTTTA AGGAAGGTGG	60
AAGGAACAAT GGAAGAATGC TTGTAAAGTA ATGTATTCTT AAGAACTAAA GCTATTTGCA	120
GAAGGGCCGA AGCTATGTGG TGTGAAAGGG AAATGAAGAG GGTGAGTTGG GGGGCTCGAG	180

(2) INFORMATION FOR SEQ ID NO:1350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1350:

GAATTCTAGA CCTGCCTCGA GCTTTCCTG ATCTTCTTCC ATCCCTTACT GACAGTGT	60
ACCAAGGATT TCCCTTGGCC TGCTTCTTTC TTTGACGCTC ATTTAAACCT TTCCCTTCAG	120
TTGCAGACCT CGTCTGCTTC TCCCAGCTAT TCCATTCTTC AGTTGCTTGT TAAACACGGC	180
CCACCATCAC CTCAAAAATG ATGTTAAAAT GTCCCCATTT TTTATCAAAC TTAAGTTTCT	240
TCCTGTGGAT CTGTTGCTCA GTACTCTCAT CTTTCCGATC ACTCGAG	287

(2) INFORMATION FOR SEQ ID NO:1351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1351:

GAATTCGGCC TTCATGGCCT AAAAAATTCT TTTTAATGG GTTTTAAACA CTAACACTGA	60
GAATTTTCTT TGATTCCTCAT CTGTTGGTTT ACTTGATTGC TATAGCTGTA TGGTAAATCT	120
CAAAATTAGG TAATGTGATT TCTTTTCTT TACTATTTT ATTAAAAAT CATTAGCAT	180
TCCTAGTTTG ACTTCCATA TACACTTTAG GATTGGTTT TCTGTTTTT AAATATTCTT	240
GCTTGGATT TGATAGAAAT TGAGTTAAAT CTATAGATCA ATGTGTTGGA AATTGGCATC	300
TTAGTCTTCC AATTCATGAA CATAGCCTAC TCGAG	335

(2) INFORMATION FOR SEQ ID NO:1352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1352:

GAATTCGGCC TTCATGGCCT ACGTATGAGA CAGTGTATAT GACACTGTAT ATGTGTGAGA	60
CTGTGTGTGT GAAACACTAT ATGACACTGT ATATGTGTGA CACTGTATAT GACACTATAT	120
GTGGAGACTA TGTGTGAGAC ACTATGTATA TGTGACACTA TGTATGTGTG TGACACTGTG	180
AGAGACACTG TGAGACACCA AGACAGTATA TGTATGAGAC ACCCTGTGTG TGTGACACAG	240
CGTGTGACTG TGTGAAACAT GCTCGAG	267

(2) INFORMATION FOR SEQ ID NO:1353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1353:

GAATTCGGCC AAAGAGGCCT ACCCAGAACC AGTTATACTG AGGGTCCTGA GATCTGCTAT	60
AACATCACCA TCCTTTCAAC CCAGAGGTGT GTGTTTGTGG GCCATTCAAT TGGCCCTCAC	120
CACATCCTGC CTGTATTGCT TAGTTTATCT TTTTATTGTC TTGTTCTCC CCAACCTCC	180
TGCGCCATAC AGACTCCTCG AG	202

(2) INFORMATION FOR SEQ ID NO:1354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1354:

```
GGTTTGGATA TCCTGAAAGA TCAATGGGCA GCTGCAATGA CTCTCCGCAC GGTATTATTG      60
TCATTGCAAG CACTATTGGC AGCTGCAGAG CCAGATGATC CACAGGATGC TGTTAGTAGCA      120
AATCAGACGA GCAAAAATCA AATTAAAGTA GATCTTGTAG ATGAGAATTT TACAGAATTA      180
AGAGGAGAAA TAGCAGGACC TCCAGACACA CCATATGAAG GAGGAAGATA CCAACTAGAG      240
ATAAAAATAC CAGAAACATA CCCATTTAAT CCCCTGATC TCGAG                          285
```

(2) INFORMATION FOR SEQ ID NO:1355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1355:

```
GAATTCGGCC TTCATGGCCT AGTTATTTTCG TCACTGTGCG AAACAGCAGG CAAAGTTTGA      60
CGAGTGTGTG CTGGACAAAC TGGGCTGGGT GCGGCCTGAC CTGGGAGAAC TGTCAAAGGT      120
CACCAAAGTG AAAACAGATC GACCTTTACC GGAGAATCCC TATCACTCAA GACCAAGACC      180
GGATCCCGAC CCTGAGATCG AGGGAGATCT GCAGCCTGCC ACACATGGCA GCCGCTTTTA      240
TTTCTGGACC AAGTAAAGAT GGGTCCGTGG CCCCACTCG GTCATGTGCT CAGACAACAA      300
CTCGAG                          306
```

(2) INFORMATION FOR SEQ ID NO:1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1356:

```
GGAATGATGT CACTCACGTC CAGCAAAGCC AAAGAGCTGA AGGACCGGCA CCGGGACTTC      60
CCAGACGTGA TCTCAGGAGC GTATATAATT GAAGTAATTC CTGATACCCC AGCAGAAGCT      120
GGTGGTCTCA AGGAAAACGA CGTCATAATC AGCATCAATG GACAGTCCGT GGTCTCCGCC      180
AATGATGTCA GCGACGTCAT TAAAAGGGAA AGCACCTGTA ACATGGTGGT CCGCAGGGGT      240
AATGAAGATA TCATGATCAC AGTGATTCCC GAAGAAATNG ACCCAGGC TCTCGAG                          297
```

(2) INFORMATION FOR SEQ ID NO:1357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1357:

GTCCCGCTAA ACCGGCAGGC GATGAGAAAG GAAACCATCA CTAAGATGCT CTGGAGTACC	60
CGCACCCCTGT TGAATATCAC CAAGGAGCAG GTACCACTTG TGGTGGAGGA GTACCTGGAC	120
AATGTCAATG AGCATGACTG GAAGATGCTA CGAAACCGTA TGATGGACAT AGTTCAAGAT	180
GCCACTTTCG TGTATGCCAC ACTGCAGACT GCTCACTACC ACCGAGATGC CGGCCTCCCT	240
GTCTACCTGT ATGAATTGTA GCACCACACG CTCGAG	276

(2) INFORMATION FOR SEQ ID NO:1358:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1358:

GAATTCGGCC TTCATGGCCT AGGGGAGCAT AAAAATACAA AAAACATTG GCTTTATTCA	60
CAACGTATTT TGTGAAAAC CAGGAATAAC TCTTTGAATT TTGGGGAAAC CAACAACATT	120
CTCAAAAACG ATGATAATCA ATTTTATGTG GCACCTCTGC ACCCTGCCTC CATGGTCCCA	180
CCACCAGGTT CCTCTCCTC CACAGTCAGA AGTTCCTCCC TGCATTCAAA CACTGGGTCT	240
CGAG	244

(2) INFORMATION FOR SEQ ID NO:1359:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1359:

GCGATTGAAT TCTANACCTG CCTCGAGGAC CCAAATATTT CTTTGAGATC TTTCTTTCAA	60
TTCTTTTGA CATATACTCA GAAGAGAGAT CATTGGATTA TTTTGTGTTT TTTCAGAAAC	120
TGCTACCGT ATTCCAAAGC AGCTGCACCA TTTCACATTC CCACCAACAT TGCATCAGGG	180
TTCCAATTTT CCCACATCCT TGTCACATT TGTTATGTTG TTTTGTGTTT TTGTTTTTTT	240
TTTGTTTCGC TTGTTTTGT TTTGTTTTGT TTTGTGCACA CAGTCTCGCT CTGTTGCACA	300
GGCTGGAGTG CAGTGGTACA GATCTCAGCT CACTGCAGCC TCTACCTCTC CAGTTCAAGC	360
AATTCTCCTA CTCAGCCTC CCCGGCTCGA G	391

(2) INFORMATION FOR SEQ ID NO:1360:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1360:

```

GAATTCGGCC TTCATGGCCT ACATTTTTTT CCTAGTATGG ATATGCTTAT TAATGCACTT      60
GTTTCAAAAT CCCAAATTGC ACAAATGTGT TAATATTTTA AGAAACAAAA TGAATCCTAC      120
AAGGAGAATG ATTTTtagcc ACACATAGGG TTGGATCTTG AGAGTGACCT ACAGAATAAA      180
AGTACTTTTA AAATAAAGTA GTCAGAGGCT ATTCAAAGGG TAAAATAATC ATAGTACCAC      240
ATTGGTCCAC TTGACACTCG AG                                         262

```

(2) INFORMATION FOR SEQ ID NO:1361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1361:

```

GAATTCGGCC TTCATGGCCT AGACAACCTG AACTGGATG ACATGCTGAG TGAATCAGA      60
GACAAATGGG ATACCATATG TGGAAAATCT GTGGAAAGGT AAAATGTTCT TTAAGACAGT      120
TTGGTTACTC TGTAACCTC TTTCAAATAC ACAGTAATGG TGCTTTGCGG GGACATTTCG      180
GGAACCTTAA ATATTTCTT TGCCTGAGGA ACTTCTGCTT GTCCTAAGTA TCCACACAC      240
ATAGCACTCG AG                                         252

```

(2) INFORMATION FOR SEQ ID NO:1362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1362:

```

GAATTCGGCC TTCATGGCCT ACATAGCAGT ACACAGAAAC TCATCTTTGG TCTTAAACT      60
GCATAGGTAC TTTAGTCCTC TGTTGACAAA TGTGGGTTG TTTCAGTCTT CTGCTATCAC      120
AAATAATGCT GCAAAGAATA CATTTGTTCA TATGTCATTT CATCCTTGGC AATTTTGCCT      180
CTGGAAAGTT CCTAGAAGTC AGATTCCCAG GTCAAAGGTT AAATGCGCAT GTAATTTTGC      240
TGGATATTGT TAAATCCCCC TACAGAGCAT GCACCACTCA GCATTCCCTC CAGCTCGAG      299

```

(2) INFORMATION FOR SEQ ID NO:1363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1363:

GAATTCGGCC TTCATGGCCT AGCGAGATCT GCGTGAAAAA TACAGCAATT TTGGCAATAA	60
CTCTTATCAC TCCTCAAGAC CCTCATCTGG ATCCAGTGTG CCCACCACCC CCACATCATC	120
CGTCTCACCC CCACAGGAGG CCAGGTTGGA AAGGTCATCA CCGAGTGGTC TTCTCACATC	180
ATCCTTCAGG CAGCACCAAG AGTCACTGGC AGCAGAGAGA GAGAGGCGGC GGCAGGAGAG	240
AGAAGAAAGG TTGCAGAGAG AGCTCGAG	268

(2) INFORMATION FOR SEQ ID NO:1364:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 273 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1364:

GAATTCGGCT TCATGGCCTA CCAACCCCCC CATTTCTCCC TTCCTCCAGC CACTGGCAAC	60
CACCATTCA TGTTCTTTT GTTTGTTGT TTTGTTT GTTTTTTGT TTTGTTATT	120
ATTATACTTC AAGTTTtagG GTACATGTGC ACAACGTGCA GGTGTTGTAC ATATGTATAC	180
ATGTGCCATG TTGGTGTGCT GCACCCATTA ACTGGTCATT TAGCATCAGG TATATCTCCT	240
AATGCTATCC CTCCCCACTC CCCCAGCTC GAG	273

(2) INFORMATION FOR SEQ ID NO:1365:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1365:

GAATTCGGCC TTCATGGCCT AATCGGTGTC TTTGGTAAAA ATTCTATGAG GATGACATAT	60
TCCATCATGT TATTCGTTTC ACATTTCCTT TTGCTCAGTC TCCAATGCAA GCACAGCTTG	120
TGGTATAACC TATTGTTTTC CCATTCTAAT AACTTCTCAA TCGATCTTCG TGTTCTTTTA	180
CTGAGGCAAA TAACTGGCCA CATACTGCAA CCTAATGTGC AGCAGCAACA AAGGCAGCCA	240
CAAAGTAGCC AACGTACATT AACAGGAAGG TTCTTCTTAA GACAACTGTT AACTCTGTNG	300
ATGCTGGCTT TAAATTCTTC AGGAGCTACT TTTTCAGTTA ATGAAGAAGG GAATTCAGAT	360
TCAAAT	366

(2) INFORMATION FOR SEQ ID NO:1366:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1366:

GTTGTTAGGC TGGTGTGTT ATGTTGCTGT TGTATGCTG GTCGTGCTGC TCCATGTTCT	60
CCAGGTGTTT TTCCCTTTTA TCGTCACAGT TACCCCGTAC ACCTGACAAC TGGACATCTG	120
CGCTGGGGT CTTCAGCCTA AACACACCTA AACCCTCCAC CAAACCCCTC TGCTTCGGCC	180

TCCCCGTGTC TGTGAGCGCC TCCACTGCCC ATCCCTCTGC TCAGGCCCA TTTCCAGGGC 240
TCGAG 245

(2) INFORMATION FOR SEQ ID NO:1367:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1367:

GTATTTTGT GACTGAAGTC ACCTTCTAAA TAATTTCTAG AATAAAATTT TTATATTGAA 60
 GAAGTTGGTC TTAACCATTT TTTTTCAGG AGCATGCATT TTGAAATCAT TCTGTGGGAA 120
 GATGAAAACA AATTTAGTTC TATGTCCTCC CTTTTAGAG ATGTTGACAC TTCCTTAAA 180
 TGTACCATGC ATGATTTGTC TACCACCCAG ACTCGAG 217

(2) INFORMATION FOR SEQ ID NO:1368:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1368:

GGCTAGAAGC AAGATGGCTG AACTCAATAC TCATGTGAAT GTCAAGGAAA AGATCTATGC 60
 AGTTAGATCA GTTGTTCCCA ACAAAAGCAA TAATGAAATA GTCCTGGTGC TCCAACAGTT 120
 TGATTTTAAT GTGGATAAAG CCGTGCAAGC CTTTGTGGAT GGCAGTGCAA TTCAAGTTCT 180
 AAAAGAATGG AATATGACAG GAAAAAGAA GAACAATAAA AGAAAAAGAA GCAAGTCCAA 240
 GCAGCATCAA GGCAACAAAG ATGCTAAAGA CAAGGTAGGG AGTCTCGAG 289

(2) INFORMATION FOR SEQ ID NO:1369:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1369:

GCGATTGAAT TCTAGACCTG CCTCGAGTGT TTTTTTAAAA CTCTCTCTCT TCACTGACAC 60
 CAGGTGTTGC TATTAATGTG CTCAATCTC TCACTTATAA AAAAGAATAA AACCTCTCTC 120
 TTTTCTAGTT ACTGGTCTGT TTATTCTTTT GTAGAATGAT CTTTGGGAAG AGTGTTTTCA 180
 TTTATCCAG TCTCTTCATC TTTATTCTCT TAGTGCACTG TCATCTCGAG 230

(2) INFORMATION FOR SEQ ID NO:1370:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1370:

GAATTCGGCC TTCATGGCCT AAACAAACAA AAAGAAGAAA ACACTCAACA AAACCAATCT	60
ACATGTTTGG GACTAAAAAA AAAAATAGAG GTTGTATTCT CAGTGTCCGA CTCGGAATTA	120
TGTTGCTGCC TCTCTGTGCT TTTGGCCTCT GTGTGGCCGT GTTTTGCCAG CATGAGATAC	180
TGTCCCCTCT GGAGGATTTT AGGGGAGGAA GAGCCACGTC CCCAGGGATT GGAGGAGGCT	240
CCGGCACCCCT CGAG	254

(2) INFORMATION FOR SEQ ID NO:1371:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1371:

GAATTCAGCT ACACTTGAGT ATTAGGAAGC CATATAGAAT TCGCAGGGTC CAACTTCATA	60
GACTCTATTC ACATTATTAG AGTAGTAGTG GGGACCGTTA CTTTGGGAA AGGATCAGTG	120
AGACAGTATA AACTTTTGAA ATAATACATT TTTGTATTCC AGAATTATTA GATAATACTA	180
AAGCAAACCT TTTTAATGGA ACATTTTGAA GTCCTGTGTA TTTATTTTAA TTTTATTATT	240
TTTGTGAGA CAGAGTTGCA CTCACGCACG CTCGAG	276

(2) INFORMATION FOR SEQ ID NO:1372:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1372:

GAATTCGGCC TTCATGGCCT ACTCGAATCA TAGTGATTAA AATAGTTGGG GTAAAGTTGT	60
AGCTTATATG CAATACTACT TGGAGGAATT CTTCTACTAA TTTGTATTTA ATGTGGAAT	120
TGTATAGTTT CATTGATTTA ATCATAAATA ATGGAAATGG TCTCCAAGAA GTTTTATTTT	180
TCATTTTTTT GCTTATACAC TCTGATTCCT ATAATACAGT GCTATAAGCT ATGCACAGAA	240
AATCTCGAG	249

(2) INFORMATION FOR SEQ ID NO:1373:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1373:

CCCGTTGTCA ATCTTTGGGT TTTATTCCTT TTTAAGAAAG AAAGAAGTTC TGCTGAATTT	60
GGAAATAAAT TCTTTATTTA AACTTTCCTT CCCAGTTTTA TAGTTTCTGG TTCTGAGGAC	120
TGATGAAAAT CATCTTCCAT CAGCAGATTT TCTTGCACTG TTTGCTGTGC CCCTCAAATA	180
TAATGTCTTG GGTTTTAAGA TCGAGCAGAG AGCTCGAG	218

(2) INFORMATION FOR SEQ ID NO:1374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1374:

GAATTCGGCC TTCATGGCTT GGGTCTCTCT TTCCCATTTT TGCTTCTTGT TCTCCAGAT	60
CTTCCCCAAA ATAAGCTCAG TGCCGAGAAC TTGTGTGGCT TTGGGATATT CCACTGCCCG	120
GGCAACAGGC AATCTCGAG	139

(2) INFORMATION FOR SEQ ID NO:1375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1375:

GAATTCGGCC TTCATGGCCT AGCAAGACGC AGCAAAAGTG GAACTTCCAA GATACTAATC	60
TGAGAAGTTT TCAACAAGAA ACAGGTTTAG AATTAAAAAT CAAAACCTCT TTTAATTGTA	120
TTAAGAGTAA ATCATATTTT AAGACAACCT TCTTTTAAAA CAAGGGACCA AAATTTAGAA	180
AGACTTTTAT AAATAATTTT AATTATAGCC AACTTAATCC CACACAAAAT GCTTTTCATA	240
AGTATTCTCT CACAAACACT CGAG	264

(2) INFORMATION FOR SEQ ID NO:1376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1376:

CTTAAACCCA GGAGTTAGAG ACCAGACTGG ACAATATAGC GAGACCTCAT TTCTAACCCC	60
CAAAAAAATA TACACACGCA CACACACACA CACAAACACA CACACACACA CAGCATGCA	120
AACTATATTA AAAAAACGGT CATGCTGCAT GGTTTTTTAT TTGTGTTATT TTTATTGTTG	180
TAATGTTACT TTATTTTCTA ATATTTTCTG TTTGCGGTTG GTTGAATCCT CAGCTGTGGA	240
ACAGCTCGAG	250

(2) INFORMATION FOR SEQ ID NO:1377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1377:

```

GAATTCGGCC TTCATGGCCT AATTCCCCT TCTCTTTTT TTTGGTTTT GGTTAATTTG      60
TAATTTTGGT TTCGTCCTGA TGTATATGGA CTGCCAGAAT AGGGGGGGTG GTGGTTTGT      120
CGTGGTGTCT GGGGGAGGAA GGAATCCTTA CCCTGGCTTC CTTAATCGGG GAAGGCTTCC      180
TGAAGGAGGT GGGCTCAGAG GTGAGTTGTG AATGAAGCGG GTAGGGAGTG GGCTGGGTGG      240
ATGTTTGGG GATGTTGGG GGAGGTGAGT AAAGGTAAC TCGAG                          285

```

(2) INFORMATION FOR SEQ ID NO:1378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1378:

```

GAATTCGGCC TTCATGGCCT AGAAAGAGCA AATATAATGA AGACTTTGAA AGAGCTTGGA      60
GAGAAGATCT CACAATTAAG AGATGAATTA AAAACATCTT CTGCAGTCTC CACACCATCT      120
AAAGTGAAGA CAAAAACGGA GGCCAGAGAG GAGTTATTAG ATACTGAACT GGACCTCCAC      180
AAGAGGCTGT CCTCAGGAGA AGACACCACA GAATTACGGA AAAAAGCTCAG TCAGTTACAG      240
GTTGAGGCTG CACGGTTAGG TATTTTACCT GTGGGTCGAG GAAAGACCAT GTCCTCTCAA      300
GGTCGAGGAA GAGGCCGAGG GCGTGGAGGA AGAGGAAGGG GCTCACTAAA TCACATGGTG      360
GTGGACCATC GTCCCAAAT CGAG                          384

```

(2) INFORMATION FOR SEQ ID NO:1379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1379:

```

GAATTCGGCC TTCATGGCCT AGTCAGGAAC TCCAGTTTGC TTTTCTGTTT TGTGTCCTGG      60
TAGCAGCTGT TGAGTAACCT TCATTGGAGG TTGGGAAGGA AGTGAGGAGA AAGTGTCTTT      120
GTTTAGTGTT TTATTTCCTA TAATAGGATG CTGCCTAACC CAGTTCATCT CTATGTCCTG      180
TTCCTGAAT ATTCCGGGTA ATTGAAAGAA AATATAATGG ATGGGCTCCA TTAAAACCGAG      240
CTCAAAAATA AATTCTTGTC AGTAAAGATT TCTTGTCAGG ATGTCTTGGA TTGCACTTTT      300
GTTGAGGAAA GACAGTGTA ATAGTTAAAG AATGTTGATA AAATTGAAAC ATTTGGGCCT      360
TCATGGCCTA                                         370

```

(2) INFORMATION FOR SEQ ID NO:1380:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1380:

```
GAATTCTAGA CCTGCCTCGA GTTGCTGAAC GGTTTAGATC CTCAAAAAAT AAAGCAATTG      60
AACCTGGCCA TGATTAACTA TGTNTTGGTC GTCTATGGAC TTGCCATTTTCTCTCTTGGA      120
ATAGGACAGC CTGAGGAATT ATCTGAAGCC GAAAACCACT TTAAGAGGAT TATTGAACAC      180
TACCCAGTG AGGGCCTTGA TTGCTTGGCC TACTGTGGAA TTGGAAAAGT ATATTGAAA      240
AAAAACAGAT TTCTAGAAGC TCTCAATCAC TTNGAGAAAG CAAGAACCTT GATTATCGT      300
CTTCCTGGAG TGTAACTTG GCCCAGAGT AATGTGATTA TTGAAGAGTC TCAGCCACCC      366
CTCGAG
```

(2) INFORMATION FOR SEQ ID NO:1381:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1381:

```
GAATTCGGCC TTCATGGCCT ACTTTAATGA GATAGGAACT AGTATATTCA CCGTCTATGA      60
GGCCGCCTCA CAGGAAGGCT GGGTGTTCCT CATGTACAGA GCAATTGACA GCTTTCCCCG      120
TTGGCGTTCC TACTTCTATT TCATCACTCT CATTTTCTTC CTCGCCTGGC TTGTGAAGAA      180
CGTGTTTATT GCTGTTATCA TTGAAACATT TGCAGAAATC AGAGTACAGT TTCAACAAAT      240
GTGGGGATCG AGAAGCAGCA CTACCTCAAC AGCCACCACC CAGATGTTTC ATGAAGATGC      300
TGCTGGAGGT TGGCAGCTGG TAGCTGTGGA TGTCAACAAG CCCCAGGGAC GCGCCCCAGC      360
CTGCCTCCAG AAAATGATGC GGTCAATCCG TTTCCACATG TTCATCCTGA GCATGGTGAC      420
CGTGGACGTG ATCGTGGCGG CTAGCAACTA CTACAAAGAA GAAAACCTCG AG      472
```

(2) INFORMATION FOR SEQ ID NO:1382:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1382:

```
GAATTCGGCC TTCATGGCCT AGAGTTTAAC CCAGAACTGG TGCTGGTCTC AGCTGGCTTT      60
GATGCTGCAC GGGGGGATCC GCTGGGGGGC TGCCAGGTGT CACCTGAGGG TTATGCCAC      120
CTCACCCACC TGCTGATGGG CTTGCCAGT GGGCCGATTA TCCTTATCCT AGAGGGTGCC      180
TATAACCTGA CATCCATCTC AGAGTCCATG GCTGCCTGCA CTCGCTCCCT CCTTGGAGAC      240
CCACCACCCC TGCTGACCCT GCCACGGCCC CCACTATCAG GGGCCCTGGC CTCATCACT      300
GAGACCATCC AAGTCCATCG CAGATACTGG CGCAGCTTAC GGGTCATGAA GGTAGAAGAC      360
AGAGAAGGAC CCTCCAGTTC TAAGTTGGTC ACCAAGAAGG CACCCCAACC ACCCAAACCT      420
CGAG
```

(2) INFORMATION FOR SEQ ID NO:1383:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 494 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1383:

```

GAATTCGGCC TTCATGGCCT AGGCAGCGGC CTCTGTCCCA GGCCCGGGG TGCCAGCGTC      60
CTGCGAGCAC CCAGCTGACC AAAGATGTTT CCCTCTGTAG AAGACTCTGC TAGACTGGGT      120
CTGAAGCTTG AGTTTTCTAA CAGGTGCTGC TGCACAGGTG GAAAGGAGCC GTGGGAATGT      180
GTGTGTGGCA CGGCCAGAC AAGGGCAGGG CTGAGGGCCT CCGACTCAGC TGGGGGTAGA      240
CGGGCTCGAA TGTGGCCTGG GAGAGCCTAG GGGGCCCCAG GGGTCTGCTT TTCTATGTGA      300
GCCTTTAAAC TTCAGACAGG CCACCACCTT GCACCTGCAG GGGCTTTGGC ACAGGAGTGC      360
TGGCTTTGGA GGGACTGTGG CCTTCATCGT GGTCTCTGCG CCACACCTCC ACGCACACAG      420
ACAGTGCCTT AGGAGGGAAA CAGAACTAAT TACGAGGGGG AGGCAAGAGG ACGCCAAGCA      480
AGGAGTGACT CGAG

```

(2) INFORMATION FOR SEQ ID NO:1384:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 460 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1384:

```

GCTCGAGAGT GGGGCGTGGC AGTGTGTGCC TGTAGTCCCA GCCACCTGGG AGGCTGAGGC      60
AGAAAAATTG CCTGAACCCG GGGGTCGCAG GTTACAGAGA GAGACTCTGT CTCCCCAAAA      120
AAAAAAAAAA AAAAAAAAAA NNGTCTAAGG GTTANACAAT TCTTGATATA ATCTCTCCAC      180
AATACATTCA GAAATCTACT TTTGCTGTTG GAGTTGTATC TGAGAGCTGG GGAATTTAAA      240
ATTGCTGAAA ACAGATATAA GGGGAAAGTG AGATAAAAGC AGAAGCTGCC AAAAGGAGGT      300
ATTAGCATCA TCCTCAATTT ACACAGAATC ACATGCTAAG AGAGGCTAAG TATCTTTCCC      360
AAGATTACTC AGCCAAGTTG TGAAGCCAAG ATTAACTGT ATCTATTCAA CTCTTATCTA      420
ATTATAAAAG CCTATGTTAT TTCCCACTGT GCTACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:1385:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1385:

```

GCAGGAGTAT CTGAGGATGG AGAACTCAGC ATAGAAAACC CCTTGTTGTA AACATTTGGA      60
AAAATACAAG AAAGTGAAAA AACTCTTATG ATGAACACAT TATATAAGCT TCATGATCGA      120
TTGGCACAGC TTGCAGGAGA TCATGAATGT GGCAGTTCTA GTCAAAGAAC GCTTTCTGTT      180
CAAGAGGCAG CTGCGTATTT AAAAGATTTA GGTCTGTAAT ATGAAGGTAT ATTAACTT      240

```

TCATTGCAGT GGATCTTAGA AAATGGAAAA GATGTTGGAA TAAGGTGTGT TGGTTTGGC	300
CCTGAGGAAG AATTGACAAA TATACTGAT GTGCAGTTTT TACAGTCCAC AAGACCACTG	360
ATGTCTTTTT GGTGTCGTTT TCGACGTGCT TTTGTACTG TAACTCACAG ATTATGTTG	420
TTATGCTTAG GTGTAGTGAT GGTTTGTGTC GTTCTGCGTT ACATGAAATA TCGATGGACA	480
AAAGAAGGGG AGGATCTCGA G	501

(2) INFORMATION FOR SEQ ID NO:1386:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1386:

GAATTCGGCC TTCATGGCCT ACTCCAAGAG GCAGTTCTAC ATCAAGATCT CAGACGTGCA	60
GGTGTTTGGG TATAGCCTGA GGTTCACGC CGACCTCCTG CGCAGTGCGAG TGCAGCAGGT	120
CAACCACTCC TACACACAGG GCGGCCAGTT CTATTCCTCT TCGTCAGTGA TGCTCCTCTT	180
GTTGGATATT CCGGACCGAA TTAATCGCCT GGGCCCTCCT GTGGCCCCGG GGAACCCCA	240
GCTGGACTTG TTCTCCTGTA TGCTGAAACA CCGCTGAAA CTGACCAACA GCGAGATCAT	300
CAGGGTGAAC CACGCCTTGG ACCTGTACAA CACGGAGATC CTCAAACAGT CGGACCAGAT	360
GACAGCCAAC ACTCGAG	377

(2) INFORMATION FOR SEQ ID NO:1387:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 538 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1387:

GAATTCGGCC TTCATGGCCT AGACGACGCC TATGAAGCCC TTAGTCCTTC TAGTTGCGCT	60
TTTGCTATGG CCTTCGTCTG TGCCGGCTTA TCGACATCA AAGGGATCAA AATTTAAGGA	120
GCTAGTTACA CATGGAGACG CTTCACCTGA GAATGATGTT TTAACCAATC CTATCAGTGA	180
AGAACTACA ACTTCCCTA CAGGAGGCTT CACACCGGAA ATAGGAAAGA AAAAACACAC	240
GGAAAGTACC CCATTCTGGT CGATCAAACC AAACAATGTT TCCATTGTTT TGCATGCAGA	300
GGAACCTTAT ATTGAAAATG AAGAGCCAGA GCCAGAGCCG GAGCCAGCTG CAAAACAAAC	360
TGAGGCACCA AGAATGTTGC CAGTTGTTAC TGAATCATCT ACAAGTCCAT ATGTTACCTC	420
ATACAAGTCA CCTGTCACCA CTTAGATAA GAGCACTGGC ATTGAGATCT CTACAGAATC	480
AGAAGATGTT CCTCAGCTCT CAGGTGAAAC TGCGATAGAA AAACCCGAAG CACTCGAG	538

(2) INFORMATION FOR SEQ ID NO:1388:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1388:

GAATTCGGCC	TTCATGGCCT	ACCTATTTTC	CATATTCCGT	GTGACTCATA	ATGTACTCCT	60
GCTGTGTCTG	ACGGGCAGTG	GTCGGTCAGA	GCAGAAGCTC	AGCTGTGATT	GCTGGGGGAG	120
TTCTGAGCTC	CATGAGCCAC	TCTGGCCACG	ACACCATCTT	TACTTGAAAG	AAAAACTTCC	180
CTTTGATGCT	GAGGCCTCCA	GTGTCATAGA	CGATGCCTTT	GCCCACCCAG	GCGATGGTCT	240
GCGTGGCTCC	ATCTGGGGTG	TGGCTGAGGA	CGGCCAGGGC	TGGGGGATGC	AGGGCGGCTT	300
TGCCAACCCC	ATAGATTCTT	CCAAATCCTC	TCGTCTTCAG	TTCTCATCC	CGGATGATGG	360
TTGGGATGAT	CCCCAGCTCC	TTTCCAACCT	TGTTAATCTC	CTCGAG		406

(2) INFORMATION FOR SEQ ID NO:1389:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1389:

GAATTCGGCC	TTCATGGCCT	AAATTAATC	TAATGGGCAA	TCATAAGAAT	AATTGAAAAT	60
AAGGAATTCA	GGGGAGCTTA	ATTCATTTGT	AGGTTTTAGG	TGATACCATT	GCTATTCAGA	120
TTGCTTTGGG	CAATTTATGT	AATTTTTTCC	AATGACATCC	AATTTCATAT	CACTGTAATC	180
GAAGAAACAG	AAAATTTAGT	TCAGATTTTA	AATCATCATT	CCCTGATGCC	ACCTCATCCA	240
ATGATGTTTC	ATAAACGATG	AAATCACGTA	AGAACCACCT	AAACCAGGAC	TGATAGCTA	300
TTGCTAGAAA	CTTGGAATAA	TTTCCACTGA	TTTCTGTTTT	CACTGGAAAC	AGAACAGAGA	360
CTCCTCGAG						369

(2) INFORMATION FOR SEQ ID NO:1390:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 548 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1390:

GAATTCGGCC	TTCATGGCCT	AAGACCAAAA	CTAAACTGAA	ATTTAAAATG	TTCTTCGGGG	60
GAGAAGGGAG	CTTGACTTAC	ACTTTGGTAA	TAATTTGCTT	CCTGACACTA	AGGCTGTCTG	120
CTAGTCAGAA	TGCGCTCAAA	AAGAGTCTAG	AAGATGTTGT	CATTGACATC	CAGTCATCTC	180
TTTCTAAGGG	AATCAGAGGC	AATGAGCCCG	TATATACTTC	AACTCAAGAA	GACTGCATTA	240
ATTCTTGCTG	TTCAACAAAA	AACATATCAG	GGACAAAGCA	TGTAACCTGA	TGATCTTCGA	300
CACTCGAAAA	ACAGCTAGAC	AACCCAACTG	CTACCTATTT	TTCTGTCCCC	AACGAGGAAG	360
CCTGTCCATT	GAAACCAGCA	AAAGGACTTA	TGAGTTACAG	GATAATTACA	GATTTTCCAT	420
CTTTGACCAG	AAATTTGCCA	AGCCAAGAGT	TACCCAGGA	AGATTCTCTC	TTACATGGCC	480
AATTTTCACA	AGCAGTCACT	CCCCTAGCCC	ATCATCACAC	AGATTATTCA	AAGCCCACCG	540
AGCTCGAG						548

(2) INFORMATION FOR SEQ ID NO:1391:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 178 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1391:

GTTTATTTTC ATCATCTACA GAACCAAACCT CCCTTTCATG TGCACGAGTG AGAATCTCTT	60
TGTACAGTGT TTCTGCTTGC TTGAACTTTC CTTGTTTCAA ATAGCAGGAT GCCAGGTTAT	120
TTTTCGTCTT AGCCAAGTTG GGGTCATCAG GTCCCAGTTT TGTCTGGTAG ATCTCGAG	178

(2) INFORMATION FOR SEQ ID NO:1392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1392:

GAATTCGGCC AAAGAGGCCT AGGGCCCTAT ACCTCCAGCC GTGAATGCCA GACTTTAAGA	60
TTGCCCGGAG GAAGCAAACCT CTTGATATAA AAAAAGCAGG CCATCTGCTT AACCCCTGGC	120
TCCACCATAA GGCACTGGGA CTCGGATTTC TCTATCTGAT AGAGGTATTT TCTGTGGCCC	180
TGGGAGCTGT CTGTCTTTCC CCTACCCCCA AGGATGCCAG GAAGACGTC ACCATTAGCC	240
ATGTGGCAAC CTTTACTTCT ATGCCTCACA AGTGCCCTTC AGAGAGCCCC AATTCTGCTT	300
TCCCACAAA TAAACCCAAT GCACTCGAG	329

(2) INFORMATION FOR SEQ ID NO:1393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1393:

GAATTCGGCC AAAGAGGCCT ATTCCTTTCC TTTTCCCTTT GAGATTTTTT TGTGTGTGTT	60
TCCTTTTGT ATTTTACTGA TATCACCAGG ATAGTTTACT CTCCTTCTAG CTTTCTGCTT	120
ACCGCACACT GGATAACACA CACATACACA CCCACAAAAA TGCTCATGAA CCCAATCCGG	180
AGAAGGTTCC AGCAGGTCCC CCACCCTCCC CTCCTCCTCC TACTTCTCCT CTTGACAGCG	240
AGGACAGGAG GGGGACAAGG GGACACCTGG GCAGACCCGC CGGNTCTCCC CCCACCCAC	300
CCCGCCCTC GCATCATACT CGAG	324

(2) INFORMATION FOR SEQ ID NO:1394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1394:

GAATTCGGCC AAAGAGGCCT AACTGCAACG GAGAGACTCA AGATGATTCT CTTTTTACCC	60
ATGTTTTCTC TACTATTGCT GCTTATTGTT AACCTATAA ACGCCAACAA TCATTATGAC	120

AAGATCTTGG CTCATAGTCG TATCAGGGGT CGGGACCAAG GCCCAAATGT CTGTGCCCTT	180
CAACAGATTT TGGGCACCAA AAAGAAATAC TTCAGCACTT GTAAGAACTG GTATAAAAAG	240
TCCATCTGTG GACAGAAAC GACTGTGTTA TATGAATGTT GCCCTGGTTA TATGAGAATG	300
GAAGGAATGA AAGGCTGCCC AGCAGTTTGG CCCATTGACC ATGTTTATGG CACTCTGGGC	360
ATCGTGGGAG CCACCACAAC GCAGCGCTAT TCTGACGCCT CAAAACAGAG GGAGGAGATC	420
GAGGGAAGG GATCCTTCAC TTACTTTGCA CCGAGGCTCG AG	462

(2) INFORMATION FOR SEQ ID NO:1395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1395:

GAATTCGGCC AAAGAGGCCT AGAACTGCCA TCATGAGGTC TGACAAGTCA GCTTTGGTAT	60
TTCTGCTCCT GCAGCTCTTC TGTGTTGGCT GTGGATTCTG TGGGAAAGTC CTGGTGTGGC	120
CCTGTGACAT GAGCCATTGG CTTAATGTCA AGGTCATTCT AGAAGAGCTC ATAGTGAGAG	180
GCCATGAGGT AACAGTATTG ACTCACTCAA AGCCTTCGTT AATTGACTAC AGGAAGCCTT	240
CTGCATTGAA ATTTGAGGTG GTCCATATGC CACAGGACAG AACAGAAGAA AATGAAATAT	300
TTGTTGACCT AGCTCTGAAT GTCTTGCCAG GCTTATCAAC CTGGCAATCA GTTATAAAAT	360
TAAATGATTT TTTTGTGAA ATAAGAGGAA CTTTAAAAAT GATGTGTGAG AGCTTTATCT	420
ACAATCAGAC GCTTATGAAG AAGCTACAGG AAACCAACTA CGATGTAATG CTTATAGACC	480
CTGTGATTCC CTGTGAGAC CTGATAGCTC TCGAG	515

(2) INFORMATION FOR SEQ ID NO:1396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1396:

GAATTCGGCC AAAGAGGCCT AGTCCTTCAC TAGACTATAT GCATTTTATC TTACCTTATT	60
CCTCATTTTA GTGTCCAGTG GCTGGCGTGT ATAAACCCCTG AATGTTTTTA AAGATAATAT	120
TTTAAAAGAT CACTTTAGTT ATAATACGGC TTCAGTTGGT GGAATAAAGA AATTTTTTTC	180
TTTTTTTTTA TTTTGAGTAA AAATGATAAC TTCTCTCCAC CCTCTCTATA GTTAAAGCCT	240
TCCATCTGAA GTATGATGAA GTTCGTCTGG ATCCAAATGT TCAGAAATGG GATGTNACAG	300
TATTAGAACT CAGCTATCAC AAACGTCATT TGGATAGACC AGTGTCTTCTA CGGTTTTGGG	360
AAACATTGGA CAGGTACATG GTAAAGCATA AATCGCACAT CTCGAG	406

(2) INFORMATION FOR SEQ ID NO:1397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1397:

```

GAATTCGGCC AAAGGGGCCT AAGAATAGCA AATATCTTGT GCTTAGCAAA AAATAATCTT      60
GAAAAATTTT TCTGAAATAA ATGTTATTGA AAAATGCAAA TAATTAGAAT TAAATACCAG      120
CTGCAGTTCT ACATCCTCTT ATTGGCCAAT GTAAAGAGAA ATCAGGCATG TTAACCTCAA      180
AAAAGGACAA TTCAACAACA TGGAAACCAT GACTAATATA TGGAGAATAC AAAGAAAGAC      240
TAAAGATTTA GATCAGGCTA ATTTCTTTT ATTCCCATCA AATCCAAGTA CCACTCGAG      299

```

(2) INFORMATION FOR SEQ ID NO:1398:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:

```

GAATTCGGAC AAAGAGGCCT AGGAGAGGCG GGAGCCTGGG AGAGCCTCTG CTAGACCTTT      60
CCTGGCACTT CCCCAGGAAA GGCAAGGCAG GGCAGATGTG CGGCTGGCCA GCTGGAGTGA      120
TTTCCATGGG CTCCAAGCTG TAGGAGTGGT CCCTGGCTGC CAGAGTGCTC TGGCCAGATA      180
CAGGTGGGCT CTGGACTGGT GAGGCTGCAT TCGGAGGCG CGCACACCCA GCTGGGCCCT      240
TATCTGTAAG GACTGGCTGG CCTGGGAGGG GCAGTCTCCC ANCCAGAANG TGGAATTTT      300
TTTTTTTTT TGAGATATCA AAACATCCTA AGGTACAGGA AAGAAATTGT CNACACACAC      360
GGCTCGAG                                     368

```

(2) INFORMATION FOR SEQ ID NO:1399:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 149 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

```

GAATTCGGCC AAAGAGGCCT ATTTTITGG AGATGTTGAT CAGATGTTCA CTGATAAACT      60
TGAGCCCCCT TTTCTTCCTC TGGTCTACCC ATCTAGAATG CTATGACCCA TCTCAGACAC      120
ACCCCTCTGG GAAGCTGCCT GAGCTCGAG                                     149

```

(2) INFORMATION FOR SEQ ID NO:1400:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 599 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

```

GAATTCGGCC AAAGAGGCCT AGTCGATGGA GATAAGTGT TTAATTACTT TTTTAATGTC      60
TGTCCTTTTG TATTTTCTC CTCTTTTCC TTTTATTTCC TGCTGTNGAG ATTACTGCCT      120
CATCTCCACA GCAGGTGGCT GTTGCAAATT TGTTTCTTT GTAAGCCTGG AAGATTTATT      180
TTGTAATATA ACTGTTCTT TTTAGTATTT TATTATTAAT GATTCTTTA CTTTGGGATA      240

```

TAGTGTA	CTT	ACACAGT	CCT	AAACAGT	AAAT	TTCCTA	ACAC	TATCTA	AGAA	CTCCA	ATCAT	300
TAAGAAAA	AAAT	CTTTG	CC	TGAGG	CGT	AT	TGTTG	AGAT	TTTTG	CTT	ACTTCA	360
CAATGCGGG	ATTAAAA	TTT	AAGGAA	ATTG	TTTTAT	AGCA	AAAGC	CAAAT	GAGAAAA	AGA		420
AAACAGAGAA	ATAGAAG	GGA	GGGAA	ATAAA	GAAAAG	GAGA	AGAGAAA	AGG	CTCAAG	AGAC		480
AAAGTATACT	TTAATAA	ATA	ATACCAT	AAA	GCAGAG	TAAAT	GAGGATA	AAAT	TTATGG	CTGA		540
AAATATGAAAT	TACATTA	ACA	TCTTTT	CTAG	AAATG	TTTCA	ACTAA	ACCAA	ATGCT	CGAG		599

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

GAATTCGGCC	AAAGAGGCCT	ACAGTCACCC	TATAAAATAG	ATTAAGTGTT	CCGAGTTCGG	60
TTGGGTTTTC	CGCAATTAAA	AATTGTGTTA	ACAGTTTAGT	GTTTCTTACA	GATAACACTG	120
ATAACACTTT	TTTGTTTTCA	TTGGGTCTTA	TCATTGGTAC	AGACTGATCC	AAAAATCCAA	180
TTGGCTTGCT	AGTAATTTT	TCCTGTGAAT	TGCTAAGATT	TATGGGTAAT	TTAAATTTTC	240
TTTTTCTTTT	CTTTTTTTTT	TTTTTAAGCA	TTTGCTCCTT	AAATGCAAAT	CGTACCACTA	300
AGATCCTCTC	ACAACAGATT	AAGGTGCAAT	TTGCAGAGAC	ACTCGAG		347

(2) INFORMATION FOR SEQ ID NO:1402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

GAATTCGGCC	AAAGAGGCCT	ATATAA	ACTC	AACTTT	TCTT	TGTCT	CTCTT	GCCTG	TGATG	60
AGTAACAGAA	ACCATCTTCC	CAGAA	ACTAT	CCCCA	CCCCAC	CCCCA	GCCCCA	GCCCCA	GAGCAG	120
CCCAGACCCA	GGAAGGAGGT	CAGAG	CCTGC	GTGACT	TGTGT	GGCA	AGGATC	CCCC	TCAAAG	180
CAGGCAGTGA	TCCCCCTCAA	AGCAG	GCAGT	GATGA	CCAGG	CTCCC	CAGGG	GAAGG	AAAAA	240
TGGTTGATTA	CCCCACCTCA	CTTCT	CAAG	TTCTG	AAAG	CCTCC	CATCT	TTTC	CAGGATG	300
TTTTCTTCT	GCTTCCTTTC	TGGGG	TGATA	TTGCA	ATGCA	TGTGT	CAGTC	CCTCG		357

(2) INFORMATION FOR SEQ ID NO:1403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

GAATTCGGCC	AAAGAGGCCT	AAGGATT	GTGTC	ATAGCC	CAGGA	CCACACT	ATT	GCTTTT	TCAT	60
AACATTTTCT	TTTTGTTTCT	TTCTTTT	TGAA	TTTCTT	ACAG	GGCTG	CAAAG	TATGC	CAGGG	120

GAGTATGTAG CCCGGGGTGG TCCAATGGGT GTGAGTATGG GACAGCCAAG TTATACCCAA	180
CCCCAGATGC CCCCCCATCC TGCTCAGCTG CGTCATGGGC CCCCCATGCA TACGTACATT	240
CCTGGACACC CTCACCACCC AACTCTCGAG	270

(2) INFORMATION FOR SEQ ID NO:1404:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 129 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

GAATTCGGCC AAAGAGGCCT ACAGCCTTTC TTCCCACTTT TAACTATAGA ACTTGCTTTT	60
AATTTCAGTG ATATATGGAC ACAGTCAGAC GAGAACTCCT TCATGCTCCT ATTACCACAG	120
CTACTCGAG	129

(2) INFORMATION FOR SEQ ID NO:1405:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 229 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

GAATTCGGCC AAAGAGGCCT AATTGCTTAA GCTCCTCAAG TTCTTTTAT TAAGAGTTGT	60
AAGTAAATTT TAATAAACAA TAACATAGTC TCTGCTATTT TGATCCTTGC TCTTTGCCAT	120
GCTGTTTTAC TTATTCTTTA TTGCATGTTT CACATCTATC AATTTTGGGA TATGCTTCTC	180
ACCTTCCCTA CTAAATGTG AGCTCCGTAA ACGCAACAGC TACCTCGAG	229

(2) INFORMATION FOR SEQ ID NO:1406:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 398 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

GAATTCGGCC AAAGAGGCCT AGTGGAGGTA TTTTGAAAAT ACAATTTAAC TACAACAACA	60
TTTGCTTATT TTTAGAGTCT TTTATGACAT CAAGAGAAAT GATCCCAGAA AGAAAAATC	120
AAGAAAAAGA ATCTGATGAT GCCTTAACTG TGAATGAAGA GACTTCTGAG GAAAAATAATC	180
AAATGGAGGA ATCTGATGTG TCTCAAGCTG AGAAAGATTT GCTACATTCT GAAGGTAGTG	240
AAAACGAAGG CCCTGTAAGT AGTAGTTCTT CTGACTGCCG TGAAACAGAA GAATTAGTAG	300
GATCCAATTC CAGTAAACT GGAGAGATTC TTTCAGAATC ATCCATGGAA AATGATGACG	360
AAGCCACAGA AGTCACCGAT GAACCAATGG AACTCGAG	398

(2) INFORMATION FOR SEQ ID NO:1407:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

```
GAATTCGGCC AAAGAGGCCT AGTAAAAGTG TCTGATCTGA AACATAATAC CCTCCCTTTT    60
CAATCCTGAT GTACCTTCTT CTAGTCTTGG TCTTTGGCAC CTTTTTTTCA AGAAGAAACC    120
ATACTCTCGA G                                     131
```

(2) INFORMATION FOR SEQ ID NO:1408:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 622 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

```
GAATTCGGCC AAAGAGGCCT AAGTCCAGGC TGTAGGGTCC CTGGTCACAG AGGACCCGGG    60
TCACCCGGGA CTCATCTTTC ACTTATGTGT TTTCAAGTCC AGGGCCCCAT GGATGCCACT    120
GAGATGATTT CAGATGTTAC AGTCATCAAG AGGGATTGGG GCGCATTTCT GCCTCATTCC    180
TTGGCTTTTG AAATCAGAGA CGACATTTTC ACTTTAAACA AACCCAAACC ATTCTGCTG    240
GTGGAGGATT TCTCCTGCAT CTCGGGGGTG GATTTTCACT GATTTATGTC TGCAGCGTGA    300
GCAGTCTCTG GGCTTTTCTG CAGCTCCAGA TGTTAGATGT TTTATCTCTC CGTCTTTTAT    360
CNGCTTCAGT CCTTGCCCCA GTCTATCCTC GCATGCTCCN TCCTNNGGGA GGGCTTCCTG    420
TCTTCACAGC CGCACCTTCC TCCCCTGCT ACCAGTGCCA TGGACCCACT GTATGTTTCC    480
TGGGGGCCAT GCAGAAGGTC CCCAGACCAG TGCTGGCCTG CGACAAATAA GTACAGAAAT    540
GGAGAATAAC CCCTTTCAA CACATAATAG CATTTGATAG AATCAATCAG GAGACTCAAG    600
TTTTTACTGC GTGCGTCTCG AG                                     622
```

(2) INFORMATION FOR SEQ ID NO:1409:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

```
GAATTCGGCC AAAGAGGCCT AGAACATGCA GATTTTTCCT CTAGAAAACC CCCTCCCCAC    60
ATTGAGCTTA TTAGAAATCC TTAACAGCAG GTAACCACCA ATGCTCCTGC CTTCTAGCCA    120
CAGTCTGCTC CTGCCCTAC AGGCTTTGAA CATGCAGATT TTTCTCTAG AAAACCCCTT    180
CCCTGCATAT TCTCTCTCT CCCCCTCAC ACAAACACCT GGCTGCCCAG GCCCGTGGG    240
GCTGCCGGGC TTCTGTGAAC CTGCCGCTG CCTTGGAGCT TCGGCCTATG CCTCTGCCG    300
CCTTACAGAG CCTGGATCCA AACTCGAG                                     328
```

(2) INFORMATION FOR SEQ ID NO:1410:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

```
GAATTCGGCC AAAGAGGCCT NNAAAAAAAA AAACCAAAAA AAAAGAAAAA GCTGACACAG      60
TTCTCTGAAA AAAGCCTAGA GAACACAAGG GTGACACAAA CTCCAGAGAG TATGCTGCTT      120
GCAGCTTTGA TGATTGTATC AACAGTGGTA AGTCACCCCA TGTCTGCAGG AGCAGCTGCA      180
GCTAATTATA CCTACTGGGC CTATGTGCCT TTCCCACCCT TAATTCGGGC AGTCACATGG      240
ATGGATAATC CTATTGAAGT ATATGTTAAT AATAGTGCAT GGGTACCTGG CCCCATAGAG      300
GATCGTTGCC CAGCCCACT CGAG                                     324
```

(2) INFORMATION FOR SEQ ID NO:1411:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

```
GAATTCGGCC AAAGAGGCCT AGAAGTTGAG TGAAGGAGAA AGAGAGGGAA GTAGAAAAGA      60
GGAGAAAAAT GTTAAGCAAA AAAGGTATTT TCCCTTGGAT ATTAAGTTGC ATATCTGAAG      120
AAATGGCATT CCGGACAATT TCGTGTGGT TGGAGTATT TATTTGTTCT ATCTGTGTGA      180
AAGGATCTTC CCAGCCCCAA GCAAGAGTTT ATTTAACATT TGATGAACTT CGAGAAACCA      240
AGACCTCTGA ATACTTCAGC CTTCCACC ATCCTTTAGA CTACAGGATT TTATTAATGG      300
ATGAAGATCA GGAACAACCTC GAG                                     323
```

(2) INFORMATION FOR SEQ ID NO:1412:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

```
GAATTCGGCC AAAGAGGCCT AGTTAGTTGC TCTCCTTTTT TCTTTTTTTT GTCGTGCATA      60
TTTTATTCTG GTAGTTTCTG GTTAGCTACC CTAAAGTGAT TAAAAAATTT AGAATGCTTT      120
GTGTTTCCTA TTTGGTAATC AACTCGAG                                     149
```

(2) INFORMATION FOR SEQ ID NO:1413:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

GAATTCGGCC AAAGAGGCCT AATAAGAATT ACTTGTAAC TTAGGGGGCA TTTAGAATTA	60
TATTGTCTT ATTTGAGATT TGGATTTAAA TTTTATTTTA GAGCATTTT TAAAAAATAA	120
ATAGAAGTGA GGCTAATATT GTTAATTATT CTCTTTAAAA AATACAGTAT TTGCTTTGGG	180
TTAAATTTT CTGCCCCAAC ATCATTATCA AGAGTCAGCA TATTACAATG ATAAATTTAG	240
CATTACTGT GTGGCAGGCA TTGTTCTATA TACTTTATTC GTTAAATTCA CCAGCGAACA	300
CGCTCGAG	308

(2) INFORMATION FOR SEQ ID NO:1414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

GAATTCGGCC AAAGAGGCCT ACTCAGAGCT GTTACGACTA GTCAGAGAGA GCGAGGTGGC	60
TGGTTCATGT TTGCAGATAG AGACCTCACT GTGTGGTGGA CTTCCCCACT TCCTGCTGCC	120
TTCATCCTGA TGGGTGGCTG CCTTCATCCT GATGGGTGGC AGCCTTGCCC TGCAGTGGGA	180
GACCCAGGTA ATGTAGTTTT TTGTTTGTGA TCCCTGATCT CTTCTTGCG TTTTGGCGG	240
GCAGGTCTCG AG	252

(2) INFORMATION FOR SEQ ID NO:1415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

GAATTCGGCC AAAGAGGCCT AGTGATTCAG AACCATTGTA TAATAGCTTG AAAGCCTAGA	60
TNGACTCTCT GCATTGCCAC CCCTCCCTAT TCTCTTAAGC CCACTCCATT CACGCTGTCA	120
TCCACACCAC TCGGCCACCA ATTTCACT GCCAAATCCA GTTCCCAGTT CCTCATCGTG	180
TTTATNGCA ACATTGAAA CAAGTGATCA ATCCCTTTTC CATGAAAAAC CTTCTTTGCA	240
CAGTTTCCAG AATTCTAAAC TTTCTGGTT TTCCTCCTAC TTCAACTTTC CAATTACCGT	300
CCCTCATTTT TACCTCATCA GCCCAACTCG AG	332

(2) INFORMATION FOR SEQ ID NO:1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

GAATTCGGGC CAAAGAAGCC TACAANAAN TATATATATN TGGATCTTCT GAAAAGTTTT	60
TTGAGGTGCA AGTTTCTCT CTTTTTTTT TTTTTTTTT TTCTCATTGA TTAATGGACA	120
TGATGCTGAG ATTCAATCAC TACATGAAAC ACCTGGCTGT GAAAACAAAA CAACCCAGAG	180
GGCTGTGTTT CAAGCAGCGC TGGGGAAGCT ACGTAACAGT CCGATGCCAG TTTTGAAGA	240
TTCACCATGC GTTCTGACCC TCTGTTGTC TCTTCTCTT CCTCTTCTT CAAGAAGGAA	300
ATTGATCCTA GTGATTTCAG CCCATGCATT AAACAGGAAA CTCGAG	346

(2) INFORMATION FOR SEQ ID NO:1417:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 128 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

GAATTCGCCA AAGAGCCTAA GGGCAAGCAG CATTCATATA TCATATGACT TCTACAATA	60
AAATGAAGCT ATTAGCACTA GTATTTAGTA ATCTAGTAAC TCTCCTTCCA GCCTCTTCA	120
CCCTCGAG	128

(2) INFORMATION FOR SEQ ID NO:1418:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

GAATTCGGCC AAAGAGCCTA GGAAGCGCT CTTACGGCA CTGGGATCCG CATCTGCCTG	60
GGATCATCAA GCCTAGAAG CTGGGTTTCT TTAAATTAGG GCTGCCGTTT TCTGTTTCTC	120
CCTGGGCTGC GGAAAGCCAG AAGATTTTAT CTAGCTTATA CAAGGCTGCT GGTGTTCCCT	180
CTTTTTTCC ACGAGGGTGT TTTGGCTGC AATTGCATGA AATCCCAATG GTGTAGACCA	240
GTGGCGATGG ATCTAGGAGT TTACCAACTG AGACATTTT CAATTTCTTT CTGTCAATCC	300
TTGCTGGGGA CTGAAAACGC TTCTGTGAGA CTTGATAATA GTCCTCTGG TGCAAGTGTG	360
GTAGCTATTG ACAACATCAC TCGAG	385

(2) INFORMATION FOR SEQ ID NO:1419:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1419:

GAATTCGGCC AAAGAGCCCT AGTAGGTTTA TAAACAGAAG TTAAACTTG TAAGCTTAAG	60
CTTCCGTTTA TAAACAGAAG TTAAAATTA TAGGTCCTGT TTAACATTCA GCTCTGTTAA	120
CTCACTCATC TTTTGTGTT TTACACTTT GTCAAGATT CTTACATAT TCATCAATGT	180

CTGAAGAAGT TACTTATGCA GATCTTCAAT TCCAGAACTC CAGTGAGATG GAAAAAATCC	240
CAGAAATTGG CAAATTGGG GAAAAAGCAC CTCCAGCTCC CTCTCATGTA TGGCGTCCAG	300
CAGCCTTGTT TCTGACTCTT CTGTGCCTTC TGTTCCTCAT TGGATTGGGA GTCTTGGCAA	360
GCAATGTTTC TGTAACCTTG AAGATAGAAA TGAAAAAAT GAACAACTA CAAAACATCC	420
TCGAG	425

(2) INFORMATION FOR SEQ ID NO:1420:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1420:

GAATTCGGCC AAAGAGGCCT AAGACGCATG CCTGTAATCC CAGCAACTCG GGAAGCTGAG	60
GCGGGAGAAT CGTTGAACC CGGAGCGGA GGTGCGGTG AGTTGAGATG GCGCCACTGC	120
ACTCCAGCCT TGGCAAAAAG AGCAAACTT CATCTCAAAA AAAAAAAG AATGTGTGGA	180
ATAATGGGGG TTTTTCCTT ACTTTTGTGG CTTATTCTCA CTTACATGGG GATAGCCTTG	240
GTCTTTGACT TGGATAGCCT CGAG	264

(2) INFORMATION FOR SEQ ID NO:1421:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

GAATTCGGCC AAAGAGGCCT AAGTGAATCG ATGTTCTGGC TTGGCTGTCT TTGGTGTITT	60
CATTCTTCA TTCTTTCTC CTTGCTCTCA TCTCTCTC CCCGTGCCCT GCTCCCTACA	120
CCTATCCCTC CCCCTACCCT CGAG	144

(2) INFORMATION FOR SEQ ID NO:1422:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

GAATTCGGCC AAAGAGGCCT AGAGAGAATA AAATACATAT AGTTGATTAA AGGAAGGAAG	60
TTTATTACTT AGGGAAAAGG AAGGTAAAAA AAGACCCTAA GCAATAAAGG CAATTCITTT	120
TTAAGCAGAA TACTTTCATT TTATTTCAAT TTTGTTTACC AGTGTGTGTA CGAAAACCTGC	180
TGCTGGGGCT ACTTCAGCTG AGATGATTTG GCTCTTTTT GTGGCTTTCT TCTTGTCTG	240
TACATCAGCA CTGTGGTTAT TACACCAGCT ACCAAGTCAT CTCGAG	286

(2) INFORMATION FOR SEQ ID NO:1423:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

```
GCGATTGAAT TCTAGACCTG CCTCGAGACA GAGCAAGATT CCGTTCCCAA GAAAAAAAAA 60
TTGTTCAACA ATAAGGGCAA AGGGAGAGAA TCATAACATC TGATTAAACA GAAAAAGCAA 120
GATTTTAACTATA TAAGGATGCA TCTCGAG 157
```

(2) INFORMATION FOR SEQ ID NO:1424:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 408 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

```
GAATTCGGCC AAAGAGGCCT ACTCAAAAGA CAAAAAGAT ACATTAGGCA GTGTTCTGTA 60
AACATGGGAA AATTATTTTA GGTAAATGG GCTGAGAAGA AATTGCTAA ATTTTGCTTT 120
TGTTACCACG TTTCTGAAA TGATGATAAT AAATAATATT TAAAAGGGT GAATAGAAGG 180
ATCTTTATTG TAGGTACTGG TGTTAAATT TAGGTTTCTG AATAACTCTG TAAAGCTACT 240
TTCTTTACAC AGATTAAACAC ATTTATCTTC TTGAATTATT TAATAATGAA TGCAAAAAA 300
TTCGAAATCT CATATAAGAT CTCACTTTGA AACAAAGTAT ATAACTGTT GATTGCACAA 360
TTTGGGTTTT GTGAAGCAGT CAGTTTGTGAC TATAAGTGGC AGCTCGAG 408
```

(2) INFORMATION FOR SEQ ID NO:1425:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

```
GAATTCGGCC AAAGAGGCCT ATTCTTGTCT CCTAAGAATA ACTGTGCTTG AAGAAGAAAA 60
TTCCAACAT GGACAAACCA CGCAAAGAAA ATGAAGAAGA GCCGCAGAGC GCGCCCAAGA 120
COGATGAGGA GAGGCCTCCG GTGGAGCACT CTCCCGAAAA GCAGTCCCCC GAGGAGCAGT 180
CTTCGGAGGA GCAGTCCTCG GAGGGAGGAG TTCTTTCCTG AGGAGCTCTT GCCTGAGCTC 240
CTGCCTGAGA TGCTCCTCTC GGAGGAGCGC CCTCGCAGG AGGGTCTTTC CAGGAAGGAC 300
CTGTTTGAGG GGCGCCCTCC CATGGAGCAG CCTCCTTGTG GAGTAGGAAA ACATAAGCTT 360
GAAGAAGGAA GCTTTAAAGA AAGGTTGGCT CGTCTCGCC CGCAATTTAG AGGGGACATA 420
CATGGCAGAA ATTTAAGCAA TGAGGAGATG ATACAGGCAA CTCTCGAG 468
```

(2) INFORMATION FOR SEQ ID NO:1426:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

TTTGACCAGA TTATTCTTCT ATGCTTTTTT GCAATAAATC AAATCCCACA TATCTACAAG	60
TGGTATGAAG TCCTGCACCC CCCAGGAGGC CTGTCCAGGC ATGTCTTCAG AGGCAGGGTG	120
GGTTACACTC ATTTACCTCC CCTCTCCCCA CCAAATTATG ACACAAACGA GTATGTTTCC	180
TCTCTAGAAC CCTGTAATGC CTCCTCCCC ATCCCCAGAG CTCCTTACTG TAGGTCTTAC	240
CCTGGACAAG GATTTTTC AATTGGAGGC ACAGAACATG AGCAATCTGA CATTCCCACA	300
GGCCTCGAG	309

(2) INFORMATION FOR SEQ ID NO:1427:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

GAATTCGGCC AAAGAGGCCT AAGTGAGGAC AGGGCAAAGA TTTTATAGTC TCCTGTAAAC	60
AGGAAGTGTC CTAGTCTGAC GTAAGTGCTA CGTGTACCT GGATGGCCTC TTTCTTGATC	120
TTACCGGTA CGTGTCTTCC AGCCAGGTA GGTGTCTTCC GGCCGGCTTT CTTCTGCTT	180
CTGCTATTTT GCTGGCCAC ACTGCTGGCG CAAGGCTTGC GCCTTGGTAC TGGGCCTGAG	240
AAGGGAGGAG TTATTCTATCC CCTTAAGCTT TCAGGCCCCA GGGAGAATCT TACACTACTG	300
GGCTGCATT CCAGACAATT AGGGCATTCT AAGGCACAGG ATGAGGTAGG AGGTCCGCAC	360
AAGATACAGG TCATAAGAC CTGTCAGATA AAACAGCTTG CAGTAAATAA GCTGGCCCAA	420
ACCCACGAAA ATCAAGATT TGACCAGAGT GACCCTCTGG TCATCCTCAC TGCTACACTC	480
CCACCAGCAT CACGACTCGA G	501

(2) INFORMATION FOR SEQ ID NO:1428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

GAATTCGGCC AAAGAGGCCT AGACCTTGTT TAGTGTGTGA AAGTTCTTCC AGTCTCGGAA	60
TGGTAAGGAA TTTATGCATG CTTACTCCAT TTTCAATAAG AAGTTTACA AATGCAACTC	120
TATCCATTAC TCGAG	135

(2) INFORMATION FOR SEQ ID NO:1429:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

GAATTCGGCC AAAGAGGCCT AGGGGCAGCG AATGTTTTTA GAAGCAGAAA ACTTTCCAAA	60
TTTGGTGAAG GACATAAATT TACAGATTTC AAGAAGCTCC ACAAATTCCA AATATGATAA	120
ATATGAAGAA ACTCATAGCA AGGATGCTAT ACCACACACT TCTGAATAAT CCACAGGTCA	180
AAGAAGTCAG ACTCTCCGGT CTGACATGTA AAGGGCCTGG AAGTCGTCAC TCCCATCCTC	240
TCGAG	245

(2) INFORMATION FOR SEQ ID NO:1430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:

GAATTCGGCC ANNAGAGGCC TAAGAACTG GAAGTGCCTT TCATCTCCTC CCCCACCTAA	60
CTCCCCAGAA TTAATCACAA ATACTTTTGT GTGTATATG TCTGGAAAT TGTAATGTT	120
TAAACAAATC TACTAAGGTA TACTCTTCTG AAATTTTCCT TTGAAAATTT AGTTTATAAT	180
TTGGATTAT TTCTTGATGA GCACATGCTA AACTCATTCC ACCCTTTTTT GATGAAAATT	240
ATTACATGTT TATTAATATA TCACATTCCC TCCTCCCTG TCCCTTTTTT CCCCATAAA	300
ACACAATACT GTCAACTCGA G	321

(2) INFORMATION FOR SEQ ID NO:1431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

GAATTCGGCC AAAGAGGCCT AGTGTGAGAC ATTTGTCATT GCTCAGAATT TAAAATTGC	60
ATTCCAAGCT GTTGGATTG AGTTTAAGTG AGGCCAACT GGGGCGAGAT CAAACACACC	120
ATCAAAGAAT TACACACATA TCCTTGTTGC CACATCGCTT TTGTTGTTG TTCAAGGAT	180
GCTGTGTGTG TTACTAGGGT TAAGACTCTT CTCCTTGGCT GAGGGATCTC CTCTGGAGAT	240
TTTGAAAACA GGAAACAGAT TTCTCTCTCC CTCTCTGGT AGTCTTCTA TTCGTGTTAG	300
AAACAATCAA CTCGAG	316

(2) INFORMATION FOR SEQ ID NO:1432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

GAATTCGGCC AAAGAGGCCT ATAAAAATGC AAAAAATCCA GTCTAAATAT TGTCTATAGT	60
TTTTTAGGAT TATAGTGTA TCTGCTCTTT TAACTTATGT ATCTCTACAG CCTGCCACCA	120
TATAAGCTTT TAATTATAAA ATTATGATGC TTGACATTGG GGAGAAAGGA ACATAAGCAC	180
CCATAATGAG TCATTTTGT TGA CTGTATA AATGAGTCAG AGTTACATGT AAGGATGAGA	240
ATATCCTCCT ACAATTTTGG TTTTGATCT TGATTTTTC CCATTGACTC TCTTTCTCC	300
CCGCCATTCT CTCTCTTGCA CGTAGCACAC TTTTGCGCTC TGTCTGTAT TACTGCTATT	360
ATAAACCTTT TACTGGACTT CAGTTGTAGT GACCATTAGG TCCTAAACAT AGAACTAAGA	420
GCGTAAGTGG ACTTTAATAG AATACTTATT AATTTAATA ACTAGAGTTC ATAATTAGA	480
ATTAATATAT GAGAATTAC TGTATAATCC TCGAG	515

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

GAATTCGGCC TTCATGGCCT ACTGCTTTT TTTCTCTTT TTCTTTTCC CTTTGACTT	60
TTGAGGCTCC TGTTCTTTGG CAGCACCAGC TCCTTCTATT TCTGCAGCCA AGGCATCAAG	120
ATCAATGTCA TCCTTGGTGC TGTCTCGCT CTGTGTTTC TGTTTCTTCC CCATTGCTTG	180
TCAATGGCGC TCGTGGCCCC AGCCCTCTA TTCGGTCTCT CACAGACCCA CTGCTCCCCG	240
GCTGACTTTG GTCTCCGCTC AGCTCTTTC CCCTCGTGCT GCGCGGCTC GCACCCGGCT	300
CGAG	304

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

GAATTCGGCC AAAGAGGCCT AGAATTTATG TAATCCCAGG GTGGCTACCT ATTTCACTAG	60
TATTCCTCTC GGCTCAGTTT TAAATTTATT TTAGAAGCTT GGATTTCTCC CTAAGAGTTC	120
AAATTTCCC AATTATATT GGCTCCAGT TGACTTTGAT ACTGGAATTC TCTGCCAGGA	180
AGGAGTGAGG CCATCATGTT TCCACTTATG CCATCAGTGG CATCTCTGAT ATTTTGCCAC	240
GTGTTGCCCC TGTACAGCCC TGAGGTGTTG GGCAGAGGAG GCCAACTCGA G	291

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

```

GAATTCGGCC AAAGAGGCCT AAGACCCCCC TCAGCCTCCC GGAGTGCTGG GATTACAGGT      60
GTGAGCCAAT GCATCCAGCT GACTTTTGGA CTCTATCTTG AGGTAGCTGG GAGCCACTGA      120
CATATGTCAA GCAAGGGATT GACATGATCA GATTATTATG TAGAAAGGCC AGTCGCTCTG      180
TCTACAGTGT GGAGAGTGGA TTGGGAGGCA GAATGACCAG TCTGGAGGCT ATTATAGTAA      240
TCCAGGTTAC AGATGGGGGT AATGAGACCT AGGCAGGTAA TAGCGTGGCT AGAAGGAATG      300
GATAGATTCC AGAGACATTT GGAGGTGAAA TCAGGGGCTG GCGATTTAAC TGGGTATGAA      360
TAAAGAGGTA GAAAGAAGAT TTGAGGATGA TGCTCAGCAT TGAACAAGAG GGTAGACTCG      420
AG                                                                                   422

```

(2) INFORMATION FOR SEQ ID NO:1436:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 142 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

```

GAATTCGGCC AAAGAGGCCT AAGCTAGTTA TATGTTATTC TGGGAAAAAA TATTATTGTT      60
AGTTATTGCT ATCATGAAAA ATAAAATTTT ATGTGTCCTA AATTTAATTA TATTTTATGA      120
AACATTAACT CTGACACTCG AG                                                                                   142

```

(2) INFORMATION FOR SEQ ID NO:1437:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 263 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

```

GAATTCGGCC AAAGAGGCCT ACGTACATTT ACTCTTTATA CATGTTTTTT TTGTATGTCA      60
TACCTTTACA GTCATTATTC TTCTTGATGT TCATATCTCC CCATCTTTGG CCAGTTAGAG      120
CATTCCAAG TGAGCTCCTG TGTCTTTTG ACAAGACCCC AGTAATCGTT CTGCTTTTAG      180
ATAGAATAAG ATGTTTGAGG ATTCTTTTAT ACAACTTTAC CCTAGACCTG AACTCAGACA      240
TCTCTCCAAG GAGCGAACTC GAG                                                                                   263

```

(2) INFORMATION FOR SEQ ID NO:1438:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

```

GAATTCGGCC AAAGAGGCCT AGCAGCCTCT GCCTCCCGGG TTCAAGTGAT TCTCCTGCCG      60

```

CAGCCTCCTG	AGGATCTGGG	ATTACAGAGG	CTATTGGAA	GCTCCAGACT	GTTTAGAAGA	120
CCTGGACAGC	CAGAAAGTCA	TTAGTCCTAT	CCAAAATGAA	GCAATTTGTG	CAGGAAAAAC	180
AGATATTTTA	TGGAAGAACT	GTGAGTTTCT	GGTAAATCGA	ATGTGCCGTC	TTGAAAGCCT	240
CATGCAGTCC	TTGAAGATGA	ACATCTTTTCG	GCTGCAAACT	GAAAAGGATT	TGAATCCTCA	300
GAAAACAGCT	TTTCTGAAAG	ATCGACTGAA	TGCAATACAG	GAAGAGCATT	CTAAGGACCT	360
GAAGCTGTTG	CATCTCGAAG	TTATGAATTT	GCGCCAGCAA	CTGAGAGCTG	TAAAAGAGGA	420
AGAAGACAAG	GCACAAGATG	AGGTGCAAAG	GTTGACTGCC	CCCTCGA		467

(2) INFORMATION FOR SEQ ID NO:1439:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 103 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:

GAATTCGGCC	AAAGAGGCCT	AGGCAGATCT	GGCAACTTTC	ATATCTGATA	TTATGTTACT	60
GAAACTAATT	TTAGGTCGCT	TTGCATCTCT	CTGTGCCCTC	GAG		103

(2) INFORMATION FOR SEQ ID NO:1440:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 465 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:

GAATTCGGCC	AAAGAGGCCT	ACATNTTTGA	ATCTTAAACT	GNNTTTTTCT	CTTAGTATTG	60
CTAATGAGTA	AAGAAAAGTC	TCATAAGGTA	GCCAAATGAA	AAAGAATGAA	AGGGAAAGTG	120
AAAAATTAAG	GGGACNAAAG	ATGGGATGTG	AAAAGAAGAA	TTCTAGTTTG	ATGGTGACTC	180
ATATTCACGA	TAGGATACAA	AGTGTGATTT	GTTGGAAACA	TGTCCCAAAT	TTCTAAAATT	240
CTGCTTCTCT	GCCAAAAGCA	ATGCTTTTCT	TGGTTGATAT	TTGAGTTTAA	AAAGGGTCAA	300
ATCTTTCTAA	TTTTTTGTAT	CTNNAGAGGG	CAGCACTAGA	AGAAATCAGC	AGGTCTAATC	360
CCACCAGTAA	GAAAACTACC	ACTTCTTGAT	TTTTACAGAT	TAAAAAAAT	CTTTTCAGTG	420
ACCTTTCTTT	TTAATGTAAA	TACAAATTTA	AACCTTAGGC	TCGAG		465

(2) INFORMATION FOR SEQ ID NO:1441:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:

GAATTCGGCC	AAGAGGCCT	AGAATTATAC	AGGTAGAGAT	GTATGCAGAT	GTGTCCATAT	60
ATGTCCATAT	TTACATTTTG	ATAGCCATTG	ATGTATGCAT	CTCTTGGCTG	TACTATAAGA	120
ACACATTAAT	TCAATGGAAA	TACACTTTCG	TAATATTTTA	ATGGTATAGA	TCTGCTAATG	180

AATTCTCTTA AAAACATACT GTATTCTGTT GCTGTGTGTT TCATTTTAAA TTGAGCATT	240
AGGGAATGCA GCATTTAAAT CAGAACTCTG CCAATGCTTT TATCTAGAGG CGTGTGCGCA	300
TTTTGTCTT ATATGAAATT TCTAATCCCT CTCGAG	336

(2) INFORMATION FOR SEQ ID NO:1442:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

GAATTCGGCC AAAGAGGCCT ATGATTTTGA GACATCCAGA AAGCAAACCTT TAACTGTCTG	60
TGAGGTACAG AGACTGGATG ATGTTAAAGA AAACCATAGT TGGACACAAG ATACTCGAG	119

(2) INFORMATION FOR SEQ ID NO:1443:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 214 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

GAATTCGGCC AAAGAGGCCT AGAGAAATTT TAAAAGCAT AGTTGAGGCA TATTTTTTCA	60
TAATTATATA CTTATCTGTT TATTGCCCAT GGAAATATA TGTGTAGAAG TATTTCTTCT	120
GTTATTTGTT ACTATCTTCT TAATTTGTTC CAAAGAAAAT GCTGCCATAC TGCATTCCCT	180
CTGGAAGGAA ACAAACAAA ACAAACCTCT CGAG	214

(2) INFORMATION FOR SEQ ID NO:1444:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

GAATTCGGCC AAAGAGGCCT AGGAAAGGAA AAATTAAGAA CCCTAGATCT CTGGTACACA	60
TAAGTCTGGG TTTGCGATTG CTATTTGTGC TGGGGCAGTG TGATTGAGAC TGACATTGAG	120
GAAAGAAGCA GCTATGAAGA CCAGGGGGTT CAGCTTTCCA AGACAAAGGC AAGTCCTGTT	180
TCTTTTCTT TTCTGGGGAG TGTCTTGGC AGGTTCTGGG TTTGGACGTT ATTGGGTGAC	240
TGAGGAAACA GAGAAAGGAT CCTTTGTGGT CAATCTGGCA AAGGATCTGG GACTAGCAGA	300
GGGGGAGCTG GCTGCAAGGG GAACCAAGGT GGTTCGGAT GATAACAAAC AATACCTGCT	360
CCTGGATTCA CATACCGGGA ATTTGCTCAC AAATGAGAAA CTGGACCGAG AGAAGCTGTG	420
TGGCCCTAAA GAGCCCTGTA TGCTGTATTT CCAAATTTTA ATGGATGATC CCTTTCAGAT	480
TTACAGGGCC GAGCTCGAG	499

(2) INFORMATION FOR SEQ ID NO:1445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

```

GAATTCGGCC AAAGAGGCCT AAAATTTGAT TAGAAATGCA AGACTGGATG CCAAGATTGA      60
TTCTAAATTA GGTCAATGTG TTATGGGTAA CAATGCAGTC TCACCCTATC AGCAAGTGAT      120
TGAAAAGACC AAAAGCCTTT CCTTTAGAAG CCAGATGTTG GCCATGAATA TTGAGAAGAA      180
ACTTAATCAG AATAGCAGGT CAGAGGCTCC TAACTGGGCA ACTCAAGATT CTGGCTTCTA      240
CTGAAGAACC ATAAAGAAAA GATGAAAAAA AAAACTATCA AAGAAAGATG AAATAATAAA      300
ACTATTATAT AAAGGGTGAC TTAATCGAG

```

(2) INFORMATION FOR SEQ ID NO:1446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

```

GAATTCGGCC AAAGAGGCCT AACAGAGGAA ACCACCCTTC AACTGGAAGA TATCATTAAG      60
CAGAGGATAA GAGATCAGGC TTGGGATGAT GTAGTACGTA AAGAAAAACC TAAAGAGGAT      120
GCATATGAAT ATAAAAAGCG TTAAACCTTA GACCATGAGA AGAGTAAATT GAGCCTTGCT      180
GAAATTTATG AACAGGAGTA CATCAAACTC AACCAGCAAA AAACAGCAGA AGAAGAAAAT      240
CCAGAATATG TAGAAATTCA GAAGATGATG GATTCCCTCT TCTTAAATTT GGATGCCNTC      300
TCAAACTTCC ACTTTATCCC TAAACCGCCT GTACCAGAGA TTAAAGTTGT GTCAAATCTG      360
CCAGCCATAA CCATGGAGGA AGTAGCCCCA GTGAGTGTTA GTGATGCAGC TCTCCTGGCC      420
CCAGAGGAGA TCAAGGAGAA AAATAAAGCT GGACATATAA AAACAGCTGC TGAAAAAACA      480
GCTACAGAAC AACTCGAGGT GTGGGGAAAA GAAAGAGAGA TCAGATTGTT ACTGTCTCTG      540
TATAGAAAGA AGTAGACATA GGAGACTCCA TTTTGTCTCT TACTAAGAAA AATTCTTCTG      600
CCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:1447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

```

CTGCTGCAGC AATATTCAGA TTGAAAAAAA TAGGTTTGGG TCACTGAGT TTAAAGGGAT      60
GATGATAAAA AGGAGGTTCT TCTTCCTCTT CATCCGAAAC ATGAGGTTTA TTCATTATTA      120
CATCATCATC TTCTTTACTC TGTGCGATCT GTTTACATTT CTCAGTTAGT TCTTCTATAG      180
TAGCTCCTCC TGACTTTTAA GCAACTTTCT CTTCTATAGT AGGTGGAGGT GCAGGCTTTA      240
GGTTTGGTGG TAAAGGGACA CCAGCCTTAG CACACATGGC AGCTGCATTA GCTTTGGCTA      300
TTTCAAGTAA TTGAGCCTTA TCCAAATCTG TCAGACGTTT GGGTGATCTG CCTCGTTCAG      360

```

AAGACCTGGA TCTTTTACGA CGGATGGGAG ATCTGCTAAA CCTTCTTCTT AAGGGTGTTC 420
TTGATCGCCT TAATCTGACT GGTGAGTAGG CCTCTTTAGC CGAATTC 467

(2) INFORMATION FOR SEQ ID NO:1448:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

GAATTCGGCC AAAGAGGCCT AGACACTTAT AGGCTTTTGA AGAAGCATTG ATCAATTGTC 60
AAACTTAGTG CTACATCAGA CTGTGGAGCG TATTCATGTG GGCAAAAAAT ACGGTGATAT 120
TCCTCGAG 128

(2) INFORMATION FOR SEQ ID NO:1449:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

GAATTCGGCC ACNAGAGCCT ATTTAAATGA AAATNATTTG AATGTTTAAT ACTCTTCCCT 60
TCTTCAATTG TAGAAACATT ACCCTTTTGC ACTATCTCAT CACTATTGTG GAAAAAAGT 120
ACCCCAAGTG TCTCAATCTA AATGAAGAAT TGCGAGATAT TCCTCAAGCT GCGAAAGTAA 180
ACATGACTGA GCTGGACAAA GAAATAAGTA CCTTGAGAAG TGGCTTGAAA GCAGTAGAGA 240
CAGAGCTGGA ATATCAGAAG TCTCAGCCCC CACAGCCCGG AGATAAGTTT GTGTCTGTTG 300
TCAGCCATCT CGAG 314

(2) INFORMATION FOR SEQ ID NO:1450:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

GGAATTCGGC CAAAGAGGCC TAGTGGTTTT CCCAGGAGGA AAGAGAGCTG CAGGGATACA 60
GATGCCTTCC TGAGCAGAGA AAATAGAATA CTTGAGCCAA TTTTCATGTA AAATGGATTA 120
TTTTCTGGC GTTTCCTGTC CTTCAAGTAA AAGGTTCTGG AATGAGTACT TCACTGCTGT 180
AATGGAGACA CTAATATTTT ATGAATGCAG TTTTACAGTT TGCAGTAATG CCAGGCCTTT 240
GGCTGTTTTT CATTAGATGG TGCACTTGGC TGGAAGCATA TACTCTTGTA GCTTTGATTT 300
TAAATTTAAC TTTCAAGTTG AAAGAGCAGT GACTCATCCA AAGGACAGGT GATATTTATT 360
TATTTTCTCT TGAAAATGCA GCACGGGTAT GTTGTATCA CACGTTTAGG GGAATTGCCA 420
CACTTCCTCG AG 432

(2) INFORMATION FOR SEQ ID NO:1451:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

```
GAATTCGGCC AAAGAGGCCT AGGATTGAAC GCTTTCACCC TGTGCCCCGC GCCTGGCGTA      60
ACGCGTGGCC CCAGACCACA CGCTGTAACC CGGGGTGAGA GGGAGTGAGG TGGGACTTCG      120
TACCGGACCC GGAGCGCCGG CCTCGCCCGC GCGGGCAGCG TTTACTGTGG GGAGTGCTCA      180
CTCAGCCTAG GCGGCGCCGG GAGGACTGCC GGGAGGAGGG AGTCGGCCTT GAATTGAGGC      240
CTCAGCCTTG AATAGGGTAG GGAGGCAAGC CTAGCCGAGA GTTTAGCACT AGCAAAAGCC      300
TGGAGGCACC AGGGTCTGCC CTAAGAACTG CAGCGCCTCT GCTCTGGCTG GGATTTAACG      360
CATTACGTCT CTGCTGTTTA TAGGTGTTGT GTTTGGTCTT ACCACTTCGT ATTCTATAGT      420
TTTTATTTAT TCCTGTTTTT TGAATTTTCC CACTTTGCTC GAG                          463
```

(2) INFORMATION FOR SEQ ID NO:1452:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 407 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

```
GAATTCGGCC AAAGAGGCCT AATGCAAGTC TGGACCGTTT AAAAGCTGGT AATTAAACAC      60
TTTATTCCAT ATCAGAATAA AAGTCAACTA GTTGAATATT TCTAGGTGAG ATGTGGTACT      120
ACTTTTTTTT TNGCTGTTAT TTTATGTCTG TATCTAAAAT ATCTTACTGC ACTCTTTTTT      180
CAGGTTGCAG CAGATCCTTG AGTTTGAAC CTGACGGGCA AATCAGAGCT TCTTCCTCAT      240
GGCAGTCGGT CAATGAGAGT GGAGACCAAG TTTACTGGTC TCCTGGCCAA GCCCGACTTC      300
AGGACCAAGG CCCATCATGG GCTTCGGGCG ACAGTAGCAA CAACCACAAA CCACGAGAGT      360
GGCTGGAGAT CGATTGGGGG GAGAAAAAGA AAATAACAGG ACTCGAG                          407
```

(2) INFORMATION FOR SEQ ID NO:1453:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

```
GAATTCGGCC AAAGAGGCCT ACGGCCAAAG AGGCCTATAG GCCTCTTTGG CCGGAAATCA      60
TGGTGTATA GATCAAAAGA TAAAAGTTTC ACAGAAGAGG TGGGATTGGA ACTAAGCTGT      120
TCATGCTCAG TAAGATTAGA GGAGGTGAAG CAAATGGGGG AATGTGTGCC AGAAGAGGAC      180
AGGTGCAAAG ATAAGCACTG GTGCTTGATC TTGACTGAAT TTTCAACCAA ACCAGCTGAC      240
TCTCAGGATA GTTGAAGGTC ACTTCTGCT GTTTAAAGAA AGATTCTAAA GTTACTTAAG      300
AAATATTTGG CAAAAGACTC AAAAGGAAGG ATTCCAATTA CAATATAAAT AAAGTAAGAA      360
```

ACCTCGAG

368

(2) INFORMATION FOR SEQ ID NO:1454:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 618 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

GAATTCGGCC	TTCATGGCCT	ACCGTGCTCT	ATGCTGATCC	TTTTTCTCGT	GAGAAAAACGC	60
TGGCCTGTTA	TTATTAGCTA	AGGTCACACC	CGCTGGGCAG	CTCCTGGGAT	TTTGGGATTC	120
CTCCCCACTC	CAGAGGGAAG	GCTATTTCTA	GTGGCTTCTT	TTCTTTGAGT	CCTCCCTTCT	180
GTCTGTCTCT	CTCCTGTTCC	TCCTCTTTAC	CAGTAGGGCT	TCCTCAATGC	TGACAGCCCT	240
GTGAAAAAAG	GGGAGACATG	CCGAGCTCCG	GCAGGAAACT	GCTGGCCCG	GACCTGGCTT	300
CTGGGGCACA	AAGGAGAATT	TCTGTGTTTG	GAAAAGTACA	GACTGAGCAG	GTGACCCCG	360
CACAGCCCT	TGGGGGAAAC	ACTTGTGCCC	TTTGAGTCTG	ACTGATATAA	ACACAGACTC	420
TCTTGACTGT	CCATAAAGG	CCAAAGCCAG	AGAACCTCAG	AAAGGGACTT	GCAAATTGTG	480
AGTGAGGCAT	ATCAGCTGGT	GCTTCTTTT	CTCTGTGGGC	TGCCATTAT	GAATCTCTTG	540
GTCTCTCTCT	GTCTCTGTCC	CTCCACTTTT	CTCTCCTTTG	CTGGTGTGTG	CATTCCCTCT	600
GACGCGCTGG	CTCTCGAG					618

(2) INFORMATION FOR SEQ ID NO:1455:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

GAATTCGGCC	TTCATGGCCT	AGCCTTTTGT	AAACTCAGGA	AAGACAAAGG	TTCAATTACA	60
CCACTTTTGT	CAATAAGCAA	ACCAGGTATT	TTTTTTTCT	CCTGTTGTCT	GGATATGGCA	120
ATAAATTTT	TAAATTGCTG	TGAGAACCA	TATATGAAA	GAGAGGAGTT	GAATTGTGTG	180
TGCCTTTAT	GTCTTGAGAT	TTATATGTGG	AAAAGACGAC	ATCTACTTCA	AACTGTATTT	240
TTTTCGTTT	TTTTTTTTT	TGGGAAGGG	GGGAGAACGG	GGTCTTGCTC	TGTCGCCCAG	300
GCTGAACTCG	AG					312

(2) INFORMATION FOR SEQ ID NO:1456:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 415 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:

GAATTCGCCT	TCATGGCCTA	GCTTAATCTT	ACAGTCATTT	AAAATAATTT	CAGAAATGTT	60
CCTTTCATAC	CATTGTCTCC	ACCCCCAAAC	CAGCTTACTA	AAAATGGCTT	AGGATTGTGT	120

```

TTCAGTCCTT CCTCTTCCTC TCCCCTGCTC CCAGACAAGG GTGTGTACTC AATACTGTAT 180
TCAGAAGTTA CTTGGGTTAG TTCTTTTTT CCGATCTTC AGTGTGATTA TTTTATTCAT 240
TTGAAATACA ATTGGATTCA TTCGTTTCCG TATGCTTTCA GTTTTAGCTT TTTTCCACTA 300
TCTTTGTTGA TATAATTGCA TTTTTTGATA GGGGGATATT AATATACTTC ACAAAGTCAG 360
AATAACATAA GGGTTTACTC AGATGTAACC TGTATCTTA GCCCGTGATC TCGAG 415

```

(2) INFORMATION FOR SEQ ID NO:1457:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

```

GAATTCGGCC TTCATGGCCT ACATTTTCT ATTGATATAA AAATTGTTAG AGAAATATAC 60
AGTTGTATAT TTCCCCCTT TATACAGAAA TTTTACAATA ATTTCAGATT TTTCTGAGTT 120
TTTTCAGATT TTTGATTCTA TAATATGAGA TTATTCTTTC TTCCTCTTAT TTTTTAGGT 180
TATTATTTT TTCTTTTCTT TTTAATTGTC TCATACAGGT TTA CTCTCGA G 231

```

(2) INFORMATION FOR SEQ ID NO:1458:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

```

GAATTCTGTT CATATTTTTA AATGTTCTT TTTTCAACA TTCAGCAAAA TATTATGTGC 60
TAGGAACTCT CCCAGACGCT TGTAAACATC TATGAATACA ACAAAGATTG TGCCCTCCTG 120
GGCCTCTTTT CTGATGGGGA AGCAAAAATC TCGAG 155

```

(2) INFORMATION FOR SEQ ID NO:1459:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

```

GAATTCGGCC TTCATGGCCT AGGTGACTAA GTACAAAAAA ATAGTTTCTT CATTTGATTC 60
AAAATAGTGA GTAGGTTCCC TGGATAATAC ACAGTGGTAG TTGACATATT TTCTCAAAC 120
ACAACCAGAA AACCCACTTC CGGTATTTGT AAATCACCTT TCAAGGGAAA AAGTGAACAC 180
GTATTCCTTG TATTTCTAGT TTGATTACCA AACCTGATGT TACAAAGAAA CCTCGTTCT 240
GTAGACAGAA TTTCTTTTAT TTTCTTCTT TTA CTCTCA CAATCACTT CCCAGTGCCA 300
CCACCGCTCG AG 312

```

(2) INFORMATION FOR SEQ ID NO:1460:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 459 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

```
GAATTCGGCC TTCATGGCCT AGTCTCCCTC GGCCTGTGCC GCCGCCGACG CCGCTTGTGG      60
GCCCGACTCC GCTCTGTCTG CTTCGCCACC TTCTCCCCGA GCACTGCCCG GCCGGCCGCC      120
ATGGCTAACG TGGCTGACAC GAAGCTGTAC GACATCCTGG CGTCCCGCCC GCGGCCAGCG      180
AGAACGAGCT GAAGAAGGCA TACAGAAAGT TAGCCAAGGA ATATCATCCT GATAAGAATC      240
CAAATGCAGG AGACAAATTT AAAGAAATAA GTTTTGCCATA TGAAGTACTA TCAAATCCTG      300
AGAAGCGTGA GTTATATGAC AGATACGGAG AGCAAGGTCT TCGGGAAGGC AGCGGCCGAG      360
GTGGTGGCAT GGATGATATT TTCTCTACA TTTTGGTGG GGGATTGTTC GGCTTCATGG      420
GCAATCAGAG TAGAAGTCGA AATGGCAGAA GAACTCGAG                                459
```

(2) INFORMATION FOR SEQ ID NO:1461:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 511 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

```
GAATTCGGCC TTCATGGCCT ACGAGATCAA GGACAAGAGG CAGCTTATAG ACAACCGCAA      60
GCTCATTGAG ACGCAAATGG AACGGITCAA AGTTGTGGAA CGAGAGACCA AAACCAAAGC      120
TTACAGCAAA GAGGGCCTGG GCCTGGCCCA GAAGGTAGAT CCTGCCCAGA AGGAGAAGGA      180
AGAGGTTGGC CAGTGGCTCA CGAATACCAT CGACACGCTC AACATGCAGG TGGACCAATT      240
TGAGAGTGAA GTGGAGTCAC TGTCAGTGCA GACACGCAAG AAGAAGGGCG ACAAGGATAA      300
GCAGGACCGG ATTGAGGGCT TGAAGCGCA CATCGAGAAG CACCGCTACC ACGTGCAT      360
GCTAGAGACC ATCCTGCGCA TGCTGGACAA TGAATCCATC CTCGTTGACG CCATCCGCAA      420
GATCAAGGAC GACGTTGAGT ACTATGTTGA CTCATCCCAG GACCCCGACT TCGAGGAGAA      480
CGAGTTTCTC TACGATGACC TGGACCTCGA G                                511
```

(2) INFORMATION FOR SEQ ID NO:1462:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

```
GAATTCGGCC AAAGAGGCCT ATTTGTTTGG TGGTTTTAAA ATTTTTCTT CGCATAAAGG      60
GTAACATCTT GCAACTTGAT TCTTCACTT CATGATATGC CTTAGATTTC TTTCTTCCC      120
AATACTCGAG                                130
```

(2) INFORMATION FOR SEQ ID NO:1463:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

GAATTCGGCC AAAGAGGCCT ACTTGTNAAG TGCTTTTGAA TTAATAAAAT ATTAGCATAA	60
TTGTGINTAG TCAGTTGAAC CCACTGTTAC CATTGTTCTT ATCCCATGGG AAGCAGTTGG	120
TTACACGATT CTTATTTTAT AAGAAACAGC TGAGAGGCAC TATGGATTAG TCTTCTGAAG	180
TGAAGGAAAT ATAGATGTCT CCTAAGTGAT AGTTAACCCA TTTTITTTTT TTTTAGGCAT	240
AGAAGCCAGT TCAGGGTCCA TAATATTTAG TGACCAACAT TTAAAGTAT AGCAGCAACC	300
TGTTCTTAA ACACAAAGTA AGTTGCCCAT TAACAAATGG CTTTATCTT TAGCATGAAA	360
ACTTTCACA CGTCTCGAG	379

(2) INFORMATION FOR SEQ ID NO:1464:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:

GAATTCGGCC AAAGAGGCCT ANAANAACT TTTCTTGGG AGCAAGGTAG TTATTTCAA	60
GCACAGAAA AGGCGGCGGG GGGCACAGAG AAGCACAGAG AAGCGGGGGC AGTTGCACAG	120
GTAAGACATT CATCTGGCT TTTCTTTTA AAAGATAAAC TTTGTCCAC GTAAAGAGGA	180
ANACTGCATA GATATTCAAT GAGATTATCT GATTGTCCAC TGTGCCAAA GAAAAACAA	240
AGGTAAATA CACGAGTTTC NNCATTGAGA AGAAAGTATT TCAGGTAAAA ATTAATATT	300
AAGCACTTT TCTCAGCAGA AGAAATGCC AAATCTTAA GGACAGTACT CGAG	354

(2) INFORMATION FOR SEQ ID NO:1465:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

GAATTCGGCC AAAGAGGCCT AACTGCTCC AGCTCTGACT CCCTCATCCC TTGCCTGGAC	60
CATGGTAATT GACCCTAGCT GGTCTCCTT TCTCTCTCA TCAGTCCTCC ACATTGCTGC	120
TGTTTTCATC TTTGTGACAT ACAAATGTGT TGCTTTCCG TCTAAAACCC TGCTTGTC	180
TCCCATTTT GACTGCCTGC CCCAGCACG CACACACACA AACTCGAG	229

(2) INFORMATION FOR SEQ ID NO:1466:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

GAATTCGGCC	AAAGAGGCCT	ATTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTAATTTAT	60
AAGGAATAGA	AATTTATTGG	CTCACAGTTC	TGGGGGCTGG	GAAGTCCCAG	AGTAAGGTGC	120
CAGCGTCTGG	TGCAATCCTT	CTTGTGTGT	CACTGTGGAA	GGTGAAGGG	CAAGAGAGGG	180
CCAAGCTCAT	CTTATTATAC	CAGCACCCAT	TCCAACATCA	TCCTCGAAGG	ATCCCAATT	240
TGAAAGAAAA	AGCATGTGAG	ACACAGAACA	GGCGAGAGAG	TGAGGGCCCG	GCATGCCCC	300
AAGTCCCCAC	CACCGCACCT	GCTCGAG				327

(2) INFORMATION FOR SEQ ID NO:1467:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

GAATTCGGCC	TTCATGGCCT	AGAGAGAGAG	AGAGAAAAGG	AGGGGGTGGT	GGAGAAGCGG	60
GAGCGAAGGA	AAGGAGGCRA	AAGGCAAAGT	GAAGGAAAGC	TGGATAGCTC	GGCCTCTCCA	120
AACTGATTGA	TTAGTCATGA	TCCCCGCACT	TTTAACAGGG	ACTCATTCAA	TTGGGAAGGT	180
GGAGCGCTGG	GGAGCAGATT	AGCATACTCT	TGTTTACTCA	TCTTCTGAGG	GATTTTTTCC	240
CCCTCTTTCC	TTTCATTTTG	AGAAGAAGGA	GGGAGGGGAG	GGGGGACTTG	GGGGGGGAGA	300
AGGGGGCTGT	GGCTTGTGTT	ATAAAGGACG	CAAAAATAAA	ATAAATTAGA	GCATCTTTTG	360
GGGGGAGGGA	ATTCAGCGGA	TCAGTCTTAA	GATGGAGCTC	GAG		403

(2) INFORMATION FOR SEQ ID NO:1468:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 329 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

GAATTCGGCC	TTCATGGCCT	ACACGAGGTC	AGACGTCACA	CATTGTTTTT	TGGCTTGTTT	60
TTTTGAAGTT	TTTACGACTT	GTCTGAGTTC	TCGGCCTGGC	TTCTGTTTTT	CACTGTCCGG	120
AAGAGTGTGG	TCCTTCTGCA	TTTGACCTTC	CTTCACCTTC	ATCCAGTCTC	CCCAGTGTGG	180
CCGTCTCAT	TTCTGTGCTG	CAGCTGGGTC	AGCTGGCTCG	GTGTGGAGTT	TGGATTTTCC	240
GTGATCCATC	CCATGCTTTT	TTTTCTTTTC	TTCTTTTTTT	CCTTTTCTTT	TCTTTTTCTT	300
TTTTTTCAGT	TTTCTCCCCA	ACTCTCGAG				329

(2) INFORMATION FOR SEQ ID NO:1469:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 352 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

GAATTCGGCC TTCATGGCCT ACAGGAAAAT TCTTCTGGCG TATTTCATTC TGATGTTTAT	60
AGTATATGCC TTTGAAGTGG CATCTGTAT CACAGCAGCA ACACAACGAG ACTTTATGCT	120
AGAGAGGTAC CAAAACAACA GCCCTCCAAA CGATGATGAC CAGTGGAAAA ACAATGGAGT	180
CACCAAAACC TGGGACAGGC TCATGCTCCA GGACAATTGC TGTGGCGTAA ATGGTCCATC	240
AGACTGGCAA AAATACACAT CTGCCTCCG GACTGAGAAT AATGATGCTG ACTATCCCTG	300
GCCTCGTCAA TGCTGTGTTA TGAACAATCT TAAAGAATCT CTCACCCTCG AG	352

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

GAATTCGGCC .TTCATGGCCT AGAGCCGTCC TATCAGATTA TCTTAACAAG AAAACCAACT	60
GGAAAAAAA ATGAAATTCC TTATCTTCGC ATTTTTCGGT GGTGTTCAAC TTTTATCCCT	120
GTGCTCTGGG AAAGCTATAT GCAAGAATGG CATCTCTAAG AGGACTTTTG AAGAAATAAA	180
AGAAGAAATA GCCAGCTGTG GAGATGTTGC TAAAGCAATC ATCAACCTAG CTGTTTATGG	240
TAAAGCCAG AACAGATCCT ATGAGCGATT GGCACCTCTG GTTGATACTG TTGGACCCAG	300
ACTGAGTGGC TCCAAGAACT AGAAAAAGCC ATCCAAATTA TGTACCAAAA CCTGCAGCAA	360
GATGGGCTGG AGAAAGTTCA CCTGGAGCCA GTGAGAATAC CCCACTGGGA GAGGGGAGAA	420
GAATCAGCTG TGATGCTGGA GCCAAGAATT CATAAGATAG CCATCCTGGG TCTTGGCAGC	480
AGCATTGGGA CTCCTCCAGA AGGCATTACA GCAGAAGTTC TGGTGGTGAC CTCTTTCGAT	540
GAATGCAGA GAAGGGCCTC AGAAGCAAGA GGAAGATTG TTGTTTATAA CCAACCTTAC	600
AACCTCGAG	609

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCC TCGAGCCTGG GCAATAGAAT	60
GAGGCTCCAT CTCATAATAA TAATAAGCAG CAGCGGCAGC TCTGGTAGAT TTTTGTGT	120
GCTTGTCTC ATGAAGACTT AAGCCTGCTC TTTCATTTG AAACCTAGGC ACTTGGACTA	180
ACTTAAAGA TCATGTAAAA AATTTAATTT TGTTTTGTA TAGATTAAAT TGTGGTTTTT	240
TTTTCTCTT TTAGATATAA TTGATCCTGT TGCTTTAGAA ATTCCATTAT CAAAAACCT	300
TCTGGCAGC ATTAGTGCTC TTGCTCTCA GCTGGATTCA GAAGATCTTC ATAATTATTC	360
AGGAAGCCAA CTATTTGAAA TGCACGAGAA AACCTCGAG	399

(2) INFORMATION FOR SEQ ID NO:1472:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

GAATTCGGCC	TTCATGGCCT	ACAGGTTT	AACTGGTTTT	TGTCATACTG	CTATATAATT	60
CTCTGCTCT	CTCTGTTTAT	CTCTCCCTC	CCTCCCTCC	CCTTCTTCTC	CATCTCCATT	120
CTTTTGAATT	TCCTCATCCC	TCCATCTCAA	TCCCGTATCT	ACGCACCCCC	CCCCCAGGC	180
AAAGCAGTGC	CTGAGTATC	ACATCACACA	AAAGGAACAA	AAGCGAAACA	CACAAACCAG	240
CCTCAACTTA	CACTTGGTTA	CTCAAAAGAA	CAAGAGTCAA	TGGTACTTGT	CCTAGCGTTT	300
CTCGAG						306

(2) INFORMATION FOR SEQ ID NO:1473:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

GAATTCGGCC	TCATGGCCTA	CAACTCGCA	GCAACAACCT	CGCAAACGG	AAAAAGAACG	60
ACATGATGCA	ATCTTCAGGA	AAGTAAGAGG	CATACTAAAT	AAGCTTACTC	CTGAAAAGTT	120
TGACAAGCTA	TGCCTTGAGC	TCCTCAATGT	GGGTGTAGAG	TCTAAACTCA	TCCTTAAAGG	180
GGTCATACTG	CTGATTGTGG	ACAAAGCCCT	AGAAGAGCCA	AAGTATAGCT	CACGTATGTC	240
TCAGCTATGT	CTGCGATTGG	CAGAAGATGC	ACCAAACTTT	GATGGCCAG	CAGCAGAGGG	300
TCAACCAGGA	CAGAAGCAAA	GCACCACATT	CAGACGCCTC	CTAATTTC	AATTACAAGA	360
TGAATTGAA	AACCGAACGC	TOGAG				385

(2) INFORMATION FOR SEQ ID NO:1474:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 428 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

GAATTCGGCC	TTCATGGCCT	AGATCCCTT	ATTTTGCCAA	AAAGTGTCAT	CAATTCATTT	60
GGATAACTTT	TATGTTTTAG	GAACGTGGCC	TCTCTTTTAA	TACTGAGAA	CTTACAAAAT	120
GGTTCAGAAA	GTTTATATTT	TAAAGCTTT	CATTTCATTGA	TATATTGAAC	ATCTAAGGCT	180
TAACATCTT	TCCAATGGGA	CAAAAACAGA	ATTCTTAAAA	ATGAGGAGGA	GGGCCAGTG	240
TGGTGGCTTA	CACCTGGAAT	TCCAGTGCTT	TGGGAGTCCA	AGGTAGGAGA	ACTGCTTGAG	300
GCCAGGGGTT	TGAGACCAGC	CTGGGCAACA	CAGCAAGACA	ACTCTACAAA	AAATTAAAAA	360
AACAATCCAG	GGCCGAGCAT	AGTGGTTCAC	ACCTGTAATC	CCAGCACTTT	AGGAGGCCAA	420
GCCTCGAG						428

(2) INFORMATION FOR SEQ ID NO:1475:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

GAATTCGGCC TTCATGGCCT ACTGGGATGT ATATGAGAGA CAGTGCTTTC AATTAAATCC	60
TTGGGTATAT TTTTATTAAT TTCCTCCAGA TTTTCTTTT AAGGCCTTTT CTAAGTTATA	120
CTGCATATCA AACTTCCCTG TTATTGAAGG ATATAAGGTA GAAGGTAAAA GCCATTTTCC	180
TATAAGTAAC TTGGGCATTT GCAAAGATTT TTCTCAAGTG CAGTTGTAAC TATACTAAAA	240
TATACTAATA TTGTGTTATG ATATACCTTG CTTTTTTTCT TTTATTTTCT CTTTGTAGAC	300
AGAGTTTTGC TCTGTTTCC CAGGCTGAAG CGCTCGAG	338

(2) INFORMATION FOR SEQ ID NO:1476:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:

GAATTCGGCC TTCATGGCCT ACAAAGAGCT AGAAGCCATT GAAAGTCGGC TAGAAAAGAC	60
AGAATTCAC TAAAAGAGG ATTTAACTAA ACTGAAAACA TTAAGTGTGA TGTTTGTAGA	120
TGAACGGAAA ACAATGAGTG AAAAATTAAA GAAACTGAA GATAAATTAC AAGCTGCTTC	180
TTCTCAGCTT CAAGTGGAGC AAAATAAAGT AACAACAGTT ACTGAGAAGT TAATTGAGGA	240
AACTAAAGG GCGCTCAAGT CCAAACCGA TGTTAGAAGAA AAGATGTACA GCGTAACCAA	300
GGAGAGAGAT GATTTAAAAA ACAAATTGAA AGCGGCAGAA CTCGAG	346

(2) INFORMATION FOR SEQ ID NO:1477:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 298 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:

GAATTCGGCC TTCATGGCCT ACAGGTTTTT ATTTTATATT ATTTTCCTTT AGCCTGAAAA	60
ATTTATTTAT TTTTCTCTT AGTACAAGTC TGCTGGTGGT AAATCTCTT AGTTTGTGTT	120
TATTGAAAGA TATTTTATT TTGCCTTCAT TCCAGAAGGT TGCTTTTGCT GGATATAGGA	180
TTCTACAACT TTGCTTTTA ACATGTTATG GATGCCATTC CTCTGTCTTT TAGCTTCCAT	240
TGTTTCTGAT GCTAAATCTT CAGTCATTTT ATCATTGATC CTCTGTAATG TACTCGAG	298

(2) INFORMATION FOR SEQ ID NO:1478:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

GCGAACTAGC CCAAATGCAC CTAGGAACAT TGTTGCTTCA GGACCAGTTA TTTCTGACCT	60
TCCAGTTGTT CCTGACTGTG AAGGGTGACC GCTTCCCGGG ACTCGAG	107

(2) INFORMATION FOR SEQ ID NO:1479:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

GAATTCGGCC TTCATGGCCT ACTTATATTC TTTATTATTA TTTAGTACAA AAATAGATTC	60
CCAGTAGATA TCCACAAGCA ATATTAGCAG GGCTTCTGTT TCTAAGTGAC CACAGACTAA	120
CCCTTTCTAG GCTTTAACAT TGTAAATAAT CCTATAAACA GTTTGATTTT TTAAGATGAT	180
TTTTGATTG AAGAGACAGG CTTTACATAA GCCTTCATTC CTTCAAAAGG TCCTGACAAA	240
ATACTTGGGT TTTTCTCT TTTTTCATT CTGGTATGCT TTGCAGCATT TCAGCTGCTT	300
TGGTGGGGAC ACAGATAACC CCTTCGCTC CAGACTCGAG	340

(2) INFORMATION FOR SEQ ID NO:1480:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

GCGATTATTG TAAGTTGACA ATTTATAATT GTATAAAAGT ATGAGGTACA AAGTGATGTT	60
ATAGCTTAAG AATACAGTAT GGTATGATTA AATCAAGTTA TTAACCTATC CTTACGTTA	120
AATGCTTAAA TTTTGTATG AGAACATTG AAATTTACTC TTGGAAGGTA AAAAAAATC	180
TCAGGACCCC CCAAATTAAA GCCATGAAGC TGAATTGTGC AACAACTCTC GAG	233

(2) INFORMATION FOR SEQ ID NO:1481:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

GAATTCGGCC TTCATGGCCT AGATAACTAT TGCTCCCACT ACCCTTTCAG CTATCTCACA	60
TAACCTTTGAT ATATATTATT TTTATTATCG TTTATTAAGT GTCTAATTC CATTGTGAAG	120
TCTCCTTGA CCTATAAGGC TGAATAAAA TAATTTAAAA TTTATTTTCT TATTGTTTCT	180
AATTCAATTT CATTATAGTT AATGCAAGTG GTCATTGTGC TATTGAGTTT GGTACTTTGG	240
AGGTTTCTTT TTCTGGCTAT CTCGAG	266

(2) INFORMATION FOR SEQ ID NO:1482:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

GAATTCGGCC TTCATGGCCT AAGAAATGTT CACTTTTCCA ACTTAAAGG ATTTTAAAA	60
ATACAAACAT AATTGACCTA CTTGGTTCAA AGAACAGAAG TGAGGAGAAC TTGCTTAAAG	120
GTATTGATGT TATATTTTCT CTTGACTGAG TGCTTGAAAA AAAATTTTAT TGAACATATG	180
TTCTCCTTCC GTGGCTTTTT TGTCTTGTCT TTTTGTGTTT GTTTGTGTTT TTTTCTTT	240
GAGATGGAGT CTCACTCTCT GCTCGAG	267

(2) INFORMATION FOR SEQ ID NO:1483:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 242 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

GAATTCGGCC TTCATGGCCT AAATTAGCAT CTAGTGTAC AGGTAAAAGA ATTCAGGAC	60
CAGGTTTAAA CTTTATTTTA AATATTTTA TACTTAGGTC TCTTTTCCT GCCTCTCCCC	120
AAAGAAGAGC CACTGGCCTT AGTTGTTTGA GCTTACTGCT TATATTATAG AGTGTAATA	180
GGTAACTAGA GACTAAAATT TTATTAACCA GCATGTTTGG TATATTTAA GCAGTTCTCG	240
AG	242

(2) INFORMATION FOR SEQ ID NO:1484:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 291 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

GAATTCGGCC TTCATGGCCT ACAGAGTGTG GTTCTGTAG CAACACTTCT CATGACCATC	60
TGTTTTGTGT TTATGATGAT TTTTTCAGGT CTGTTGGTCA ATCTCACAAC CATTGCATCT	120
TGGCTGTCAT GGCTTCAGTA CTTGAGCATT CCACGATATG GATTTACGGC TTTCAGCAT	180
AATGAATTTT TGGGACAAAA CTTCTGCCA GGACTCAATG CAACAGGAAA CAATCTTGT	240
AACTATGCAA CATGTACTGG CGAAGAATAT TTGGTAAAGC AAGGGCTCGA G	291

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

```

GAATTCGGCC TTCATGGCCT AGTAATTTT GATAGTAAGG GCTTTTATT GTCATTTT   60
GTTAATCGTT TCCTGTCTGT TTTGTATTTC TTTGTTTCCT CTCTTCCTCG CTGGGTATCA   120
TCTTTGCAAT TTGATAATTT TTGTGTGAT ATACTTTGAT TCTTCTATT TATCTCTCT   180
GAATCTAATA TTAGTTTTT TTATCTTTC TGTATCTATT ATTAGTTTT TTTCTTTGTG   240
GTTATCATGA GGCTTCCACT CGAG                                         264

```

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

```

GAATTCGGCC TTCATGGCCT ACCAGTGCCT TCCTCTTCCC TATATTCTGT GTGTCTTAAC   60
GGAATTATTT TTCCAAATCA TTGTGTGCAA AGAAACTAAT GACATCATAA GTATGATTTC   120
TGTACACATT TTAGTTGTAA TTGCTAGGTT TTCCAAGATT TCACAGTCAT CAAGTCATCT   180
GTTCCCAGAC ATCCCAACAA GACTTATCA AGTGTCTCCA TCTGCTGCTC TCATCTCTCT   240
CAGGTGCCAT TCCAGTGACA TTGCTATAGC CTCTTGCTGT ACCCCCCTCG AG          292

```

(2) INFORMATION FOR SEQ ID NO:1487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

```

GAATTCGGCC TTCATGGCCT AATGGATATA GAATTCAGG TTGATAAACA TTTTCTGTCA   60
CAACTTTACA ACTGAAGGCA TTGCCCTTTT GTCTTTTACC GTTCATTGA TAAAAAGTCT   120
GGTGGTAATC TAATTCTTAC ACCTTTGTAG GTGAGCATTT TTTCTTTCC TGTGACACAT   180
TTGTGATTAT CTGATCCTTA GAGATCTGAA GTTTTATCAT TTGTATCTAT GAGATCTTTT   240
CCCATCTCC TGGTGCTCGA G                                         261

```

(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

GAATTCGGCC	TTCATGGCCT	AATTTTCTGT	ATATTTTAC	ATGAATTCA	GTACTATATT	60
GAACAGCTAT	GTTTAAGGAT	AATCAAAAGA	TGACTGTGAC	AGGGAGAATT	TGAAAATATT	120
AGCCCAAGTC	TAGTCAATTG	TGATTGTTGT	TGCGTTGGTA	CTAGTTTAAA	TTGGGGCTAA	180
ATTTAGAGCC	ACTGGGACTG	AGTACCTCGG	TTGATCTCCA	ATGATTCCAA	TTGCTAAAAA	240
GTAAAGGGCA	ACCAACACATA	CGTACCAATT	CTGAAGTCCT	AGGAAATTTT	TAAAAGAATG	300
TAAGAGAATA	AGAAAATGTA	AAAGGGAGAA	GAGTTTATAT	GTCATGACGT	AAGTTTITAGA	360
GTTATTTACT	TTGTAACTGG	ACCTTCTCTG	CTTCTTCCAA	TGTGTTTCATT	AAGACCCTGC	420
TGAAAAATGA	CCTTCCAAC	CCCTGAGTA	ATTATTTAAG	ACCCTTTCAT	CTTACCAACC	480
CTCTCGAG						488

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

GAATTCGGCC	TTCATGGCCT	AGTCTCAAAA	AAAAAATCAA	AATAAAAGTA	AAAGTAAGAA	60
GATGGAAATT	TGCTTAGCTG	TGAAAGGAAA	GCGATCTGT	CTGATGTCCT	GTGTTTGGTG	120
CCTAGGTGGG	CTTGGTGCTT	GCATTTCCTG	CGTTGCAGTG	TCAGGATTTT	TCAGGGATCA	180
GCCTTGACAC	TGGAGACCTT	CACATTTTCC	ATCTGGTTAC	TATGGCACAC	AACTCGAG	238

(2) INFORMATION FOR SEQ ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 263 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

GAATTACTCT	GGAAGATATG	CTCTATGCTG	CTTCATCCAT	AAAGAGTAAT	TATTTGGTGT	60
TCATGGCGGA	ACTGTTCTGG	TGGTTTGAAG	TGGTGAAGCC	GTCTTTTGTA	CAGCCTCGTG	120
TTGTTGCTCC	ACAAGGAGCT	GAACCTGTAA	AAGATATGCC	TTCAATTCCT	GTCTTGAATG	180
CTGCCAAAAG	AAATGTCTTA	GATAGTAGTT	CTGACTTCCC	TTCAAGTGGG	GAAGGAGCTA	240
CATTTACACA	GTCTCATCTC	GAG				263

(2) INFORMATION FOR SEQ ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 257 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

GCGATTGAAT TCTAGACCTG CCTCGAGCTC ACACCTGGAT TATCTCAGTA GTTCCCAAC	60
TGGTTTCCTT GTTCCATTG TTGCCTCCTT CTGTCTACTC TCAATATAAC AGCTAGAACA	120
ATCCTTTTAC AATGGAATTC AGATCATGTT TACCCCTCTG TTCAAATTCT CCAGTGAATT	180
TCCAGTTTTT ACATGATCTG GCTCCTACTA CCTGTCTCAC TGTGTTTCCT ACTACTCTCC	240
TGCCCTTTCT CCTCGAG	257

(2) INFORMATION FOR SEQ ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

GAATTAAAGA GGGCGATATC ATCACACTCA CTAACCAAAT TGATGAGAAC TGGTATGAGG	60
GGATGCTGCA TGGCCATTCA GGCTTCTTCC CCATCAATTA TGTGGAAATT CTGGTTGCC	120
TGCCCCATTA GGATGTTATG CTGGCTGGCT CGCCTCCTCT TGACCCAGAT AGTTACGGTT	180
AACCACTGCT TTGGCAATGC TGCTTATAAC ACATCCCAAG TGCAGGCCGC AGTGGTCCAC	240
GTCATCCAGC CCCACCAAGT GACTTTGGTT GACTTGTGGG CTCCACAGG ACTCGAG	297

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

GAATTCGGCC TTCATGGCCT AAAAAGAAAG AAAAAGAAAA GAAAAAACCT TGGAGAAGTA	60
AGGGATTCTG TAAAAAATTT CCCCAATTTT ACTAGAGAGA TTGACATATA AATTTAGAAA	120
ATTCAGATAA CCTATGTAAG ATGCTATGTA AGACAACCAT TGCAGAGACA CAAAGTAATC	180
AGATTCTTGA AGGTCAATGC AAAAGAAAAA AATATTAAAG GCACTCGAG	229

(2) INFORMATION FOR SEQ ID NO:1494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

GAATTCGGCC TTCATCTGAC AATTAAAAAC ACTACCTTAG TTTGTTTTTC TGTAATTGAA	60
-------------------------------------------------------------------	----

TTTGACAGT TCTATTTTAC TTGAATTAGT CTTTTTATAT ATATATAGGC AGAAGTACTT	120
AAATAAATCT TCCCTTAAGT ATCAAAAGCA AAAGAATAAC ATTCATAGAA GTCTAACATG	180
TTCAAAGTGT TAAATATACT ACAATTGTTT ATTACATTA TAAATGCAGC TAAAATGACT	240
AACCTTTCAG ATCAACCCCT CGAG	264

(2) INFORMATION FOR SEQ ID NO:1495:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 190 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

GAATTCGGCC TTCATGGCCT ACCTTCCTTC CTTCTTCCT TCCTTTCCTT CTTTCTTCC	60
TTCTTCCTT TCCTTCCTT CTTCTTCCT CTCTCTTCT CTCTTCTGT CATGGTCTGG	120
CTCTGTTACC CAGGCTGGAG TGCAGGGGTG CAATCTCAGC TCGCTGCAAC TTCTTCCCCC	180
CCAACTCGAG	190

(2) INFORMATION FOR SEQ ID NO:1496:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

GGCCTTCATG GCCTACTAAG CTATTTGATT CTAAGTGAAT ATGTTATCTC TTATTAGAGG	60
ATATGTTAAT TTTCTGTCAT TTTATTCATT TATTAACCTA ACATCTCTGA TTGCCTACCA	120
TGTGTCAGGC TCTGTACTAA GGATTGAGGA CCCAAAGATG AACAAAACAT GGGGCCTAAT	180
TCAAAGATTT CACAACTGG AGAGAAAGTC AGCCACATAC AAAAGCCTCG AG	232

(2) INFORMATION FOR SEQ ID NO:1497:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

GTAGAATTGT ACAGTGCTTA TGAGTTATGC ATGTGTTCTT GGTCTTGTGTT CTAGGATTTT	60
TTTTTTTTTT TGATTGCTGC TCCAGTTGCC TTACTTACTT TGACATTGGA GTTGACCACA	120
TGATGTTGTT CCACACTTCC CTTAGGCTCG AG	152

(2) INFORMATION FOR SEQ ID NO:1498:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

GCGATTGAAT TCTAGACCTG CCTCGATCTC TTGTATTGAG TATTTTGTGG GGGAGGTA	60
TTGAAACTGT GTAAATATAC CATTTCTCAT TAACTTTTC AATTTATTCC CTTATTAGA	120
TGCGTATGAA CTCATGGCTT CTTGTTTAT TTGATGGATC CAAATCTGTT AATATCCTTA	180
CTGATTTGGA TGCTCAGACT GCCCAGATT TGGCCAGTGG AAGCCCTTTC AGGCTTGCTC	240
CCATGTCCTT CGAG	254

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 658 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

GAATTCGGCC TTTCATGGCC TAGAGAGCGC GGTGGGCTGC CATTAAACG CGGCCATCGG	60
TCCGGCCATC ATCCCTTCA CGGTACTAGA CTCGGGATG GTGAGATCCT TCTCATCCTT	120
TGGGGGCGA CCCCCTTCC GGGGACTTTG CTCTGGGCT CTTTTCAGAG GGGATTGGA	180
GCCTCTCTCT GAAGAGCCTG AAGACACCCT CTTCTTTCCT TCTCCCATGT TCTTCTTAC	240
CTTCCCTTCA GACAGGCTAA GTTTGCGCTT CTCATCACCT GAGTTTGGCC TACTTCTCTC	300
CTCACTGGAA TTACGTCGAT TCTGTATC AGAAGAATTG TGGGATGACG TCTGGTCTTT	360
CCCTTTGGCT CTCCTGTAGG CCATGAAGGC CCGCCTTCA TGGCCTACCA TTTCTTACAC	420
ACACTGCCAG AGATACTCTA GGCATGTAAG GCACAAACAT ACATATAAAA TCTGCGGGCT	480
TCAAAAAATA TAAGTAGGAT GTCATCTATA CTGTCATACA CTTTGTTTT TATCACTTAC	540
TTAATGTTAT ATCTTGGATA TTGTATTACC CTGGGTATTA AAAAGAACTC CTTTCACATT	600
TTAAATAAAC AATCTGAGCA CTTCATAAAT CCAATGCGT ATCTCCAGTC TGCTCGAG	658

(2) INFORMATION FOR SEQ ID NO:1500:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

GAATTCTAGA CCTGTCTCGA GAAACCAGAG GACTTTTCTG CTTTGTTTT TCTTTTAGGA	60
GGTAATAAAA CCGTGAATTT ATTTAAATGC TAATGTGTAG GATCTCACTC GAG	113

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145,

SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298,

SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451,

SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604,

SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739, SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748, SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757,

SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766, SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775, SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784, SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793, SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802, SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829, SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865, SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874, SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883, SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892, SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910,

SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919, SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928, SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937, SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964, SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982, SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID

[illegible]

NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID
NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID
NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID
NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID
NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID
NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID
NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID
NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID
NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID
NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID
NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID
NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID
NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID
NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID
NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID
NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID
NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID
NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID
NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID
NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID
NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID
NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID
NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID
NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID
NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID
NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID
NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID
NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID
NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID
NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID
NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID
NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID
NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID
NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID

[illegible]

NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;

or a complement of said sequence.

2. An isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID

NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID

NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID

NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID

NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604, SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID

NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739, SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748, SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766, SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775, SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784, SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793, SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802, SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829, SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865, SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID

NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874, SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883, SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892, SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910, SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919, SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928, SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937, SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964, SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982, SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID

NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID
NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID
NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID
NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID
NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID
NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID
NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID
NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID
NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID
NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID
NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID
NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID
NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID
NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID
NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID
NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID
NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID
NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID
NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID
NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID
NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID
NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID
NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID
NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID
NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID
NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID
NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID
NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID
NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID
NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID
NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID
NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID
NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID
NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID

[illegible]

NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID
NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID
NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID
NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID
NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID
NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID
NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID
NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID
NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID
NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID
NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID
NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID
NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID
NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID
NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID
NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID
NO:1357, SEQ ID NO:1358, SEQ ID NO:1359, SEQ ID NO:1360, SEQ ID
NO:1361, SEQ ID NO:1362, SEQ ID NO:1363, SEQ ID NO:1364, SEQ ID
NO:1365, SEQ ID NO:1366, SEQ ID NO:1367, SEQ ID NO:1368, SEQ ID
NO:1369, SEQ ID NO:1370, SEQ ID NO:1371, SEQ ID NO:1372, SEQ ID
NO:1373, SEQ ID NO:1374, SEQ ID NO:1375, SEQ ID NO:1376, SEQ ID
NO:1377, SEQ ID NO:1378, SEQ ID NO:1379, SEQ ID NO:1380, SEQ ID
NO:1381, SEQ ID NO:1382, SEQ ID NO:1383, SEQ ID NO:1384, SEQ ID
NO:1385, SEQ ID NO:1386, SEQ ID NO:1387, SEQ ID NO:1388, SEQ ID
NO:1389, SEQ ID NO:1390, SEQ ID NO:1391, SEQ ID NO:1392, SEQ ID
NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID
NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID
NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID
NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID
NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID
NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID
NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID
NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID
NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID

NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEQ ID NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEQ ID NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;

or a complement of said sequence.

3. An isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ

ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,

SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370,

SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523,

SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604, SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676,

SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739, SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748, SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766, SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775, SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784, SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793, SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802, SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829,

SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865, SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874, SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883, SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892, SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910, SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919, SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928, SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937, SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964, SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982,

SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID

NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID
NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID
NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID
NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID
NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID
NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID
NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID
NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID
NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID
NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID
NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID
NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID
NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID
NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID
NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID
NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID
NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID
NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID
NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID
NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID
NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID
NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID
NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID
NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID
NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID
NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID
NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID
NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID
NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID
NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID
NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID
NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID
NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID
NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID

[illegible]

NO:1393, SEQ ID NO:1394, SEQ ID NO:1395, SEQ ID NO:1396, SEQ ID NO:1397, SEQ ID NO:1398, SEQ ID NO:1399, SEQ ID NO:1400, SEQ ID NO:1401, SEQ ID NO:1402, SEQ ID NO:1403, SEQ ID NO:1404, SEQ ID NO:1405, SEQ ID NO:1406, SEQ ID NO:1407, SEQ ID NO:1408, SEQ ID NO:1409, SEQ ID NO:1410, SEQ ID NO:1411, SEQ ID NO:1412, SEQ ID NO:1413, SEQ ID NO:1414, SEQ ID NO:1415, SEQ ID NO:1416, SEQ ID NO:1417, SEQ ID NO:1418, SEQ ID NO:1419, SEQ ID NO:1420, SEQ ID NO:1421, SEQ ID NO:1422, SEQ ID NO:1423, SEQ ID NO:1424, SEQ ID NO:1425, SEQ ID NO:1426, SEQ ID NO:1427, SEQ ID NO:1428, SEQ ID NO:1429, SEQ ID NO:1430, SEQ ID NO:1431, SEQ ID NO:1432, SEQ ID NO:1433, SEQ ID NO:1434, SEQ ID NO:1435, SEQ ID NO:1436, SEQ ID NO:1437, SEQ ID NO:1438, SEQ ID NO:1439, SEQ ID NO:1440, SEQ ID NO:1441, SEQ ID NO:1442, SEQ ID NO:1443, SEQ ID NO:1444, SEQ ID NO:1445, SEQ ID NO:1446, SEQ ID NO:1447, SEQ ID NO:1448, SEQ ID NO:1449, SEQ ID NO:1450, SEQ ID NO:1451, SEQ ID NO:1452, SEQ ID NO:1453, SEQ ID NO:1454, SEQ ID NO:1455, SEQ ID NO:1456, SEQ ID NO:1457, SEQ ID NO:1458, SEQ ID NO:1459, SEQ ID NO:1460, SEQ ID NO:1461, SEQ ID NO:1462, SEQ ID NO:1463, SEQ ID NO:1464, SEQ ID NO:1465, SEQ ID NO:1466, SEQ ID NO:1467, SEQ ID NO:1468, SEQ ID NO:1469, SEQ ID NO:1470, SEQ ID NO:1471, SEQ ID NO:1472, SEQ ID NO:1473, SEQ ID NO:1474, SEQ ID NO:1475, SEQ ID NO:1476, SEQ ID NO:1477, SEQ ID NO:1478, SEQ ID NO:1479, SEQ ID NO:1480, SEQ ID NO:1481, SEQ ID NO:1482, SEQ ID NO:1483, SEQ ID NO:1484, SEQ ID NO:1485, SEQ ID NO:1486, SEQ ID NO:1487, SEQ ID NO:1488, SEQ ID NO:1489, SEQ ID NO:1490, SEQ ID NO:1491, SEQ ID NO:1492, SEQ ID NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;

or a complement of said sequence.

4. An isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ

ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID

NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID

NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341, SEQ ID NO:342, SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366, SEQ ID NO:367, SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401, SEQ ID NO:402, SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419, SEQ ID NO:420, SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID NO:427, SEQ ID NO:428, SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459, SEQ ID NO:460, SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468, SEQ ID NO:469, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID

NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488, SEQ ID NO:489, SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516, SEQ ID NO:517, SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535, SEQ ID NO:536, SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546, SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565, SEQ ID NO:566, SEQ ID NO:567, SEQ ID NO:568, SEQ ID NO:569, SEQ ID NO:570, SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599, SEQ ID NO:600, SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604, SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, SEQ ID NO:610, SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629, SEQ ID NO:630, SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID

NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669, SEQ ID NO:670, SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEQ ID NO:718, SEQ ID NO:719, SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739, SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744, SEQ ID NO:745, SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748, SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766, SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775, SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784, SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788, SEQ ID

NO:789, SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793, SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800, SEQ ID NO:801, SEQ ID NO:802, SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829, SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865, SEQ ID NO:866, SEQ ID NO:867, SEQ ID NO:868, SEQ ID NO:869, SEQ ID NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874, SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883, SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892, SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903, SEQ ID NO:904, SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910, SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919, SEQ ID NO:920, SEQ ID NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928, SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937, SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID

NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964, SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEQ ID NO:974, SEQ ID NO:975, SEQ ID NO:976, SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982, SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1017, SEQ ID NO:1018, SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1042, SEQ ID NO:1043, SEQ ID NO:1044, SEQ ID NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID NO:1077, SEQ ID NO:1078, SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID

NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID
NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID
NO:1093, SEQ ID NO:1094, SEQ ID NO:1095, SEQ ID NO:1096, SEQ ID
NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID
NO:1101, SEQ ID NO:1102, SEQ ID NO:1103, SEQ ID NO:1104, SEQ ID
NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID
NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID
NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID
NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID
NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID NO:1124, SEQ ID
NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID
NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID
NO:1133, SEQ ID NO:1134, SEQ ID NO:1135, SEQ ID NO:1136, SEQ ID
NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID
NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144, SEQ ID
NO:1145, SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID
NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID
NO:1153, SEQ ID NO:1154, SEQ ID NO:1155, SEQ ID NO:1156, SEQ ID
NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID
NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID
NO:1165, SEQ ID NO:1166, SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID
NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID
NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID
NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID
NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID
NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID
NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID
NO:1193, SEQ ID NO:1194, SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID
NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID
NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID
NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID
NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212, SEQ ID
NO:1213, SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID
NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID

NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID
NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID
NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID
NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID
NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID
NO:1241, SEQ ID NO:1242, SEQ ID NO:1243, SEQ ID NO:1244, SEQ ID
NO:1245, SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID
NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID
NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID
NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID
NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID
NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID
NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID
NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276, SEQ ID
NO:1277, SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID
NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID
NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID
NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID
NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID
NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID
NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID
NO:1305, SEQ ID NO:1306, SEQ ID NO:1307, SEQ ID NO:1308, SEQ ID
NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID
NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID
NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID
NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID
NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID
NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID
NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID
NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID
NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID
NO:1345, SEQ ID NO:1346, SEQ ID NO:1347, SEQ ID NO:1348, SEQ ID
NO:1349, SEQ ID NO:1350, SEQ ID NO:1351, SEQ ID NO:1352, SEQ ID
NO:1353, SEQ ID NO:1354, SEQ ID NO:1355, SEQ ID NO:1356, SEQ ID

[illegible]

NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;
or to a complement of said sequence.

5. An isolated protein encoded by an isolated polynucleotide of claim 1.
6. An isolated protein encoded by an isolated polynucleotide of claim 2.
7. An isolated protein encoded by an isolated polynucleotide of claim 3.
8. An isolated protein encoded by an isolated polynucleotide of claim 4.